

From: Holleran, Anne  
Sent: Friday, August 31, 2001 2:43 PM  
To: STIC-Biotech/ChemLib  
Subject: sequence search for 09/512,363

Please search the following sequences for 09/512,363:

1. commercial database and interference search for the following sequences:

SEQ ID NO: 2(aa)

2. commercial database and interference search of SEQ ID NO: 2(aa) against nucleotide databases
3. oligomer search, commercial and interference databases, for SEQ ID NO: 2(aa)
4. fragment search for SEQ ID NO: 2(aa):

/amino acids -25 - 137 (if aa -25 is numbered as "1", then 1-162)  
/amino acids 1-137 (" , then 26-162)  
amino acids 1-114 (" , then 26-139)  
amino acids -25-139 (" , then 1-164)  
amino acids 21-139 (" , then 46-164)  
amino acids 8-129 (" , then 33-154)  
amino acids 8-48 (" , then 33-73)  
amino acids 49-88 (" , then 74-113)  
amino acids 89-129 (" , then 114-154)

\* note for fragment search: the application lists the fragments using the numbering of the specification which includes negative numbers. I have listed the fragments using the fragment numbering as listed in the claims and also the fragment numbers that would correspond if the first aa is numbered "1" and not numbered "-25".

Thanks

Anne Holleran  
AU: 1642  
Tel: 308-8892  
Room: 8E03

**Point of Contact:**  
**Toby Port**  
**Technical Info. Specialist**  
**CM1 1E01 TEL: 308-3534**

RECEIVED  
SEP - 4 2001  
STIC

DT 28-JUL-1998 (first entry)  
 DE Amino acid sequence of the human 312C2 T cell protein.  
 XX  
 KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 KW antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; hematopoietic cells; lymphoid cell;  
 KW autoimmune disorders.  
 XX OS Homo sapiens.  
 XX PH Key Location/Qualifiers  
 FT CDS 1..726  
 FT /tag= a  
 FT /product= "human 312C2 protein"  
 XX  
 PN WO9806842-A1.  
 XX  
 PD 9-FEB-1998.  
 XX  
 PF 14-AUG-1997; 97WO-US13931.  
 XX  
 PR 07-OCT-1996; 96US-0027901.  
 PR 16-AUG-1996; 96US-0689943.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 PI Gorman DM, Randall TD, Zlotnik A;  
 XX WPI; 1998-159534/14.  
 DR N-PSDB; AAV19153.  
 XX  
 PT Isolated 312C2 T cell gene - used to develop products for treating,  
 PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 PT other T cell disorders  
 XX  
 PS Claim 2; Pages 59-60; 71pp; English.  
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 CC This is the amino acid sequence encoding the human 312C2 T cell  
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 CC treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX  
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 Query Match 100.0%; Score 246; DB 19; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-24;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY " 1 DCASGTFSGGHEGCKPWTCTQFGFLTFPPGNKTHNAVCV 41  
 DB 114 dcasgtfsgghegckpwtctqfgfltfppgnkthnavcv 154  
 RESULT 8  
 ID AAY06605 standard; Protein; 241 AA.  
 XX  
 AC AAY06605;  
 XX  
 DT 26-OCT-1999 (first entry)  
 XX  
 DE Human TNF receptor homologue PRO364.  
 PRO364; tumour necrosis factor receptor; human; apoptosis;

KW Inflammation; antiinflammatory; NF-KB activation;  
 KW autoimmune disease; therapy.  
 XX Homo sapiens.  
 OS  
 PH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT Protein /note= "signal peptide"  
 FT /note= "mature protein"  
 FT Modified-site 146  
 FT Domain /note= "N-glycosylated"  
 FT /note= "transmembrane domain"  
 XX  
 PN WO9940196-A1.  
 XX  
 PD 12-AUG-1999.  
 XX  
 PF 09-FEB-1999; 99WO-US02642.  
 XX  
 PR 09-FEB-1998; 98US-0024087.  
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 XX Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;  
 PI Pitti RM, Wood WI;  
 XX WPI; 1999-494296/41.  
 DR N-PSDB; AAX87670.  
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 PT autoimmune responses  
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 DB 114 dcasgtfsgghegckpwtctqfgfltfppgnkthnavcv 154  
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 Query Match 100.0%; Score 252; DB 19; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-20;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CVQPEFHCGDPCCTTCRHPCPPGQGVQSGKFSFGFCI 40  
 DB 74 cvqpefhcgdpctctcrhhpcppgqgvsgqgkfsfgfci 113  
 XX  
 RESULT 8  
 AAY06605  
 ID AAY06605 standard; Protein; 241 AA.  
 XX  
 AC AAY06605;  
 XX  
 XX 26-OCT-1999 (first entry)  
 DT Human TNF receptor homologue PRO364.  
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 XX PRO364; tumour necrosis factor receptor; human; apoptosis;  
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KW inflammation; antiinflammatory; NF-KB activation;  
 KW autoimmune disease; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT /note= "signal peptide"  
 FT Protein 26..241  
 FT /note= "mature protein"  
 FT Modified-site 146  
 FT /note= "N-glycosylated"  
 FT Domain 162..180  
 FT /note= "transmembrane domain"  
 XX  
 PN WO9940196-A1.  
 XX  
 XX 12-AUG-1999.  
 PD  
 XX  
 PF 09-FEB-1999; 99WO-US03642.  
 XX  
 PR 09-FEB-1998; 98US-0024087.  
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 XX (GETH ) GENENTECH INC.  
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 SQ Sequence 241 AA;  
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 Query Match 100.0%; Score 252; DB 20; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-20;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CVQPEFHCGDPCCTTCRHPCPPGQGVQSGKFSFGFCI 40  
 DB 74 cvqpefhcgdpctctcrhhpcppgqgvsgqgkfsfgfci 113  
 XX  
 RESULT 9  
 AAB27651  
 ID AAB27651 standard; Protein; 241 AA.

PN WO9806842-A1.  
 XX 19-FEB-1998.  
 XX 14-AUG-1997; 97WO-US13931.  
 XX 07-OCT-1996; 96US-0027901.  
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 XX WPI; 1998-159534/14.  
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 XX which affect immunological responses, e.g. autoimmune disorders.  
 XX Sequence 241 AA:  
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 Query Match 100.0%; Score 255; DB 19; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCGPRLLLGTGTDCRCRVHTTCCRDYPGEECCSEWDCM 41  
 DB 33 gcgpglllgtgtddarccrvhttrccrdypgeccsewdcm 73  
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 ID AAY06605  
 XX AAY06605 standard; Protein; 241 AA.  
 AC AAY06605;  
 XX 26-OCT-1999 (first entry)  
 DT Human TNF receptor homologue PRO364.  
 XX  
 DE PRO364; tumour necrosis factor receptor; human; apoptosis;  
 KW inflammation; antiinflammatory; NF-KB activation;  
 KW autoimmune disease; therapy.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
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 FT /note= "signal peptide"  
 FT Protein 26..241  
 FT /note= "mature protein"  
 FT Modified-site 146  
 FT /note= "N-glycosylated"  
 FT Domain 162..180  
 FT /note= "transmembrane domain"  
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 XX WO9940196-A1.

XX 12-AUG-1999.  
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 XX N-PSDB; AAX87670.  
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 SQ  
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 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCGPRLLLGTGTDCRCRVHTTCCRDYPGEECCSEWDCM 41  
 DB 33 gcgpglllgtgtddarccrvhttrccrdypgeccsewdcm 73  
 RESULT 8  
 AAB27651  
 ID AAB27651 standard; Protein; 241 AA.  
 XX AAB27651;  
 AC AAB27651;  
 XX 26-JAN-2001 (first entry)  
 DT Human protein PRO364.  
 XX  
 DE Cardiovascular; endothelial; angiogenic disorder; PRO179;  
 KW PRO238; PRO364; PRO844; PRO1760; PRO205; PRO321; PRO333;  
 KW PRO840; PRO877; PRO878; PRO882; PRO885; PRO887;  
 KW gene therapy.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH Peptide 1..25

Incyte clone 2809903; antiarteriosclerotic; hepatotropic; cytostatic;  
 anti-inflammatory; antipsoriatic; anti-HIV; antiasthmatic; anaemia;  
 dermatological; antidiabetic; nephrotropic; antichyroid; thyromimetic;  
 immunosuppressive; osteopathic; antiarthritic; uropathic; antitumor;  
 ophthalmological; diagnosis; treatment; prevention; immune disorder;  
 cell proliferative disorder; actinic keratosis; arteriosclerosis;  
 atherosclerosis; bursitis; hepatitis; Crohn's disease; amyloidosis.  
 Homo sapiens.

Key Location/Qualifiers  
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 Region 68..96  
 /label= Signature\_sequence  
 Region 109..147  
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 Region 122..129  
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 Region 157..175  
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 Region 165..186  
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 Modified-site 62  
 /note= "Potential phosphorylation site"  
 Modified-site 82  
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 Modified-site 205  
 /note= "Potential phosphorylation site"  
 Modified-site 223  
 /note= "Potential phosphorylation site"  
 Modified-site 140  
 /note= "N-glycosylated"

WO200005374-A2.

03-FEB-2000.

21-JUL-1999; 99WO-US16637.

22-JUL-1998; 98US-0093827.

INCYTE PHARM INC.

Lang YT, Lal P, Hillman JL, Corley NC, Patterson C, Baughn MR;

WPI; 2000-182699/16.

N-PSDB; AA249948.

Polypeptides and polynucleotides useful for treating and detecting cell  
 proliferation disorders e.g. actinic keratosis, and immune disorders  
 e.g. Crohn's disease

Claim 1; Pages 64-65; 67pp; English.

The present sequence is a molecule associated with cell  
 proliferation, MACP-5 from Incyte clone 2809903 isolated from TLYMN0706  
 CDNA library. This sequence is expressed in cardiovascular and  
 haematopoietic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV,  
 dermatologic, antiinflammatory, antipsoriatic, cytostatic, antiasthmatic,  
 hepatologic, antidiabetic, nephrotropic, antithyroid, thyromimetic,  
 immunosuppressive, osteopathic, antiarthritic, uropathic, antitumor,  
 and ophthalmological activities. The present sequence is useful in the  
 diagnosis, treatment and prevention of cell proliferative disorders e.g.  
 actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and  
 hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and  
 anaemia.

Sequence 235 AA;

Query Match 100.0%; Score 753; DB 21; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-55;  
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTARCCRVHTTRCCRDYPCBECCEWDCMCVQPFHCGDPCCTCRHH 60  
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 Db 27 GCGPGRLLLTGTARCCRVHTTRCCRDYPCBECCEWDCMCVQPFHCGDPCCTCRHH 86

QY 61 PCPPGQGVQSGKFSFGQCDACSGTSGGHEGHCKPWTCTOFGELTVFPGKTHNAV 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 87 PCPPGQGVQSGKFSFGQCDACSGTSGGHEGHCKPWTCTOFGELTVFPGKTHNAV 146

QY 121 CV 122  
 ||  
 Db 147 CV 148

RESULT 5

AAW37839

ID AAW37839 standard; Protein; 241 AA.

AC AAW37839;

XX 28-JUL-1998 (first entry)

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KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
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Key Location/Qualifiers

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QY 1 GCGPGRLLLTGTDCRCRVHTRCCRDYPCGECSEWDCMCVQPEPHCGDPCCTTCRHH 60  
DB 33 GCGPGRLLLTGTDCRCRVHTRCCRDYPCGECSEWDCMCVQPEPHCGDPCCTTCRHH 92  
QY 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTCTQFGFLTVPFGNKTNAV 120  
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QY 121 CV 122  
DB 153 CV 154

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AC AAY06605;

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XX PRO9940196-A1.  
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DB 33 GCGPGRLLLTGTDCRCRVHTRCCRDYPCGECSEWDCMCVQPEPHCGDPCCTTCRHH 92

QY 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTCTQFGFLTVPFGNKTNAV 120  
DB 93 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTCTQFGFLTVPFGNKTNAV 152

QY 121 CV 122  
DB 153 CV 154

RESULT 7  
AAB27651  
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XX AAB27651;

XX 26-JAN-2001 (first entry)  
XX Human protein PRO364.

XX Cardiovascular; endothelial; angiogenic disorder; PRO179;  
KW PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333;  
KW PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;  
XX gene therapy.

XX Homo sapiens.  
XX Key Location/Qualifiers  
FH Peptide 1..25  
FT Peptide /label= "signal peptide"  
XX WO200053757-A2.  
XX 14-SEP-2000.  
XX 24-FEB-2000; 2000WO-US05004.

XX 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 02-JUN-1999; 99WO-US12252.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 30-NOV-1999; 99WO-US28313.

FT Region /label= Signature\_sequence  
 FT 68..96  
 FT /label= Signature\_sequence  
 FT 109..147  
 FT /label= Signature\_sequence  
 FT 122..129  
 FT /label= Signature\_sequence  
 FT 157..175  
 FT /label= Signature\_sequence  
 FT 165..186  
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 FT 37  
 FT /note= "Potential phosphorylation site"  
 FT 48  
 FT /note= "Potential phosphorylation site"  
 FT 62  
 FT /note= "Potential phosphorylation site"  
 FT 82  
 FT /note= "Potential phosphorylation site"  
 FT 205  
 FT /note= "Potential phosphorylation site"  
 FT 223  
 FT /note= "Potential phosphorylation site"  
 FT 140  
 FT /note= "N-glycosylated"

XX WO200005374-A2.

PN 03-FEB-2000.

XX 21-JUL-1999; 99WO-US16637.

XX 22-JUL-1998; 98US-0093827.

XX (INCY-) INCYTE PHARM INC.

PI Tang YT, Lal P, Hillman JL, Corley NC, Patterson C, Baughn MR;

XX WPI: 2000-182699/16.

DR N-PSDB; AAZ49948.

XX Polypeptides and polynucleotides useful for treating and detecting cell  
 PT proliferation disorders e.g. actinic keratosis, and immune disorders  
 PT e.g. Crohn's disease

XX Claim 1; Pages 64-65; 67pp; English.

XX The present sequence is a molecule associated with cell  
 CC proliferation, MACP-5 from Incyte clone 2809903 isolated from TLYMN0706  
 CC cDNA library. This sequence is expressed in cardiovascular and  
 CC haematopoietic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV,  
 CC hepatotrophic, antiinflammatory, antipsoriatic, cytostatic, antiasthmatic,  
 CC dermatological, antidiabetic, nephrotropic, antithyroid, thyromimetic,  
 CC immunosuppressive, osteopathic, antiarthritic, uropathic, antitumor,  
 CC and ophthalmological activities. The present sequence is useful in the  
 CC diagnosis, treatment and prevention of cell proliferative disorders e.g.  
 CC actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and  
 CC hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and  
 CC anaemia.

XX Sequence 235 AA;

Query Match 100.0%; Score 737; DB 21; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-54;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DARCCRVHTRCCRDYPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGVQSQK 60  
 DB 40 darccrvhtrccrdypgeccsewdcmcvqpefhcgdpcccttcrrhhpcppggvqsqk 99

OY 61 FSFGFCIDCASGTFSGGHEGHCKPWTDCQTQFGFLTVPFGKTHNAVVCVPGSPPAEPLG 119  
 DB 106 fsfgfcidcasgtfsggheghckpwtcdtqfgfltvfpgnkthnavcvpgspapleplg 164

Db 100 fsfgfcidcasgtfsggheghckpwtcdtqfgfltvfpgnkthnavcvpgspapleplg 158  
 RESULT 5  
 AAW37839  
 ID AAW37839 standard; Protein; 241 AA.  
 XX AC AAW37839;  
 XX 28-JUL-1998 (first entry)  
 XX Amino acid sequence of the human 312C2 T cell protein.  
 KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 KW antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
 KW autoimmune disorders.  
 XX Homo sapiens.  
 OS Key Location/Qualifiers  
 FH CDS 1..726  
 FT /\*tag= a  
 FT /product= "human 312C2 protein"

PN WO9806842-A1.

XX 19-FEB-1998.

XX 14-AUG-1997; 97WO-US13931.

XX 07-OCT-1996; 96US-0027901.

XX 16-AUG-1996; 96US-0689943.

XX (SCHE ) SCHERING CORP.

XX Gorman DM, Randall TD, Zlotnik A;

XX WPI: 1998-159534/14.

DR N-PSDB; AAV19153.

XX Isolated 312C2 T cell gene - used to develop products for treating;  
 PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 PT other T cell disorders

XX Claim 2; Pages 59-60; 71pp; English.

XX This is the amino acid sequence encoding the human 312C2 T cell  
 CC protein. The 312C2 proteins are expressed in thymus cells and are  
 CC induced on T cells and spleen cells following activation. Engagement  
 CC of 312C2 stimulates proliferation of T cell clones, antigen-specific  
 CC proliferation and cytokine production by T-cells, and potentiates T  
 CC cell expansion or apoptosis. The products can be used in the  
 CC treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.

XX Sequence 241 AA;

Query Match 100.0%; Score 737; DB 19; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-54;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DARCCRVHTRCCRDYPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGVQSQK 60  
 DB 46 darccrvhtrccrdypgeccsewdcmcvqpefhcgdpcccttcrrhhpcppggvqsqk 105

OY 61 FSFGFCIDCASGTFSGGHEGHCKPWTDCQTQFGFLTVPFGKTHNAVVCVPGSPPAEPLG 119  
 DB 106 fsfgfcidcasgtfsggheghckpwtcdtqfgfltvfpgnkthnavcvpgspapleplg 164

N1 J, Ruben SM;  
WPI: 2000-061922/05.  
N-PSDB; AA237762.  
New tumour necrosis factor receptor-like polypeptides used to, e.g.  
treat Digeorge syndrome -  
Claim 14; Fig 1; 167pp; English.

This is the amino acid sequence of the human tumour necrosis factor receptor-like protein (TRL1 receptor). The invention relates to TRL1 and two splice variants TRL1S1 and TRL1S2. The nucleotide sequences were determined by sequencing cloned cDNAs AAZ37765-237766. The TRL1 receptor and its splice variants show homology to the murine glucocorticoid induced tumour necrosis factor receptor family-related gene (GTR).

TRL1, TRL1S1 and TRL1S2 polypeptides may be involved in the regulation of cell-type specific receptor-mediated cell growth, differentiation, and ultimately, cell death. They can be used for screening for agonists/antagonists. The polypeptides, agonists or antagonists can be used for treating a disease state associated with aberrant cell survival. They can be used for treating immune deficiency disorders, Digeorge syndrome, HIV infection, severe combined immunodeficiency (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood platelet disorders or wounds resulting from trauma or surgery. They can also be used to treat heart attacks, strokes, Addison's disease, haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome, systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis, hypersensitivity to an antigenic molecule, organ rejection or graft versus host disease, inflammatory conditions, ischaemia-reperfusion injury, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, hyperproliferative disorders, or infections. They can also be used to repair, replace, or protect tissue damaged by congenital defects, trauma, age, disease, surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, peripheral nerve injuries, neuropathies, and central nervous system disease (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome). The products can also be used for detection, diagnosis and prognosis.

Sequence 234 AA;

Query Match 100.0%; Score 979; DB 21; Length 234;  
Best Local Similarity 100.0%; Pred. No. 3.9e-70;  
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Db 1 maqhcmagfralcglalcalslgrrpgcgprlllgtgdarccrvhtttcrdd 60

Qy 61 YPGECCSEWDCMCVQPEFHCGDPDCTTCRRHPCPGQGVQSGKFSGFCIDCASGTF 120  
Db 61 ypgeccsewdcmcvqpefhcgdpdcttrhhpcpggvgqgkfsfgfcidcasgtf 120

Qy 121 SGGHEGHCkPWTDCQFGFLTVFPNGKNTNACVCPGSPPAEPLG 164  
Db 121 sggheghckpwtcdctqfgfltfpgnkthnavcvpgsppeaplg 164

RESULT 3  
AAW37839  
ID AAW37839 standard; Protein: 241 AA.  
XX  
AC AAW37839;  
XX  
XX 28-JUL-1998 (first entry)  
XX  
DE Amino acid sequence of the human 312C2 T cell protein.

FT Region /label= Signature\_sequence  
FT 68..96  
FT /label= Signature\_sequence  
FT 109..147  
FT /label= Signature\_sequence  
FT 122..129  
FT /label= Signature\_sequence  
FT 157..175  
FT /label= Signature\_sequence  
FT 165..186  
FT /label= Signature\_sequence  
FT 37  
FT /note= "Potential phosphorylation site"  
FT 48  
FT /note= "Potential phosphorylation site"  
FT 62  
FT /note= "Potential phosphorylation site"  
FT 82  
FT /note= "Potential phosphorylation site"  
FT 205  
FT /note= "Potential phosphorylation site"  
FT 223  
FT /note= "Potential phosphorylation site"  
FT 140  
FT /note= "N-glycosylated"

XX WO200005374-A2.

XX 03-FEB-2000.

XX 21-JUL-1999; 99WO-US16637.

XX 22-JUL-1998; 98US-0093827.

XX (INCY-) INCYTE PHARM INC.

XX Tang YT, Lal P, Hillman JL, Corley NC, Patterson C, Baughn MR;

XX WPI; 2000-182699/16.

DR N-PSDB; AAZ49948.

XX Polypeptides and polynucleotides useful for treating and detecting cell  
PT proliferation disorders e.g. actinic keratosis, and immune disorders  
PT e.g. Crohn's disease

XX Claim 1; Pages 64-65; 67pp; English.

XX The present sequence is a molecule associated with cell  
CC proliferation, MACP-5 from Incyte clone 2809903 isolated from TLYMNOT06  
CC cDNA library. This sequence is expressed in cardiovascular and  
CC haematopoietic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV,  
CC hepatotropic, antiinflammatory, antipsoriatic, cytostatic, antiasthmatic,  
CC dermatological, antidiabetic, nephrotropic, antithyroid, thyromimetic,  
CC immunosuppressive, osteopathic, antiarthritic, uropathic, antiulcer,  
CC and ophthalmological activities. The present sequence is useful in the  
CC diagnosis, treatment and prevention of cell proliferative disorders e.g.  
CC actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and  
CC hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and  
CC anemia.

XX Sequence 235 AA;

Query Match 100.0%; Score 711; DB 21; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2.9e-50;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRTGGPGCGRLILGTGTARCCRVHTTRCCRDYFGECCSEWDCMCVQPEFHCGDPC 60

.Db 20 qrptggpgcgrlllgtgtardccrvhttrccrdypgeccscwdcmcvqpefhcgdp 79

Qy 61 CTTCRHHPCPPGGVOSQKFSFGFCIDCASGTFSGGHEGHCCKPWTDCQFGF 114

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Db 80 ctctrrhhpcppggvgqgkfsfgfcidcasgtfsggheghckpwtcdctqfgf 133

RESULT 5

AAW37839

ID AAW37839 standard; Protein; 241 AA.

XX AC AAW37839;

XX DT 28-JUL-1998 (first entry)

XX DE Amino acid sequence of the human 312C2 T cell protein.

XX KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
KW antigen-specific T cell proliferation; cytokine production by T-cell;  
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
KW autoimmune disorders.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
FT CDS 1..726  
FT /tag= a  
FT /product= "human 312C2 protein"

XX PN WO9806842-A1.

XX PD 19-FEB-1998.

XX PF 14-AUG-1997; 97WO-US13931.

XX PR 07-OCT-1996; 96US-0027901.

XX PR 16-AUG-1996; 96US-0689943.

XX PA (SCHE ) SCHERING CORP.

XX PI Gorman DM, Randall TD, Zlotnik A;

XX WPI; 1998-159534/14.

DR N-PSDB; AAV19153.

XX PT Isolated 312C2 T cell gene - used to develop products for treating,  
PT e.g. cancers, auto-immune disorders, transplantation rejection and  
PT other T cell disorders

XX PS Claim 2; Pages 59-60; 71pp; English.

XX CC This is the amino acid sequence encoding the human 312C2 T cell  
CC protein. The 312C2 proteins are expressed in thymus cells and are  
CC induced on T cells and spleen cells following activation. Engagement  
CC of 312C2 stimulates proliferation of T cell clones, antigen-specific  
CC proliferation and cytokine production by T-cells, and potentiates T  
CC cell expansion or apoptosis. The products can be used in the  
CC treatment of conditions associated with abnormal physiology or  
CC development, including abnormal proliferation, e.g. cancerous  
CC conditions or degenerative conditions. They can be used in the  
CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
CC which affect immunological responses, e.g. autoimmune disorders.

XX Sequence 241 AA;

Query Match 100.0%; Score 711; DB 19; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2.9e-50;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRTGGPGCGRLILGTGTARCCRVHTTRCCRDYFGECCSEWDCMCVQPEFHCGDPC 60

.Db 26 qrptggpgcgrlllgtgtardccrvhttrccrdypgeccscwdcmcvqpefhcgdp 85

Qy 61 CTTCRHHPCPPGGVOSQKFSFGFCIDCASGTFSGGHEGHCCKPWTDCQFGF 114

|||||

4





N1 J, Ruben SM;  
 WPI: 2000-061922/05.  
 N-PSDB: AAZ37762.  
 New tumour necrosis factor receptor-like polypeptides used to, e.g.  
 treat Digeorge syndrome -  
 Claim 14: Fig 1: 167pp: English.  
 This is the amino acid sequence of the human tumour necrosis factor  
 receptor-like protein (TRLI receptor). The invention relates to TRLI and  
 two splice variants TRLIS1 and TRLIS2. The nucleotide sequences were  
 determined by sequencing cloned cDNAs AAZ37765-737766. The TRLI receptor  
 and its splice variants show homology to the murine glucocorticoid  
 induced tumour necrosis factor receptor family-related gene (GTRR).  
 TRLI, TRLIS1 and TRLIS2 polypeptides may be involved in the regulation  
 of cell-type specific receptor-mediated cell growth, differentiation,  
 and ultimately, cell death. They can be used for screening for  
 agonists/antagonists. The polypeptides, agonists or antagonists can be  
 used for treating a disease state associated with aberrant cell  
 survival. They can be used for treating immune deficiency disorders,  
 Digeorge syndrome, HIV infection, severe combined immunodeficiency  
 (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood  
 platelet disorders or wounds resulting from trauma or surgery. They can  
 also be used to treat heart attacks, strokes, Addison's disease, Grave's  
 haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, disease,  
 multiple sclerosis, myasthenia gravis, Stiff-Man syndrome,  
 systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent  
 diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,  
 hypersensitivity to an antigenic molecule, organ rejection or graft  
 versus host disease, inflammatory conditions, ischaemia-reperfusion  
 injury, complement-mediated hyperacute rejection, nephritis, cytokine or  
 chemokine induced lung injury, inflammatory bowel disease, Crohn's  
 disease, hyperproliferative disorders, or infections. They can also be  
 used to repair, replace, or protect tissue damaged by congenital  
 defects, trauma, age, disease, surgery, including cosmetic plastic  
 surgery, fibrosis, reperfusion injury, peripheral nerve injuries,  
 neuropathies, and central nervous system disease (e.g. Alzheimer's  
 disease, Parkinson's disease, Huntington's disease, amyotrophic lateral  
 sclerosis, and Shy-Drager syndrome). The products can also be used for  
 detection, diagnosis and prognosis.  
 Sequence 234 AA;  
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 Local Similarity 100.0%; Pred. No. 1.3e-69;  
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 Db 1 maohgamafralcgllalcalcslgqrpfggcggrllltgtgdarcrcrvhttrccrd 60  
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 Db 61 ypgeccsewdcmcpvefhcgdpctctcrhpcppgqvgsgkfsfgfcidcasgtf 120  
 QY 121 SGGHEGHCXKPTWDTCTGFLTVFPGNKTHNAVCPGSPPAEP 162  
 Db 121 sggheghckpwtctgfltvfpgnktthnavcpvgsppaep 162  
 RESULT 3  
 AAW37839  
 ID AAW37839 standard; Protein: 241 AA.  
 XX AAW37839;  
 XX  
 XX 28-JUL-1998 (first entry)  
 XX Amino acid sequence of the human 312C2 T cell protein.

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2001, 15:57:34 ; Search time 65.86 Seconds  
(without alignments)  
50.647 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_1\_162

Perfect score: 969

Sequence: 1 MAQHGAMGAFRALGGLALIC.....FPGKTHNAVCPGSPAP 162

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Scored: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	937	96.7	228	3	Sequence 4, Appl
3	937	96.7	311	3	Sequence 6, Appl
4	605	62.4	232	3	Sequence 8, Appl
5	506	52.2	228	3	Sequence 7, Appl
6	255	26.3	89	4	Sequence 2, Appl
7	166.5	17.2	206	1	Sequence 191, App
8	166.5	17.2	206	1	Sequence 7, Appl
9	166.5	17.2	438	1	Sequence 11, Appl
10	166.5	17.2	438	1	Sequence 11, Appl
11	162	16.7	277	2	Sequence 2, Appl
12	162	16.7	277	4	Sequence 2, Appl
13	160.5	16.6	255	1	Sequence 8, Appl
14	160.5	16.6	255	5	Sequence 9, Appl
15	160.5	16.6	255	5	Sequence 8, Appl
16	158.5	16.4	219	2	Sequence 2, Appl
17	153	15.8	191	3	Sequence 52, Appl
18	153	15.8	256	1	Sequence 6, Appl
19	153	15.8	256	5	Sequence 2, Appl
20	153	15.8	300	2	Sequence 2, Appl
21	151	15.6	205	3	Sequence 51, Appl
22	149	15.4	140	4	Sequence 17, Appl
23	141.5	14.6	401	3	Sequence 2, Appl
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27	138.5	14.3	451	3	Sequence 4, Appl

28 138.5 14.3 451 4 US-08-995-659-4 Sequence 4, Appl  
29 138.5 14.3 616 3 US-08-996-139-6 Sequence 6, Appl  
30 138.5 14.3 616 4 US-08-995-659-6 Sequence 6, Appl  
31 135.5 14.0 197 3 US-08-974-022-49 Sequence 49, Appl  
32 135.5 14.0 289 4 US-09-042-785A-11 Sequence 11, Appl  
33 133 13.7 401 3 US-08-974-022-6 Sequence 6, Appl  
34 133 13.7 401 4 US-09-042-785A-12 Sequence 12, Appl  
35 131 13.5 591 3 US-08-996-139-2 Sequence 2, Appl  
36 131 13.5 591 4 US-08-995-659-2 Sequence 2, Appl  
37 129.5 13.4 253 4 US-09-042-785A-4 Sequence 4, Appl  
38 129.5 13.4 605 4 US-09-042-785A-23 Sequence 23, Appl  
39 129.5 13.4 655 3 US-08-959-382-2 Sequence 2, Appl  
40 123 12.7 625 3 US-08-996-139-15 Sequence 15, Appl  
41 123 12.7 625 4 US-08-995-659-15 Sequence 15, Appl  
42 121 12.5 227 3 US-08-974-022-48 Sequence 48, Appl  
43 121 12.5 461 4 US-09-042-785A-7 Sequence 7, Appl  
44 119 12.3 461 1 US-08-385-229-2 Sequence 2, Appl  
45 119 12.3 461 6 5395760-2 Patent No. 5395760

## ALIGNMENTS

RESULT 1  
US-08-911-423-4  
; Sequence 4, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-4

Query Match 100.0%; Score 969; DB 3; Length 241;

Best Local Similarity 100.0%; Pred. No. 5.3e-77;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAFAFALCGALLCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
DB 1 MAQHGAFAFALCGALLCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
QY 61 YGEECCSEWDCMCVQPEFHGCDPCCTTCRHHPCPPGGVQSGKFSFGQICDASGTF 120  
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DB 121 SGGHEGCKPWTDTQGFGLTVFPGNKTHNAVCPGSPPAEP 162

RESULT 2  
US-08-911-423-6  
Sequence 6, Application US/08911423  
Patent No. 6111090  
GENERAL INFORMATION:  
APPLICANT: Gorman, Daniel M.  
APPLICANT: Randall, Troy D.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
TITLE OF INVENTION: REAGENTS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,419  
FILING DATE: 16-AUG-1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/027,901  
FILING DATE: 07-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 228 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-911-423-6

Query Match 96.7%; Score 937; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 3e-74;  
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGAFRALCGALLCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 66  
DB 1 MGAFRALCGALLCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 66

QY 67 CSEWDCMCVQPEFHGCDPCCTTCRHHPCPPGGVQSGKFSFGQICDASGTFSGGHEG 126  
DB 61 CSEWDCMCVQPEFHGCDPCCTTCRHHPCPPGGVQSGKFSFGQICDASGTFSGGHEG 120  
QY 127 HCKPWTDTQGFGLTVFPGNKTHNAVCPGSPPAEP 162  
DB 121 HCKPWTDTQGFGLTVFPGNKTHNAVCPGSPPAEP 156

RESULT 3  
US-08-911-423-8  
Sequence 8, Application US/08911423  
Patent No. 6111090  
GENERAL INFORMATION:  
APPLICANT: Gorman, Daniel M.  
APPLICANT: Randall, Troy D.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
TITLE OF INVENTION: REAGENTS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,419  
FILING DATE: 16-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/027,901  
FILING DATE: 07-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 311 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-911-423-8

Query Match 96.7%; Score 937; DB 3; Length 311;  
Best Local Similarity 100.0%; Pred. No. 4e-74;  
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGAFRALCGALLCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 66  
DB 1 MGAFRALCGALLCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 60  
QY 67 CSEWDCMCVQPEFHGCDPCCTTCRHHPCPPGGVQSGKFSFGQICDASGTFSGGHEG 126  
DB 61 CSEWDCMCVQPEFHGCDPCCTTCRHHPCPPGGVQSGKFSFGQICDASGTFSGGHEG 120  
QY 127 HCKPWTDTQGFGLTVFPGNKTHNAVCPGSPPAEP 162

Query Match 100.0%; Score 841; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 3.2e-66;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGGCGGGRLLLTGTGDARCCRVHTTRCCRDYFGECCSEWDCMCVQPEFHCGDPC 60  
DB 20 QRTGGGCGGGRLLLTGTGDARCCRVHTTRCCRDYFGECCSEWDCMCVQPEFHCGDPC 79

QY 61 CTTCRHHPCPPGGVQSGKFSFGQCIDCASGTFSGGHEGCHKPWTDTCTQFGFLTVPFG 120  
DB 80 CTTCRHHPCPPGGVQSGKFSFGQCIDCASGTFSGGHEGCHKPWTDTCTQFGFLTVPFG 139

QY 121 NKTHNAVCPGSPAP 137  
DB 140 NKTHNAVCPGSPAP 156

RESULT 2  
US-08-911-423-4  
Sequence 4, Application US/08911423  
Patent No. 611090  
GENERAL INFORMATION:  
APPLICANT: Gorman, Daniel M.  
APPLICANT: Randall, Troy D.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
TITLE OF INVENTION: REAGENTS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,419  
FILING DATE: 16-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/027,901  
FILING DATE: 07-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-911-423-4

Query Match 100.0%; Score 841; DB 3; Length 241;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGGCGGGRLLLTGTGDARCCRVHTTRCCRDYFGECCSEWDCMCVQPEFHCGDPC 60  
DB 26 QRTGGGCGGGRLLLTGTGDARCCRVHTTRCCRDYFGECCSEWDCMCVQPEFHCGDPC 85

QY 61 CTTCRHHPCPPGGVQSGKFSFGQCIDCASGTFSGGHEGCHKPWTDTCTQFGFLTVPFG 120  
DB 86 CTTCRHHPCPPGGVQSGKFSFGQCIDCASGTFSGGHEGCHKPWTDTCTQFGFLTVPFG 145

QY 121 NKTHNAVCPGSPAP 137  
DB 146 NKTHNAVCPGSPAP 162

RESULT 3  
US-08-911-423-8  
Sequence 8, Application US/08911423  
Patent No. 611090  
GENERAL INFORMATION:  
APPLICANT: Gorman, Daniel M.  
APPLICANT: Randall, Troy D.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
TITLE OF INVENTION: REAGENTS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,419  
FILING DATE: 16-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/027,901  
FILING DATE: 07-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 311 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-911-423-8

Query Match 100.0%; Score 841; DB 3; Length 311;  
Best Local Similarity 100.0%; Pred. No. 4.2e-66;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGGCGGGRLLLTGTGDARCCRVHTTRCCRDYFGECCSEWDCMCVQPEFHCGDPC 60  
DB 20 QRTGGGCGGGRLLLTGTGDARCCRVHTTRCCRDYFGECCSEWDCMCVQPEFHCGDPC 79

QY 61 CTTCRHHPCPPGGVQSGKFSFGQCIDCASGTFSGGHEGCHKPWTDTCTQFGFLTVPFG 120  
DB 80 CTTCRHHPCPPGGVQSGKFSFGQCIDCASGTFSGGHEGCHKPWTDTCTQFGFLTVPFG 139

QY 121 NKTHNAVCPGSPAP 137

Query Match 100.0%; Score 711; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 2.2e-54;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGPGCGPGRLLLTGTGDARCCRVHTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60  
DB 20 QRTGGPGCGPGRLLLTGTGDARCCRVHTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 79

QY 61 CTTCRHHPCPGQGVQSGKSFQFCIDCASGTFSGGHEGHCCKPWTCTQFGF 114  
DB 80 CTTCRHHPCPGQGVQSGKSFQFCIDCASGTFSGGHEGHCCKPWTCTQFGF 133

RESULT 2  
US-08-911-423-4  
; Sequence 4, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-4

Query Match 100.0%; Score 711; DB 3; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2.3e-54;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGPGCGPGRLLLTGTGDARCCRVHTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60  
DB 26 QRTGGPGCGPGRLLLTGTGDARCCRVHTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 85

QY 61 CTTCRHHPCPGQGVQSGKSFQFCIDCASGTFSGGHEGHCCKPWTCTQFGF 114  
DB 86 CTTCRHHPCPGQGVQSGKSFQFCIDCASGTFSGGHEGHCCKPWTCTQFGF 139

RESULT 3  
US-08-911-423-8  
; Sequence 8, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 311 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-8

Query Match 100.0%; Score 711; DB 3; Length 311;  
Best Local Similarity 100.0%; Pred. No. 2.8e-54;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGPGCGPGRLLLTGTGDARCCRVHTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60  
DB 20 QRTGGPGCGPGRLLLTGTGDARCCRVHTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 79

QY 61 CTTCRHHPCPGQGVQSGKSFQFCIDCASGTFSGGHEGHCCKPWTCTQFGF 114  
DB 80 CTTCRHHPCPGQGVQSGKSFQFCIDCASGTFSGGHEGHCCKPWTCTQFGF 133

RESULT 4  
US-08-911-423-7  
; Sequence 7, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2001, 15:57:36 ; Search time 65.86 Seconds  
(without alignments)  
51.273 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_1\_164

Perfect score: 979  
Sequence: 1 MAQHGAMGAPRALCGLALLC.....GNKTHNAVCPGSPAPPLG 164

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Submitted: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

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2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	947	96.7	228	3	US-08-911-423-6
3	947	96.7	311	3	US-08-911-423-8
4	605	61.8	232	3	US-08-911-423-7
5	510	52.1	228	3	US-08-911-423-2
6	255	26.0	89	4	US-09-188-930-191
7	165.5	17.0	206	1	US-08-097-827-7
8	165.5	17.0	206	1	US-08-494-574-7
9	165.5	17.0	438	1	US-08-097-827-11
10	165.5	17.0	438	1	US-08-494-574-11
11	162	16.5	277	2	US-08-147-784-2
12	162	16.5	277	2	US-08-195-967-2
13	160.5	16.4	255	1	US-08-236-918A-8
14	160.5	16.4	255	2	US-08-816-605-9
15	160.5	16.4	255	5	PCT-US96-03965-8
16	158.5	16.2	219	2	US-08-816-605-2
17	153	15.6	191	3	US-08-974-022-52
18	153	15.6	256	1	US-08-236-918A-6
19	153	15.6	256	5	PCT-US96-03965-2
20	153	15.6	300	2	US-08-794-796-2
21	151	15.4	205	3	US-08-974-022-51
22	149	15.2	140	4	US-08-477-347-17
23	141.5	14.5	401	3	US-08-974-022-2
24	139.5	14.2	139	2	US-08-219-237B-8
25	139.5	14.2	401	3	US-08-974-022-4
26	139.5	14.2	401	4	US-09-042-785A-13
27	138.5	14.1	451	3	US-08-996-139-4

28	138.5	14.1	451	4	US-08-995-659-4	Sequence 4, Appl
29	138.5	14.1	616	3	US-08-996-139-6	Sequence 6, Appl
30	138.5	14.1	616	4	US-08-995-659-6	Sequence 6, Appl
31	137	14.0	401	3	US-08-974-022-6	Sequence 6, Appl
32	137	14.0	401	3	US-09-042-785A-12	Sequence 12, Appl
33	135.5	13.8	197	3	US-08-974-022-49	Sequence 49, Appl
34	135.5	13.8	289	4	US-09-042-785A-11	Sequence 11, Appl
35	131	13.4	591	3	US-08-996-139-2	Sequence 2, Appl
36	131	13.4	591	4	US-08-995-659-2	Sequence 2, Appl
37	129.5	13.2	253	4	US-09-042-785A-4	Sequence 4, Appl
38	129.5	13.2	605	4	US-09-042-785A-23	Sequence 23, Appl
39	129.5	13.2	655	3	US-08-959-382-2	Sequence 2, Appl
40	123	12.6	625	3	US-08-996-139-15	Sequence 15, Appl
41	123	12.6	625	4	US-08-995-659-15	Sequence 15, Appl
42	121	12.4	197	2	US-08-505-606-1	Sequence 1, Appl
43	121	12.4	227	3	US-08-974-022-48	Sequence 48, Appl
44	121	12.4	461	4	US-09-042-785A-7	Sequence 7, Appl
45	119	12.2	461	6	5395760-2	Patent No. 5395760

## ALIGNMENTS

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RESULT 1
US-08-911-423-4
; Sequence 4, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-911-423-4

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Query Match 100.0% Score 979; DB 3; Length 241;

Best Local Similarity 100.0%; Pred. No. 5.7e-78;  
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAMGAFALCGLLALLCALSLGQRPTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
DB 1 MAQHGAMGAFALCGLLALLCALSLGQRPTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
QY 61 YPEECCSEWDCMCVQPEFFHCGDPCCTTCRHHPCPPGGVQSGKFSFGFCIDCASGTF 120  
DB 61 YPEECCSEWDCMCVQPEFFHCGDPCCTTCRHHPCPPGGVQSGKFSFGFCIDCASGTF 120  
QY 121 SGGHEGCKPWTCTQGFGLTVFPNGKTHNAVCPGSPPAEPLG 164  
DB 121 SGGHEGCKPWTCTQGFGLTVFPNGKTHNAVCPGSPPAEPLG 164

## RESULT 2

US-08-911-423-6  
Sequence 6, Application US/08911423  
Patent No. 6111090  
GENERAL INFORMATION:  
APPLICANT: Gorman, Daniel M.  
APPLICANT: Randall, Troy D.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
TITLE OF INVENTION: REAGENTS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,419  
FILING DATE: 16-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/027,901  
FILING DATE: 07-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 228 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

Query Match 96.7%; Score 947; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 3.2e-75;  
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGAFRALCGLLALLCALSLGQRPTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 66  
DB 1 MGAFRALCGLLALLCALSLGQRPTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 60

QY 67 CSEWDCMCVQPEFFHCGDPCCTTCRHHPCPPGGVQSGKFSFGFCIDCASGTFSGGHEG 126  
DB 61 CSEWDCMCVQPEFFHCGDPCCTTCRHHPCPPGGVQSGKFSFGFCIDCASGTFSGGHEG 120  
QY 127 HCKPWTCTQGFGLTVFPNGKTHNAVCPGSPPAEPLG 164  
DB 121 HCKPWTCTQGFGLTVFPNGKTHNAVCPGSPPAEPLG 158

## RESULT 3

US-08-911-423-8  
Sequence 8, Application US/08911423  
Patent No. 6111090  
GENERAL INFORMATION:  
APPLICANT: Gorman, Daniel M.  
APPLICANT: Randall, Troy D.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
TITLE OF INVENTION: REAGENTS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,419  
FILING DATE: 16-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/027,901  
FILING DATE: 07-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 311 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

Query Match 96.7%; Score 947; DB 3; Length 311;  
Best Local Similarity 100.0%; Pred. No. 4.3e-75;  
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGAFRALCGLLALLCALSLGQRPTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 66  
DB 1 MGAFRALCGLLALLCALSLGQRPTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 60  
QY 67 CSEWDCMCVQPEFFHCGDPCCTTCRHHPCPPGGVQSGKFSFGFCIDCASGTFSGGHEG 126  
DB 61 CSEWDCMCVQPEFFHCGDPCCTTCRHHPCPPGGVQSGKFSFGFCIDCASGTFSGGHEG 120  
QY 127 HCKPWTCTQGFGLTVFPNGKTHNAVCPGSPPAEPLG 164



Query Match 100.0%; Score 737; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 1.2e-58;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DARCCRVHTTRCCRDYPGEGCCSEWDCMCVQPEFHCGDPCCTTCRRHHPCPPGGQVQSQGK 60  
DB 40 DARCCRVHTTRCCRDYPGEGCCSEWDCMCVQPEFHCGDPCCTTCRRHHPCPPGGQVQSQGK 99  
QY 61 FSGFGQCIDCASGTFSGGHEGCHKPWTDCTQFGFLTVFPNGKTHNAVCPGSPPAEPLG 119  
DB 100 FSGFGQCIDCASGTFSGGHEGCHKPWTDCTQFGFLTVFPNGKTHNAVCPGSPPAEPLG 158

RESULT 2  
US-08-911-423-4  
; Sequence 4, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911.423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-4

Query Match 100.0%; Score 737; DB 3; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1.2e-58;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DARCCRVHTTRCCRDYPGEGCCSEWDCMCVQPEFHCGDPCCTTCRRHHPCPPGGQVQSQGK 60  
DB 46 DARCCRVHTTRCCRDYPGEGCCSEWDCMCVQPEFHCGDPCCTTCRRHHPCPPGGQVQSQGK 105  
QY 61 FSGFGQCIDCASGTFSGGHEGCHKPWTDCTQFGFLTVFPNGKTHNAVCPGSPPAEPLG 119  
DB 106 FSGFGQCIDCASGTFSGGHEGCHKPWTDCTQFGFLTVFPNGKTHNAVCPGSPPAEPLG 164

RESULT 3  
US-08-911-423-8  
; Sequence 8, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911.423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 311 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-8

Query Match 100.0%; Score 737; DB 3; Length 311;  
Best Local Similarity 100.0%; Pred. No. 1.5e-58;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DARCCRVHTTRCCRDYPGEGCCSEWDCMCVQPEFHCGDPCCTTCRRHHPCPPGGQVQSQGK 60  
DB 40 DARCCRVHTTRCCRDYPGEGCCSEWDCMCVQPEFHCGDPCCTTCRRHHPCPPGGQVQSQGK 99  
QY 61 FSGFGQCIDCASGTFSGGHEGCHKPWTDCTQFGFLTVFPNGKTHNAVCPGSPPAEPLG 119  
DB 100 FSGFGQCIDCASGTFSGGHEGCHKPWTDCTQFGFLTVFPNGKTHNAVCPGSPPAEPLG 158

RESULT 4  
US-08-911-423-2  
; Sequence 2, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert

```

Query Match      100.0%; Score 753; DB 3; Length 228;
Best Local Similarity 100.0%; Pred. No. 6e-60;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 GCGPGRLLLTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRRH 60
   |||||||
DB 27 GCGPGRLLLTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRRH 86
   |||||||

QY 61 PCPPGGVQSQGKFSGFGOCIDCASGTFSGGHEGCHKPWTDTQGFGLTVFPGNKTHNAV 120
   |||||||
DB 87 PCPPGGVQSQGKFSGFGOCIDCASGTFSGGHEGCHKPWTDTQGFGLTVFPGNKTHNAV 146
   |||||||

QY 121 CV 122
   ||
DB 147 CV 148

RESULT 2
US-08-911-423-4
: Sequence 4, Application US/08911423
: Patent No. 6111090
: GENERAL INFORMATION:
: APPLICANT: Gorman, Daniel M.
: APPLICANT: Randall, Troy D.
: APPLICANT: Zlotnik, Albert
: TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
: TITLE OF INVENTION: REAGENTS
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DNAX Research Institute
: STREET: 901 California Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/911,423
: FILING DATE: 14-AUG-1997
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/023,419
: FILING DATE: 16-AUG-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/027,901
: FILING DATE: 07-OCT-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Ching, Edwin P.
: REGISTRATION NUMBER: 34,050
: REFERENCE/DOCKET NUMBER: DX0612K
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-852-9196
: TELEFAX: 650-496-1200
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 241 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-911-423-4

Query Match      100.0%; Score 753; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 6.3e-60;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRRH 60
   |||||||
DB 33 GCGPGRLLLTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRRH 92
   |||||||

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Query Match      100.0%; Score 255; DB 3; Length 228;
Best Local Similarity 100.0%; Pred. No. 3.6e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGPGRLLLTGTGTDARCCRVHTTCCRDYPGECCSEWDCM 41
   |||||
Db 27 GCGPGRLLLTGTGTDARCCRVHTTCCRDYPGECCSEWDCM 67

RESULT 2
US-08-911-423-7
; Sequence 7, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-911-423-7

Query Match      100.0%; Score 255; DB 3; Length 232;
Best Local Similarity 100.0%; Pred. No. 3.6e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGPGRLLLTGTGTDARCCRVHTTCCRDYPGECCSEWDCM 41
   |||||
Db 27 GCGPGRLLLTGTGTDARCCRVHTTCCRDYPGECCSEWDCM 67

RESULT 3
US-08-911-423-4
; Sequence 4, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```
APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0612K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-911-423-4

Query Match      100.0%; Score 255; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 3.8e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGPGRLLLTGTGTDARCCRVHTTCCRDYPGECCSEWDCM 41
   |||||
Db 33 GCGPGRLLLTGTGTDARCCRVHTTCCRDYPGECCSEWDCM 73

RESULT 4
US-08-911-423-8
; Sequence 8, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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Query Match 100.0%; Score 252; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 2.4e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVOPEFHCGDPCCTTCRHHPCPPGQVQSOGKFSFGQCI 40  
Db 68 CVOPEFHCGDPCCTTCRHHPCPPGQVQSOGKFSFGQCI 107

## RESULT 2

US-08-911-423-4  
Sequence 4, Application US/08911423  
Patent No. 6111090  
GENERAL INFORMATION:  
APPLICANT: Gorman, Daniel M.  
APPLICANT: Randall, Troy D.  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,419  
FILING DATE: 16-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/027,901  
FILING DATE: 07-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-911-423-4

Query Match 100.0%; Score 252; DB 3; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2.5e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVOPEFHCGDPCCTTCRHHPCPPGQVQSOGKFSFGQCI 40  
Db 74 CVOPEFHCGDPCCTTCRHHPCPPGQVQSOGKFSFGQCI 113

## RESULT 3

US-08-911-423-8  
Sequence 8, Application US/08911423  
Patent No. 6111090  
GENERAL INFORMATION:  
APPLICANT: Gorman, Daniel M.

APPLICANT: Randall, Troy D.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
TITLE OF INVENTION: REAGENTS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,419  
FILING DATE: 16-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/027,901  
FILING DATE: 07-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 311 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-911-423-8

Query Match 100.0%; Score 252; DB 3; Length 311;  
Best Local Similarity 100.0%; Pred. No. 3.1e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVOPEFHCGDPCCTTCRHHPCPPGQVQSOGKFSFGQCI 40  
Db 68 CVOPEFHCGDPCCTTCRHHPCPPGQVQSOGKFSFGQCI 107

## RESULT 4

US-08-911-423-7  
Sequence 7, Application US/08911423  
Patent No. 6111090  
GENERAL INFORMATION:  
APPLICANT: Gorman, Daniel M.  
APPLICANT: Randall, Troy D.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
TITLE OF INVENTION: REAGENTS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

Query Match 100.0%; Score 246; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 1.2e-23;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCASGTFSGGHEGCKPWTCTQFGFLTVFPGNKTNAVCV 41  
|||||  
DB 108 DCASGTFSGGHEGCKPWTCTQFGFLTVFPGNKTNAVCV 148

## RESULT 2

US-08-911-423-4  
; Sequence 4, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911.423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023.419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027.901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-4

Query Match 100.0%; Score 246; DB 3; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1.3e-23;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCASGTFSGGHEGCKPWTCTQFGFLTVFPGNKTNAVCV 41  
|||||  
DB 114 DCASGTFSGGHEGCKPWTCTQFGFLTVFPGNKTNAVCV 154

## RESULT 3

US-08-911-423-8  
; Sequence 8, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.

APPLICANT: Randall, Troy D.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911.423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023.419  
FILING DATE: 16-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/027.901  
FILING DATE: 07-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 311 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-911-423-8

Query Match 100.0%; Score 246; DB 3; Length 311;  
Best Local Similarity 100.0%; Pred. No. 1.7e-23;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCASGTFSGGHEGCKPWTCTQFGFLTVFPGNKTNAVCV 41  
|||||  
DB 108 DCASGTFSGGHEGCKPWTCTQFGFLTVFPGNKTNAVCV 148

## RESULT 4

US-08-911-423-2  
; Sequence 2, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

ID Q9Y5U5 PRELIMINARY; PRT; 241 AA.  
 AC Q9Y5U5;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.  
 GN TNFRSF18.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BONE MARROW;  
 RA Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,  
 RA Gurney A.L., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,  
 RA Baldwin D.T., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.,  
 RA Goddard A.D.,  
 RT "Identification of a new member of the tumor necrosis factor family  
 and its receptor, a human ortholog of mouse GITR.";  
 RL Curr. Biol. 0:0-0(1999).  
 DR EMBL; AF125304; AAD22635.1; -.  
 DR InterPro; IPR001368; -.  
 DR SMART; SM00208; TNFR; 1.  
 SQ SEQUENCE 241 AA; 26000 MW; 90DC3BA4AA7E82CBE CRC64;

Query Match 100.0%; Score 711; DB 4; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-70;  
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QRTGGPGCGPGLLLGTGTDAACRCRVHTTRCCRDYDPEGCCSWDCMCVQPEFHCGDPC 60  
 DB 26 QRTGGPGCGPGLLLGTGTDAACRCRVHTTRCCRDYDPEGCCSWDCMCVQPEFHCGDPC 85  
 QY 61 CTTCTRHHPCCPPGGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTDCQTQGF 114  
 DB 86 CTTCTRHHPCCPPGGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTDCQTQGF 139

RESULT 3  
 Q9NYJ9  
 ID Q9NYJ9 PRELIMINARY; PRT; 255 AA.  
 AC Q9NYJ9;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE GITR-D.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=THYMUS;  
 RA Nocentini G., Bartoli A., Ronchetti S., Mastroiaca E., Riccardi C.,  
 RT "Identification of a soluble human GITR splicing (hgITR-D).";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF241229; AAF63506.1; -.  
 SQ SEQUENCE 255 AA; 26827 MW; C986652AC97AF2CC CRC64;

Query Match 96.1%; Score 683; DB 4; Length 255;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-67;  
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QRTGGPGCGPGLLLGTGTDAACRCRVHTTRCCRDYDPEGCCSWDCMCVQPEFHCGDPC 60  
 DB 26 QRTGGPGCGPGLLLGTGTDAACRCRVHTTRCCRDYDPEGCCSWDCMCVQPEFHCGDPC 85  
 QY 61 CTTCTRHHPCCPPGGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTDC 109  
 DB 86 CTTCTRHHPCCPPGGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTDC 134

RESULT 4  
 Q9JKR2  
 ID Q9JKR2 PRELIMINARY; PRT; 222 AA.  
 AC Q9JKR2;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE GITR-C.  
 GN TNFRSF18.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=THYMUS;  
 RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,  
 RA Migliorati G., Riccardi C.;  
 RT "Identification of three novel mRNA splice variants of GITR.";  
 RL Cell Death Differ. 0:0-0(2000).  
 DR EMBL; AF229433; AAF61567.1; -.  
 DR InterPro; IPR000561; -.  
 DR SMART; SM00181; EGF; 1.  
 SQ SEQUENCE 222 AA; 24450 MW; 594932BA425A79CA CRC64;

Query Match 52.5%; Score 373.5; DB 11; Length 222;  
 Best Local Similarity 53.7%; Pred. No. 1.8e-33;  
 Matches 58; Conservative 19; Mismatches 24; Indels 7; Gaps 1;  
 QY 7 PGCGPGRLLLTGTDAACRCRVHTTRCCRDYDPEGCCSWDCMCVQPEFHCGDPCCTTGRH 66  
 DB 27 PGCGPGRLLLTGTDAACRCRVHTTRCCRDYDPEGCCSWDCMCVQPEFHCGDPCCTTGRH 79  
 QY 67 HPCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTDCQTQGF 114  
 DB 80 YPCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTDCQTQGF 127

RESULT 5  
 O35714  
 ID O35714 PRELIMINARY; PRT; 228 AA.  
 AC O35714;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE GLUCOCORTICOID-INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.  
 GN TNFRSF18 OR GITR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C3H/HEJ;  
 RX MEDLINE=97322352; PubMed=9177197;  
 RA Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,  
 RA Moraca R., Migliorati G., Riccardi C.;  
 RT "A new member of the tumor necrosis factor/nerve growth factor  
 receptor family inhibits T cell receptor-induced apoptosis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C;  
 RA Nocentini G., Bartoli A., Ronchetti S., Giunchi L., CuPELLI A.,  
 RA Migliorati G., Riccardi C.;  
 RT "Gene structure and chromosomal assignment of GITR, a mouse member of  
 the tumor necrosis factor/nerve growth factor receptor family.";  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U82534; AAB81243.1; -.  
 DR EMBL; AF109216; AAF14231.1; -.  
 DR MGI; 894675; Tnfrsf18.

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:14:30 ; Search time 133.1 Seconds  
(without alignments)  
113.319 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_26\_139

Perfect score: 711  
Sequence: 1 QRTGPGGCGPGRLLGTGT.....FSGGHEGCKPWTDCQFGF 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL16:\*
- 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phase:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_unclassified:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	711	100.0	234	4 Q95851	Q95851 homo sapien
2	711	100.0	241	4 Q9Y5U5	Q9Y5U5 homo sapien
3	683	96.1	255	4 Q9NYJ9	Q9NYJ9 homo sapien
4	373.5	52.5	222	11 Q9JKR2	Q9JKR2 mus musculu
5	373.5	52.5	228	11 Q35714	Q35714 mus musculu
6	373.5	52.5	294	11 Q9JKR3	Q9JKR3 mus musculu
7	339.5	47.7	132	11 Q9JKR1	Q9JKR1 mus musculu
8	130.5	18.4	267	6 O02764	O02764 oryctolagus
9	122	17.2	107	11 Q9JKE0	Q9JKE0 rattus norv
10	119	16.7	276	13 Q9DD02	Q9DD02 gallus gall
11	117	16.5	300	4 Q95407	Q95407 homo sapien
12	112	15.8	152	5 Q9XVX3	Q9XVX3 caenorhabdi
13	108.5	15.3	2906	11 Q9WUH9	Q9WUH9 rattus norv
14	108	15.2	616	4 Q9Y6Q6	Q9Y6Q6 homo sapien
15	107	15.0	164	5 Q22048	Q22048 caenorhabdi
16	106	14.9	625	11 Q35305	Q35305 mus musculu
17	105	14.8	1574	11 Q88281	Q88281 rattus norv
18	104.5	14.7	655	4 Q75509	Q75509 homo sapien
19	104	14.6	1522	5 Q22685	Q22685 caenorhabdi

20	104	14.6	4601	5 Q9V383	Q9V383 drosophila
21	103.5	14.6	126	10 Q9S9F4	Q9S9F4 phytolacca
22	103.5	14.6	655	11 Q9EP05	Q9EP05 mus musculu
23	102.5	14.4	188	5 Q18238	Q18238 caenorhabdi
24	102.5	14.4	283	6 Q9XSZ8	Q9XSZ8 cercopithec
25	102.5	14.4	1308	5 Q9GPM8	Q9GPM8 caenorhabdi
26	102	14.3	401	11 Q08727	Q08727 rattus norv
27	102	14.3	870	6 Q02660	Q02660 bos taurus
28	101	14.2	401	11 Q08712	Q08712 mus musculu
29	99.5	14.0	1764	11 Q35806	Q35806 rattus norv
30	99	13.9	372	4 Q9UHP4	Q9UHP4 homo sapien
31	99	13.9	401	4 Q00300	Q00300 homo sapien
32	97	13.6	1587	4 Q00508	Q00508 homo sapien
33	96.5	13.6	410	11 Q63720	Q63720 rattus norv
34	96.5	13.6	469	11 Q63721	Q63721 rattus norv
35	96.5	13.6	1821	4 Q14767	Q14767 homo sapien
36	96	13.5	1511	4 Q75412	Q75412 homo sapien
37	96	13.5	1963	6 Q28019	Q28019 bos taurus
38	95.5	13.4	1698	5 Q94438	Q94438 chironomus
39	95.5	13.4	1792	13 Q57484	Q57484 gallus gall
40	95	13.4	1537	5 Q9VAI2	Q9VAI2 drosophila
41	94.5	13.3	830	4 Q43701	Q43701 homo sapien
42	94.5	13.3	830	4 Q14162	Q14162 homo sapien
43	94.5	13.3	1833	11 Q08999	Q08999 mus musculu
44	94	13.2	1203	11 Q06008	Q06008 mus musculu
45	94	13.2	1637	6 Q9XSU8	Q9XSU8 bos taurus

ALIGNMENTS

RESULT 1	
Q95851	
ID Q95851	PRELIMINARY; PRT; 234 AA.
AC Q95851;	
DT 01-MAY-1999 (Tremblrel. 10, Created)	
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)	
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)	
DE TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.	
OS Homo sapiens (human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=99156876; PubMed=10037686;	
RA Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L.,	
RA Liu D., Wang S.X., Kwon B.S.;	
RT "Identification of a novel activation-inducible protein of the tumor	
RT necrosis factor receptor superfamily and its ligand.";	
RL J. Biol. Chem. 274:6056-6061(1999).	
DR EMBL; AF117297; AAD19694.1; -	
DR InterPro; IPR001368; -	
DR SMART; SM00208; TNFR; 1.	
KW Receptor.	
SQ SEQUENCE 234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;	
Query Match 100.0%; Score 711; DB 4; Length 234;	
Best Local Similarity 100.0%; Pred. No. 2e-70;	
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 QRTGPGGCGPGRLLGTGTDCRCRVHTTRCCRDYFGEECCSEWDCMCVQPFHCGDPC 60	
Db 26 QRTGPGGCGPGRLLGTGTDCRCRVHTTRCCRDYFGEECCSEWDCMCVQPFHCGDPC 85	
QY 61 CTTCTRHHPCCPGGVQSGKFSFGFCIDCASCTFSGGHEGCKPWTDCQFGF 114	
Db 86 CTTCTRHHPCCPGGVQSGKFSFGFCIDCASCTFSGGHEGCKPWTDCQFGF 139	
RESULT 2	
Q9Y5U5	

[illegible]



```
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
KW SIGNAL; Receptor.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 228 GLUCOCORTICOID INDUCED TNFR FAMILY
FT RELATED PROTEIN.
SQ SEQUENCE 228 AA; 25334 MW; 50D8C275D9C56259. CRC64;

Query Match 52.5%; Score 373.5; DB 11; Length 228;
Best Local Similarity 53.7%; Pred. No. 1.8e-33;
Matches 58; Conservative 19; Mismatches 24; Indels 7; Gaps 1;

QY 7 PGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTTCRH 66
Db 27 PGCGPGKVGQSGNNTCCSLYA-----PGKEDCPKERCICVTPYHCGDPQCKICKH 79

QY 67 HPCPPGGVQSGQKFSFGFCIDCASGTFSGGHEGCHKPWTCTQFGF 114
Db 80 YPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCLWNTCSQGF 127

RESULT 6
Q9JKR3 PRELIMINARY; PRT; 294 AA.
AC Q9JKR3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GTR-B.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229432; AAF61566.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 294 AA; 32658 MW; FE0D4AE6A007BA9A. CRC64;

Query Match 52.5%; Score 373.5; DB 11; Length 294;
Best Local Similarity 53.7%; Pred. No. 2.2e-33;
Matches 58; Conservative 19; Mismatches 24; Indels 7; Gaps 1;

QY 7 PGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTTCRH 66
Db 27 PGCGPGKVGQSGNNTCCSLYA-----PGKEDCPKERCICVTPYHCGDPQCKICKH 79

QY 67 HPCPPGGVQSGQKFSFGFCIDCASGTFSGGHEGCHKPWTCTQFGF 114
Db 80 YPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCLWNTCSQGF 127

RESULT 7
Q9JKR1 PRELIMINARY; PRT; 132 AA.
AC Q9JKR1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GTR-D.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229434; AAF61568.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 132 AA; 14106 MW; F586A5404BIDFEDE. CRC64;

Query Match 47.7%; Score 339.5; DB 11; Length 132;
Best Local Similarity 52.5%; Pred. No. 6e-30;
Matches 53; Conservative 17; Mismatches 24; Indels 7; Gaps 1;

QY 7 PGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTTCRH 66
Db 27 PGCGPGKVGQSGNNTCCSLYA-----PGKEDCPKERCICVTPYHCGDPQCKICKH 79

QY 67 HPCPPGGVQSGQKFSFGFCIDCASGTFSGGHEGCHKPWT 107
Db 80 YPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCLWNT 120

RESULT 8
O02764 PRELIMINARY; PRT; 267 AA.
AC O02764;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OX40 PRECURSOR (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHBB;HM;
RA Isono T., Seto A.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003911; BAA20059.1; -.
DR HSSP; PI9438; IEXT.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_c6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR SMART; SM00208; TNFR; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 18 POTENTIAL.
FT CHAIN 19 267 OX40.
SQ SEQUENCE 267 AA; 28489 MW; A8B4CD3173C9500B. CRC64;

Query Match 18.4%; Score 130.5; DB 6; Length 267;
Best Local Similarity 32.8%; Pred. No. 8.3e-07;
Matches 38; Conservative 7; Mismatches 50; Indels 21; Gaps 6;

QY 9 CGPGRLLLTGTGDARCCRVHTTRCCRDYFG--EECCSEWDCM-CVQ-----PEFHCG 57
Db 40 CQP-----GYGMVSRGNRSQDTTICHPCEPGFYNEAVNYQACKPCTCQNRSGSEPOQECT 94

QY 58 DPCCTTCRHHPCCPGGQSGQKFSFGFCIDCASGTFSGGHEGCHKPWTCTQFG 113
Db 95 HTRDVTVC---CRP--GTQPLNGYKHGVDCAPCPQGHFSEGNRRACKRPWTNCTLAG 145

RESULT 9
Q9JKEO
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OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98032977; PubMed=9367155;  
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,  
RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,  
RA Galibert L.;  
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth  
and dendritic-cell function.";  
RL Nature 390:175-179(1997).  
CC - FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.  
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).  
CC - TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN  
CC SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL  
CC GLAND.  
CC - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
DR EMBL: AF018253; AB88609.1; -;  
DR HSSP: P25942; ICDF.  
DR MIM: 603499; -;  
DR InterPro: IPR001368; -;  
DR Pfam: PF00020; TNFR\_C6; 4.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
DR PROSITE: PS50050; TNFR\_NGFR\_2; 1.  
DR SMART: SM00208; TNFR; 1.  
KW Receptor; Glycoprotein; Transmembrane; Signal; Repeat.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 616 RECEPTOR ACTIVATOR OF NF-KAPPA-B.  
FT DOMAIN 24 212 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 213 233 POTENTIAL.  
FT DOMAIN 234 616 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 33 195 4 X TNFR-CYS.  
FT REPEAT 33 69 TNFR-CYS 1.  
FT REPEAT 70 112 TNFR-CYS 2.  
FT REPEAT 113 152 TNFR-CYS 3.  
FT REPEAT 133 195 TNFR-CYS 4.  
FT DISULFID 34 46 BY SIMILARITY.  
FT DISULFID 47 60 BY SIMILARITY.  
FT DISULFID 50 68 BY SIMILARITY.  
FT DISULFID 71 86 BY SIMILARITY.  
FT DISULFID 92 112 BY SIMILARITY.  
FT DISULFID 114 124 BY SIMILARITY.  
FT DISULFID 126 133 BY SIMILARITY.  
FT DISULFID 127 151 BY SIMILARITY.  
FT DISULFID 154 169 BY SIMILARITY.  
FT DISULFID 175 194 BY SIMILARITY.  
FT CARBOHYD 105 105 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 174 174 N-LINKED (GLCNAC...) (POTENTIAL).  
SQ SEQUENCE 616 AA; 66033 MW; E3DE9A7A08196F81 CRC64;

Query Match 15.2%; Score 108; DB 4; Length 616;  
Best Local Similarity 22.5%; Pred. No. 0.00049;  
Matches 32; Conservative 10; Mismatches 40; Indels 60; Gaps 6;  
QY 28 HTTRCCR-----DYPGECCSEWDCMCVQPEFHC-----DPC----- 60  
| | | | | : : : : : |  
DB 42 HLGRCCKCEPGKYMSSKCTTSDVCLP-----CGPDEYLDNNEEDKCLLHKVCDTGKA 97  
| | | | | : : : : : |  
QY 61 -----CTTCRRHH-PCPPGQGVQSGKFSFGFCIDCAGS 93  
| | | | | : : : : : |  
DB 98 LVAVAGNSTTPRRCACTAGYHWSQDCECCRRNTECAPGLGAQHPLOLNKNDTVCKPCLAG 157  
QY 94 TFGSGHEG--HCKPWTDCQFG 113  
| | | | | : : : : : |  
DB 158 YFSDAFSSDCKCRPWNTCTFLG 179  
| | | | | : : : : : |

RESULT 15  
Q22048 PRELIMINARY; PRT; 164 AA.  
AC Q22048;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)  
DE T01B7.8 PROTEIN.  
GN T01B7.8.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sims M.;  
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94150718; PubMed=7906398;  
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
RA Lightning J., Lloyd C., Murray A., Mortimore B., O'Callaghan M.,  
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,  
RA Saldon N., Smith A., Sonhammer E., Staden R., Sulston J.,  
RA Thiermy-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
elegans.";  
RL Nature 368:32-38(1994).  
DR EMBL: Z66499; CAA91301.1; -;  
DR InterPro: IPR000561; -;  
DR InterPro: IPR001007; -;  
DR InterPro: IPR001271; -;  
DR InterPro: IPR001450; -;  
DR PROSITE: PS00198; 4PE4S\_FERREDOXIN; UNKNOWN\_1.  
DR PROSITE: PS00269; DEFENSIN; UNKNOWN\_1.  
DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE: PS01208; VWFC; UNKNOWN\_1.  
SQ SEQUENCE 164 AA; 16499 MW; C002D48D36C9FCED CRC64;

Query Match 15.0%; Score 107; DB 5; Length 164;  
Best Local Similarity 34.9%; Pred. No. 0.00021;  
Matches 30; Conservative 1; Mismatches 29; Indels 26; Gaps 6;  
QY 8 GCGPGRLLLTGTGDARCCRVHTTCCRDYDYGEECCSEWDCMCVQPEFHCQDPCCTTCRHH 67  
| | | | | : : : : : |  
DB 74 GCGGG-----GGCGCGCCCR---PRCC-----CCRCCTCTCCRT---CCCTCTCTCCR-- 115  
| | | | | : : : : : |  
QY 68 PCPPGQGVQSGKFSFGFCIDCAGS 93  
| | | | | : : : : : |  
DB 116 PCCGCGGC-----GGCGCGCGGG 133  
| | | | | : : : : : |

Search completed: September 4, 2001, 16:14:31  
Job time: 1218 sec

105 PCCGCGCG- - - - - GCGGCGCGGG 122

RESULT 13

Q9WUH9

ID Q9WUH9 PRELIMINARY; PRT: 2906 AA.

AC Q9WUH9;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE FIBRILLIN-2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RA Yang Q., Ota K., Tian Y., Kumar A., Wada J., Kashiwara N., Wallner E.I., Kanwar Y.S.;

RA "Cloning of rat fibrillin-2 cDNA and its role in branching morphogenesis of rat embryonic lung.;"

RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

RL EMBL: AF135060; AAD34439.1; -; HSSP; P35555; IEMN.

DR InterPro: IPR000152; -

DR InterPro: IPR000561; -

DR InterPro: IPR001438; -

DR InterPro: IPR001881; -

DR InterPro: IPR002086; -

DR InterPro: IPR002212; -

DR Pfam: PF000008; EGF\_46.

DR Pfam: PF00683; TB; 9.

DR PRINTS: PR00010; EGFBL00D.

DR PROSITE: PS00070; ALDEHYDE\_DEHYDR\_CYS; UNKNOWN\_1.

DR PROSITE: PS00010; ASX\_HYDROXYL; 43.

DR PROSITE: PS00022; EGF\_1; UNKNOWN\_2.

DR PROSITE: PS01186; EGF\_2; 36.

DR PROSITE: PS01187; EGF\_CA; 43.

DR SMART: SM00179; EGF\_CA; 1.

DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat

SW SEQUENCE 2906 AA; 313372 MW; 9EE64E727044EF58 CRC64;

Query Match	15.3%	Score 108.5;	DB 11;	Length 2906;	
Best Local Similarity	25.2%;	Pred. No. 0.0016;			
Matches	31;	Conservative 15;	Mismatches 38;	Indels 39;	Gaps

QY	9	CGPCRLLLTGT	DARCC-----RVHTTCCRDRYPGEECCS	EMWDCMCVQPEFHCG	57
Db	676	CPPG----	LAVGVDRGVCVDTHMRSTCYGEIKKGV	CVRPFFG--AVTYECCCANPDYGGF	730
QY	58	DPCCTTCHHP	PCPGQGVQSGQSFSGF-----QC-ID----	CASG---TFSGGHE	100
Db	731	EPC-----	QCPAKNAE	PHGLCSGGVGTVDGRDINECALPDICANGICENL	RGSYR 784
QY	101	GHC	103		
Db	785	CNC	787		

RESULT	14
QY9Y6Q6	
ID	QY9Y6Q6
AC	QY9Y6Q6;
DT	01-NOV-1999 (T-EMBLrel. 12, Created)
DT	01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
DT	01-MAR-2001 (T-EMBLrel. 16, Last annotation update)
DE	RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-INDUCED CYTOKINE RECEPTOR) (RANK).
GN	TNFRSF1A OR RANK.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.





Search completed: September 4, 2001, 16:14:30  
Job time: 1217 sec

DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)  
 DE (OCIF).  
 GN TNFRSF11B OR OPG.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=INTESTINE;  
 RC MEDLINE=97262071; PubMed=9108485;  
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
 RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,  
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trill G., Sullivan J.,  
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,  
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
 RA Suggs S., Boyle W.J.;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=BALB/C; TISSUE=KIDNEY;  
 RC MEDLINE=97262071; PubMed=9108485;  
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
 RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,  
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trill G., Sullivan J.,  
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,  
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
 RA Suggs S., Boyle W.J.;  
 OS Osteoprotegerin; a novel secreted protein involved in the regulation  
 RT of bone density.;  
 RL Cell 89:309-319(1997).  
 CC -|- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES  
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY  
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO  
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN  
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.  
 CC -|- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY  
 CC SIMILARITY).  
 CC -|- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL; U94330; AAB53707.1; -;  
 DR HSSP; P25942; ICDF.  
 DR InterPro; IPR000488; -;  
 DR InterPro; IPR001368; -;  
 DR Pfam; PF00020; TNFR\_C6; 4.  
 DR ProDom; PD000771; -; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 2.  
 DR SMART; SM00005; DEATH; 1.  
 KW Glycopolypeptide; Repeat; Cytokine; Signal.  
 FT SIGNAL 1 21 BY SIMILARITY.  
 FT CHAIN 22 401 OSTEOPROTEGERIN.  
 FT DOMAIN 23 201 4 X TNFR-CYS.  
 FT REPEAT 23 63 TNFR-CYS 1.  
 FT REPEAT 64 106 TNFR-CYS 2.  
 FT REPEAT 107 143 TNFR-CYS 3.  
 FT REPEAT 144 201 TNFR-CYS 4.  
 FT DOMAIN 306 365 DEATH DOMAIN.  
 FT DISULFID 41 54 BY SIMILARITY.  
 FT DISULFID 44 62 BY SIMILARITY.  
 FT DISULFID 65 80 BY SIMILARITY.  
 FT DISULFID 83 97 BY SIMILARITY.  
 FT DISULFID 87 105 BY SIMILARITY.  
 FT DISULFID 118 142 BY SIMILARITY.  
 FT DISULFID 145 160 BY SIMILARITY.  
 FT CARBOHYD 98 198 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 165 195 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 401 AA; 46192 MW; FEC6A31F1D4E573A CRC64;

Query Match 10.6%; Score 141.5; DB 11; Length 401;  
 Best Local Similarity 27.2%; Pred. No. 2.2e-06;  
 Matches 46; Conservative 11; Mismatches 63; Indels 49; Gaps 8;  
 QY 15 GLALCALSLGQRTGGPGCGPGRLLLTGTGDACCRVRHTTRC--CRDY-----PGEE 65  
 DB 36 GRQLLC-----DKCAPGYL-----KQHTVRRKTLCPDPSYSDTSWHTSDS 79  
 QY 66 C-----CSEWD-----CMCVQPEHFHCGDPCCTTCRHHPCPPGGVQSQGK 106  
 DB 80 CVYCSPVCKELQTVQECNRTHNRVCECEGRYLELEFC---LKHRSPPGLGVLAQSTP 136

QY 107 SFGFOCIDCASGTFSG--GHEGCHKPWTCTQFGELTVFPGNKTHNAV 153  
 DB 137 ERNTVCKRCPDGFSGETSSKAPCRKHTNCSSGLLLLIQGNATHDNVC 185  
 RESULT 13  
 O08712 PRELIMINARY; PRT; 401 AA.  
 ID O08712 O08712; O70202;  
 AC O08712; O70202;  
 DT 01-JUL-1997 (TRENBLrel. 04, Created)  
 DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)  
 DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)  
 DE (OCIF).  
 GN TNFRSF11B OR OPG.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=BALB/C; TISSUE=KIDNEY;  
 RC MEDLINE=97262071; PubMed=9108485;  
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
 RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,  
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trill G., Sullivan J.,  
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,  
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
 RA Suggs S., Boyle W.J.;  
 OS Osteoprotegerin; a novel secreted protein involved in the regulation  
 RT of bone density.;  
 RL Cell 89:309-319(1997).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=129/Ola, AND NIH SWISS;  
 RC MEDLINE=98382527; PubMed=9714833;  
 RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,  
 RA Higashio K.;  
 OS Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)  
 RT gene and its expression in embryogenesis.;  
 RL Gene 215:339-343(1998).  
 CC -|- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES  
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY  
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO  
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN  
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.  
 CC -|- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).  
 CC -|- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -|- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,  
 CC BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND  
 CC PLACENTA. NOT DETECTED IN SPLEEN.  
 CC -|- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT  
 CC DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY  
 CC 15 TO DAY 17.  
 CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL; U94331; AAB53708.1; -;  
 DR EMBL; AB013898; BAA28269.1; -;  
 DR EMBL; AB013903; BAA33388.1; -;  
 DR EMBL; AB013899; BAA33388.1; JOINED.  
 DR EMBL; AB013900; BAA33388.1; JOINED.  
 DR EMBL; AB013901; BAA33388.1; JOINED.  
 DR EMBL; AB013902; BAA33388.1; JOINED.  
 DR HSSP; P25942; ICDF.  
 DR MGD; MGI:109587; Tnfrsf11b.  
 DR InterPro; IPR000488; -;  
 DR InterPro; IPR001368; -;  
 DR Pfam; PF00020; TNFR\_C6; 3.  
 DR ProDom; PD000771; -; 1.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 DR SMART; SM00005; DEATH; 1.  
 KW Glycoprotein; Repeat; Cytokine; Signal.





```
Matches 129; Conservative 32; Mismatches 58; Indels 16; Gaps 4;

Qy 7 MGAFRALCGLALLCALS LGQ-RPTGGPGCGPGRLLLTGTGTARCCRVHTRCCRDYPGEE 65
Db 1 MGAWAMLYGVSMCLVLDLGQPSVVEEPGCGPKVQSGNNTCCSLYA-----PGKE 53
Qy 66 CCSEWDCMCVQPEFHCGDPCCCTTCHRHPCPPGQVQSGKFSFGQICDASGTFSGGHE 125
Db 54 DCPKERCICVTPEYHCGDPQCKICKHYPCQQRVESQGDIVFGFRCVACAMGTFSAGRD 113
Qy 126 GHCKPWTCTQFGFLTVPGNKTHNACVCPGPPAPPLGWLTVLLVAACVLLLTSAQL 185
Db 114 GHCRLTWNCQSGFGLTVPGNKTHNACVCPGPPAPPLGWLTVLLVAACVLLLTSAQL 173
Qy 186 GLHIWQLRK-----TQLLEVPSTEDARSCQPEERGERSAEKGRLGDLW 233
Db 174 GLHIWQLRQHMCPRQTPFAEVLQSAEDACSFQPEERGERQOT-EKCHLGRW 227

RESULT 5
Q9JKR3 PRELIMINARY; PRT; 294 AA.
AC Q9JKR3;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE GTR-B.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229432; AAF61566.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 294 AA; 32658 MW; FE0D4AE6A007BA9A CRC64;

Query Match 46.7%; Score 625.5; DB 11; Length 294;
Best Local Similarity 52.9%; Pred. No. 1.9e-55;
Matches 111; Conservative 32; Mismatches 56; Indels 11; Gaps 3;

Qy 7 MGAFRALCGLALLCALS LGQ-RPTGGPGCGPGRLLLTGTGTARCCRVHTRCCRDYPGEE 65
Db 1 MGAWAMLYGVSMCLVLDLGQPSVVEEPGCGPKVQSGNNTCCSLYA-----PGKE 53
Qy 66 CCSEWDCMCVQPEFHCGDPCCCTTCHRHPCPPGQVQSGKFSFGQICDASGTFSGGHE 125
Db 54 DCPKERCICVTPEYHCGDPQCKICKHYPCQQRVESQGDIVFGFRCVACAMGTFSAGRD 113
Qy 126 GHCKPWTCTQFGFLTVPGNKTHNACVCPGPPAPPLGWLTVLLVAACVLLLTSAQL 185
Db 114 GHCRLTWNCQSGFGLTVPGNKTHNACVCPGPPAPPLGWLTVLLVAACVLLLTSAQL 173
Qy 186 GLHIWQLRK-----LLEVPSTEDARSCQ 212
Db 174 GLHIWQLRQHMCPRVLLQRPSSRRSCQ 203

RESULT 6
Q9JKR2 PRELIMINARY; PRT; 222 AA.
AC Q9JKR2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
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```
GTR-C.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229433; AAF61567.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 222 AA; 24450 MW; 594932BA425A79CA CRC64;

Query Match 46.1%; Score 618; DB 11; Length 222;
Best Local Similarity 54.7%; Pred. No. 8.5e-55;
Matches 105; Conservative 31; Mismatches 48; Indels 8; Gaps 2;

Qy 7 MGAFRALCGLALLCALS LGQ-RPTGGPGCGPGRLLLTGTGTARCCRVHTRCCRDYPGEE 65
Db 1 MGAWAMLYGVSMCLVLDLGQPSVVEEPGCGPKVQSGNNTCCSLYA-----PGKE 53
Qy 66 CCSEWDCMCVQPEFHCGDPCCCTTCHRHPCPPGQVQSGKFSFGQICDASGTFSGGHE 125
Db 54 DCPKERCICVTPEYHCGDPQCKICKHYPCQQRVESQGDIVFGFRCVACAMGTFSAGRD 113
Qy 126 GHCKPWTCTQFGFLTVPGNKTHNACVCPGPPAPPLGWLTVLLVAACVLLLTSAQL 185
Db 114 GHCRLTWNCQSGFGLTVPGNKTHNACVCPGPPAPPLGWLTVLLVAACVLLLTSAQL 173
Qy 186 GLHIWQLRK-----TQLLEVPSTEDARSCQ 212
Db 174 GLHIWQLRQHMCPRVLLQRPSSRRSCQ 203

RESULT 7
Q9JKR1 PRELIMINARY; PRT; 132 AA.
AC Q9JKR1;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE GTR-D.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229434; AAF61568.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 132 AA; 14106 MW; F586A5404BDFE CRC64;

Query Match 28.4%; Score 380; DB 11; Length 132;
Best Local Similarity 50.4%; Pred. No. 6.1e-31;
Matches 64; Conservative 21; Mismatches 34; Indels 8; Gaps 2;

Qy 7 MGAFRALCGLALLCALS LGQ-RPTGGPGCGPGRLLLTGTGTARCCRVHTRCCRDYPGEE 65
Db 1 MGAWAMLYGVSMCLVLDLGQPSVVEEPGCGPKVQSGNNTCCSLYA-----PGKE 53
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QY 66 CCSEWDCMCVQPEHCHGDDPCTTCRHHPGPPGQVQSQGKFSFGQCIDCASGTFSGGHE 125
| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 54 DCPKERCICVTPYHCGDPQCKICKHYPCQPGQVQSQGDIIVFGRCVACAMGTFSGAGRD 113
QY 126 GHCKPWT 132
| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 114 GHCLWT 120

RESULT 8
Q02764 PRELIMINARY; PRT; 267 AA.
AC 002764;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OX40 PRECURSOR (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHB:HM;
RA Isono T., Seto A.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003911; BAA20059.1; -
DR HSSP; P19438; 1EXT.
DR InterPro; IPRO01368; -
DR Pfam; PF00020; TNFR_c6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
DR SMART; SM00208; TNFR; 1.
KW Signal.
FT NON_TER 1
FT SIGNAL <1 18 POTENTIAL.
FT CHAIN 19 267 OX40.
SQ SEQUENCE 267 AA; 28489 MW; A8B4CD3173C9500B CRC64;

Query Match 13.6%; Score 182.5; DB 6; Length 267;
Best Local Similarity 27.8%; Pred. No. 1.1e-10;
Matches 76; Conservative 22; Mismatches 94; Indels 81; Gaps 16;

QY 12 ALGCLA-LICALSLGQRTGPGCG-----GPGRLLL-----GTGTDARCCRVHTTRCCRD 60
| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 4 AALGLALLLLGLLGLAEPR--PDCVGTYPGGDRCCLEQCPGYGNVSRNRSQDTICHPC 61
QY 61 YPG--EECCSEWDCM-CVQ-----PEFHGDCPCTTCRHHPGPPGQVQSQGKFSFG 109
| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 62 EPGFYNAVNYQACKPCTQCNRSSGSEPPQECTHTRDTVCR---CRP--GTQPLNGYKHG 116
QY 110 FQCIDCASGTFSGGHEGCHRPWTDCTQFGFLTVFPGNKNTHAVC-----VPGS 157
| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 117 VDCAPCPQGHGSEGNRACRPWTNCTLAGKRTLPASSISDAVCEDRSSLATQPWETPSA 176
QY 158 PPAEP-----LGM-----LNVVL-LAAVACVLLTSAOLGLHI--- 189
| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 177 PYRPTARTAPTRTAQGSTPTLEASKGFLAIVLSLGLGLLALLAALLALYLHQR 236
QY 190 -WQLRKTQLLLEVPPTEDARSCQFP--EEERGE 220
| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 237 AWR-----PPKLPGGGSEFTPIQEEQAD 259

RESULT 9
Q9DD2 PRELIMINARY; PRT; 276 AA.
AC Q9DD2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
```

```
DE HUMAN CD40-HOMOLOGUE.
GN TNFSF5.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Tregaskes C.A.;
RL Thesis (2001), University of Reading, Reading, UNITED KINGDOM.
DR EMBL; AJ293700; CAC20218.1; -
SQ SEQUENCE 276 AA; 30009 MW; 4040B7E0DB82454E CRC64;

Query Match 13.6%; Score 182.5; DB 13; Length 276;
Best Local Similarity 25.5%; Pred. No. 1.1e-10;
Matches 73; Conservative 20; Mismatches 94; Indels 99; Gaps 15;

QY 16 LALLCALSLGQRTGPGCG-PGRLLLTGTGDARCCR---VHTTRCC-RDYPGEECCSE 69
| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 7 LGLLCALLL-----GCGQPG-----DAVNCSDKQYEHKGRCCNRCQPKKLASE 50
| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
QY 70 -----WD-----CMCVQPEF 79
| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 51 CNDTDSVCTPCENGQYQHSWTKERHCTPHEICEDNAGLIVKRHNATHNTVCQC-RAGM 109
QY 80 HCGDPCCTTC-RHHPGPPGQ--VQSQGKFSFGQCIDCASGTF--GGHEGCHKPWTDC 135
| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 110 HCSASCQTCVENEPCQKQGFVAAAEARMTSPCECAEGTFSNVSSKTEPCHEWTSCE 169
QY 136 QFGFLTVFPGNKNTHAVCVGSPAPAEPLGWLTVLLVAAACVLLTSAOLGLHIHQLRKT 195
| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 170 EKGLVVKVKGNTSDVIC--ESSRRSSLSVLPTITAAVVTCL-----VGICVCLVHT 220
QY 196 QLLEVPFS-----TEDARSCQPEER---GERSAEKGR 228
| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 221 DLRRGPKQAEAPRELVTQOPEEVDFPVQETLLGGQPVQAEQDGK 266

RESULT 10
Q95407 PRELIMINARY; PRT; 300 AA.
AC 095407;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE DECOY RECEPTOR 3 (M68) (M68C) (M68E) (DJ583P15.1.1).
GN DCR3 OR TR6 OR TNFRSF6B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99087326; PubMed=9872321;
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
Dodd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
Goddard A.D., Bolstein D., Ashkenazi A.;
RA "Genomic amplification of a decoy receptor for Fas ligand in lung and
RT colon cancer.";
RL Nature 396:699-703(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RX MEDLINE=99253915; PubMed=10318773;
RA Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT "A newly identified member of tumor necrosis factor receptor
superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
RL J. Biol. Chem. 274:13733-13736(1999).
RN [3]
RP SEQUENCE FROM N.A.
```

GenCore version 4.5  
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# OW protein - protein search, using sw model

Run on: September 4, 2001, 15:54:13 ; Search time 133.1 Seconds  
(without alignments)  
232.602 Million cell updates/sec

Title: US-09-512-363-2  
Perfect score: 1340  
Sequence: 1 MAQHGAMGAFRALCGLALLC.....EEERGSABEKGRLGLIWI 234

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

SPTREMBL\_16:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_unclassified:\*  
13: sp\_vertebrate:\*  
14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1340	100.0	234	4	O95851
2	1322.5	98.7	241	4	O9Y5U5
3	815	60.8	255	4	O9NRJ9
4	703	52.5	228	11	O35714
5	625.5	46.7	294	11	O9JKR3
6	618	46.1	222	11	O9JKR2
7	380	28.4	132	11	O5JKR1
8	182.5	13.6	267	6	O02764
9	182.5	13.6	276	13	O9DDD2
10	153	11.4	300	4	O95407
11	150	11.2	616	4	O9Y6Q6
12	141.5	10.6	401	11	O08727
13	139.5	10.4	401	11	O08712
14	139.5	10.4	439	4	Q16042
15	138	10.3	372	4	Q9UHP4
16	138	10.3	401	4	O00300
17	134.5	10.0	625	11	O35305
18	129.5	9.7	655	4	O75509
19	125	9.3	655	11	Q9EPUS

20	122	9.1	107	11	Q9JKE0	Q9jke0 rattus norv
21	121	9.0	302	13	Q9PUS0	Q9pus0 salvelinus
22	120.5	9.0	459	11	Q62327	Q62327 mus musculu
23	120.5	9.0	482	11	O88734	O88734 mus musculu
24	119.5	8.9	1587	4	O00508	O00508 homo sapien
25	119.5	8.9	1637	6	O9XSV8	O9xsv8 bos taurus
26	119	8.9	1574	11	O88281	O88281 rattus norv
27	118.5	8.8	1511	4	O75412	O75412 homo sapien
28	116	8.7	4123	4	O75851	O75851 homo sapien
29	115.5	8.6	1371	11	O9QVW4	O9qvW4 rattus sp.
30	115	8.6	1687	11	Q61204	Q61204 mus musculu
31	114.5	8.5	2906	11	Q9WUH9	Q9wuh9 rattus norv
32	113.5	8.5	283	6	O9XSZ8	O9xsZ8 cercopithec
33	112	8.4	152	5	O9XVX3	O9xvX3 caenorhabdi
34	111.5	8.3	1764	11	O35806	O35806 rattus norv
35	111	8.3	147	11	O9ER63	O9er63 mus musculu
36	111	8.3	1111	5	O9XWD6	O9xwD6 caenorhabdi
37	111	8.3	1792	13	O57484	O57484 gallus gall
38	110.5	8.2	870	6	O02660	O02660 bos taurus
39	110	8.2	1522	5	O22685	O22685 caenorhabdi
40	110	8.2	1537	5	O9VA12	O9vaI2 drosophila
41	110	8.2	1698	5	O94438	O94438 chironomus
42	109.5	8.2	164	5	Q22048	Q22048 caenorhabdi
43	109.5	8.2	4601	5	O9V383	O9v383 drosophila
44	108.5	8.1	2319	11	Q9R172	Q9r172 rattus norv
45	108	8.1	176	14	Q68396	Q68396 human cytom

## ALIGNMENTS

### RESULT 1

O95851 ID O95851 PRELIMINARY; PRT; 234 AA.  
AC O95851;  
DT 01-MAY-1999 (Tremblrel. 10, Created)  
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99156876; PubMed=10037686;  
RA Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L.,  
RA Liu D., Wang S.X., Kwon B.S.;  
RT "Identification of a novel activation-inducible protein of the tumor  
RT necrosis factor receptor superfamily and its ligand.";  
RL J. Biol. Chem. 274:6036-6061(1999).  
DR EMBL; AF117297; AAD19694.1; -;  
DR InterPro; IPR001368; -;  
DR SMART; SM00208; TNFR; 1.  
KW Receptor.  
SQ SEQUENCE. 234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;

Query Match 100.0%; Score 1340; DB 4; Length 234;  
Best Local Similarity 100.0%; Pred. No. 8.9e-128;  
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAMGAFRALCGLALLCALSIGQRTGPGCGPGRLLLTGTGTARCCRVHTTRCCRD 60

Db 1 MAQHGAMGAFRALCGLALLCALSIGQRTGPGCGPGRLLLTGTGTARCCRVHTTRCCRD 60

QY 61 YPGECCSEWDCMCVQFEHCGDCPCTTCRHHPCPPGGVQSQGKFSFGFCIDCASGTF 120

Db 61 YPGECCSEWDCMCVQFEHCGDCPCTTCRHHPCPPGGVQSQGKFSFGFCIDCASGTF 120

QY 121 SGGHEGHCKPWTDCQTFGLTFVFGNKTTHNACVPGSPAPPLGWLTVVLLAVACVLL 180

Db 121 SGGHEGHCKPWTDCQTFGLTFVFGNKTTHNACVPGSPAPPLGWLTVVLLAVACVLL 180



```
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,
RA Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,
RA Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;
RT "Identification of a new member of the tumor necrosis factor family
RT and its receptor, a human ortholog of mouse GTR."
RL Curr. Biol. 0:0-0(1999).
DR EMBL; AF125304; AAD22635.1; -.
DR InterPro; IPR001368; -.
DR SMART; SM00208; TNFR; 1.
SQ SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7B92CBE CRC64;

Query Match 100.0%; Score 246; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 3e-27;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCASGTFSGGHEGCKPWTCTQFGFLTVPFGKTHNAVCV 41
Db 114 DCASGTFSGGHEGCKPWTCTQFGFLTVPFGKTHNAVCV 154

RESULT 3
ID Q9JKR2 PRELIMINARY; PRT; 222 AA.
AC Q9JKR2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GTR-C.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR."
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229433; AAF61567.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 222 AA; 24450 MW; 594932BA425A79CA CRC64;

Query Match 78.0%; Score 192; DB 11; Length 222;
Best Local Similarity 75.0%; Pred. No. 1.3e-19;
Matches 30; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 CASGTFSGGHEGCKPWTCTQFGFLTVPFGKTHNAVCV 41
Db 103 CAMGTFSGAGRGHCLWNCQSGFLTFMPPGNKTHNAVCI 142

RESULT 4
ID Q35714 PRELIMINARY; PRT; 228 AA.
AC Q35714;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
```

```
DE GLUCOCORTICOID-INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.
GN TNFRSF18 OR GTR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEN;
RX MEDLINE=97322352; PubMed=9177197;
RA Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,
RA Moraca R., Migliorati G., Riccardi C.;
RT "A new member of the tumor necrosis factor/nerve growth factor
RT receptor family inhibits T cell receptor-induced apoptosis."
RL Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C;
RA Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
RA Migliorati G., Riccardi C.;
RT "Gene structure and chromosomal assignment of GTR, a mouse member of
RT the tumor necrosis factor/nerve growth factor receptor family."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U82534; AB881243.1; -.
DR EMBL; AF109216; AAF14231.1; -.
DR MGI; MGI:894675; Tnfrsf18.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
KW Signal; Receptor.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 228 GLUCOCORTICOID INDUCED TNFR FAMILY
FT RELATED PROTEIN.
SQ SEQUENCE 228 AA; 25334 MW; 50D8C275D9C56259 CRC64;

Query Match 78.0%; Score 192; DB 11; Length 228;
Best Local Similarity 75.0%; Pred. No. 1.4e-19;
Matches 30; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 CASGTFSGGHEGCKPWTCTQFGFLTVPFGKTHNAVCV 41
Db 103 CAMGTFSGAGRGHCLWNCQSGFLTFMPPGNKTHNAVCI 142

RESULT 5
ID Q9JKR3 PRELIMINARY; PRT; 294 AA.
AC Q9JKR3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GTR-B.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR."
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229432; AAF61566.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 294 AA; 32658 MW; FE0D4AE6A007BA9A CRC64;

Query Match 78.0%; Score 192; DB 11; Length 294;
Best Local Similarity 75.0%; Pred. No. 1.8e-19;
Matches 30; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
```

GenCore version 4.5

Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2001, 16:14:33 ; Search time 133.1 Seconds  
(without alignments)  
40.755 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_114\_154

Perfect score: 246

Sequence: 1 DCASGTFSGHGCHKPWT.....TQFGFLTVFPGNKTHNAVCV 41

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_16:\*

1: sp.archaea:\*

2: sp.bacteria:\*

3: sp.fungi:\*

4: sp.human:\*

5: sp.invertebrate:\*

6: sp.mammal:\*

7: sp.mhc:\*

8: sp.organelle:\*

9: sp.phage:\*

10: sp.plant:\*

11: sp.rodent:\*

12: sp.unclassified:\*

13: sp.vertebrate:\*

14: sp.virus:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	246	100.0	234	4	Q95851 homo sapien
2	246	100.0	241	4	Q9Y5U5 homo sapien
3	192	78.0	222	11	Q9JKR2 mus musculu
4	192	78.0	228	11	Q35714 mus musculu
5	192	78.0	294	11	Q9JKR3 mus musculu
6	135	54.9	255	4	Q9NYJ9 homo sapien
7	96	39.0	267	6	O02764 oryctolagus
8	83	33.7	401	11	O08727 rattus norv
9	83	33.7	401	11	O08712 mus musculu
10	79	32.1	132	11	Q9JKR1 mus musculu
11	78	31.7	300	4	O95407 homo sapien
12	77	31.3	267	14	O90257 fish lympho
13	77	31.3	372	4	Q9UHP4 homo sapien
14	77	31.3	401	4	O00300 homo sapien
15	75	30.5	625	11	O35305 mus musculu
16	74	30.1	616	4	Q9Y6Q6 homo sapien
17	74	30.1	655	4	O75509 homo sapien
18	70	28.5	276	13	Q9DD02 gallus gall
19	65	26.4	655	11	Q9EPU5 mus musculu

20	63	25.6	650	4	Q9NQ78
21	63	25.6	653	4	Q9NQ79
22	63	25.6	661	4	Q9NQ80
23	62	25.2	193	11	Q9QX63
24	61	24.8	175	11	Q9WUL4
25	61	24.8	351	14	O57117
26	61	24.8	439	4	Q16042
27	61	24.8	459	11	O62327
28	61	24.8	482	11	O88734
29	59	24.0	897	14	O96631
30	59	24.0	998	14	O66929
31	57.5	23.4	135	13	Q9IAM1
32	56.5	23.0	131	13	Q9PSM9
33	56.5	23.0	146	13	Q9DG31
34	55.5	22.6	146	13	Q9I840
35	55	22.4	1283	4	O95451
36	55	22.4	1594	4	O9HC84
37	54.5	22.2	350	2	Q92377
38	54	22.0	175	14	Q9PZS0
39	54	22.0	176	14	Q68396
40	54	22.0	176	14	O9PZR9
41	54	22.0	176	14	O9PZR8
42	54	22.0	176	14	O9PZQ7
43	54	22.0	176	14	O9PX59
44	54	22.0	176	14	O9PX08
45	54	22.0	176	14	O9PWX6

## ALIGNMENTS

RESULT 1

Q95851 ID O95851 PRELIMINARY; PRT; 234 AA.  
AC O95851;

DT 01-MAY-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

ON NCBI\_TaxID=9606;

RX MEDLINE=99156876; PubMed=10037686;

RA Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L.,

RA Liu D., Wang S.X., Kwon B.S.;

RT "Identification of a novel activation-inducible protein of the tumor  
necrosis factor receptor superfamily and its ligand.";

RL J. Biol. Chem. 274:6056-6061(1999).

DR EMBL; AF117297; AADI9694.1; -

DR InterPro; IPR001368; -

DR SMART; SM00208; TNFR; 1.

KW Receptor.

SQ SEQUENCE. 234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;  
Query Match 100.0%; Score 246; DB 4; Length 234;

Best Local Similarity 100.0%; Pred. No. 2.9e-27;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCASGTFSGHGCHKPWTCTQFGFLTVFPGNKTHNAVCV 41

Db 114 DCASGTFSGHGCHKPWTCTQFGFLTVFPGNKTHNAVCV 154

RESULT 2

Q9Y5U5 ID Q9Y5U5 PRELIMINARY; PRT; 241 AA.

AC Q9Y5U5;

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

Best Local Similarity 39.0%; Pred. No. 0.00079;  
Matches 16; Conservative 6; Mismatches 17; Indels 2; Gaps 1;

QY 2 CASGTFSG--GHEGCKPWTCTQFGFLTVFPNGKTHNAV 40  
DB 145 CPDFFSGEISSKAPCRKHTNCSSGLLLLIQGNATHDNVC 185

RESULT 9  
O08712 PRELIMINARY; PRT; 401 AA.

AC O08712; 070202;  
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)  
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)  
DE (OCIF).  
GN TNFRSF11B OR OPG.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BALB/C; TISSUE-KIDNEY;  
RX MEDLINE=97262071; PubMed=9108485;  
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
Raethly R., Nguyen H.O., Woodson S., Bennett L., Boone T., Shimamoto G.,  
Derosé M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,  
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,  
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
Suggs S., Boyle W.J.;  
RA "Osteoprotegerin: a novel secreted protein involved in the regulation  
of bone density.";  
RT Cell 89:309-319(1997).  
RL [2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=129/OLA, AND NIH SWISS;  
RX MEDLINE=98382527; PubMed=9714833;  
RA Higashio K.;  
RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,  
RT "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)  
gene and its expression in embryogenesis.";  
RL Gene 215:339-343(1998).  
CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES  
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY  
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO  
OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN  
STROMAL CELLS AND OSTEOCLAST PROGENITORS.  
CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).  
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,  
BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND  
PLACENTA. NOT DETECTED IN SPLEEN.  
CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT  
DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY  
15 TO DAY 17.  
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
DR EMBL; U94331; AAB53708.1; -.  
DR EMBL; AB013898; BAA28469.1; -.  
DR EMBL; AB013903; BAA33388.1; -.  
DR EMBL; AB013899; BAA33388.1; JOINED.  
DR EMBL; AB013900; BAA33388.1; JOINED.  
DR EMBL; AB013901; BAA33388.1; JOINED.  
DR EMBL; AB013902; BAA33388.1; JOINED.  
DR HSP; P25942; ICDF.  
DR MGD; MGI:109587; Tnfslf1b.  
DR InterPro; IPR004488; -.  
DR InterPro; IPR001368; -.  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR ProDom; PD000771; -.  
DR PROSITE; PS00017; DEATH\_DOMAIN; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.

DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
DR SMART; SM00005; DEATH; 1.  
KW Glycoprotein; Repeat; Cytokine; Signal.  
FT SIGNAL 1 21 OSTEOPROTEGERIN.  
FT CHAIN 22 401 4 X TNFR-CYS.  
FT DOMAIN 23 201 TNFR-CYS 1.  
FT REPEAT 23 63 TNFR-CYS 2.  
FT REPEAT 64 106 TNFR-CYS 3.  
FT REPEAT 107 143 TNFR-CYS 4.  
FT REPEAT 144 201 DEATH DOMAIN.  
FT DOMAIN 306 365 BY SIMILARITY.  
FT DISULFID 41 54 BY SIMILARITY.  
FT DISULFID 44 62 BY SIMILARITY.  
FT DISULFID 65 80 BY SIMILARITY.  
FT DISULFID 83 97 BY SIMILARITY.  
FT DISULFID 87 105 BY SIMILARITY.  
FT DISULFID 118 142 BY SIMILARITY.  
FT DISULFID 145 160 BY SIMILARITY.  
FT CARBOHYD 98 165 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 178 178 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT VARIANT 138 138 R -> P (IN STRAINS 129/OLA AND NIH  
SWISS).  
FT VARIANT 161 161 I -> R (IN STRAINS 129/OLA AND NIH  
SWISS).  
FT VARIANT 165 165 N -> D (IN STRAINS 129/OLA AND NIH  
SWISS).  
FT VARIANT 288 288 S -> A (IN STRAINS 129/OLA AND NIH  
SWISS).  
FT VARIANT 296 296 L -> R (IN STRAINS 129/OLA AND NIH  
SWISS).  
SQ SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;

Query Match 33.7%; Score 83; DB 11; Length 401;  
Best Local Similarity 41.5%; Pred. No. 0.00079;  
Matches 17; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

QY 2 CASGTFSG--GHEGCKPWTCTQFGFLTVFPNGKTHNAV 40  
DB 145 CPDFFSGEISSKAPCRKHTNCSTFGLLIQGNATHDNVC 185

RESULT 10  
Q0JKR1 PRELIMINARY; PRT; 132 AA.

AC Q0JKR1;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE GTR-D.  
GN TNFRSF18.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=THYMUS;  
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,  
RA Migliorati G., Riccardi C.;  
RT "Identification of three novel mRNA splice variants of GTR.";  
RL Cell Death Differ. 0:0-0(2000).  
DR EMBL; AF229434; AAF61568.1; -.  
DR InterPro; IPR000561; -.  
DR SMART; SM00181; EGF; 1.  
SQ SEQUENCE 132 AA; 14106 MW; F586A5404B1DFEDE CRC64;

Query Match 32.1%; Score 79; DB 11; Length 132;  
Best Local Similarity 66.7%; Pred. No. 0.00094;  
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;





Query Match 31.3%; Score 77; DB 4; Length 372;  
 Best Local Similarity 36.6%; Pred. No. 0.0052;  
 Matches 15; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

OY 2 CASGTFSG--GHEGCHKPWTCTQFGFLTVFPNGKTHNAV 40  
 DB 124 CPDGFSSNETSKAPCRKHTNCSVFGLLLTQKGNATHNIC 164

RESULT 14  
 OQ0300 PRELIMINARY; PRT; 401 AA.

ID QO0300 O60236;  
 AC QO0300; O60236; (T-EMBLrel. 04, Created)  
 DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)  
 DT 01-JUL-1997 (T-EMBLrel. 16, Last annotation update)  
 DT 01-MAR-2001 (T-EMBLrel. 16, Last annotation update)  
 DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)  
 DE (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).  
 GN TNFRSF11B OR OPG OR OCIF.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=KIDNEY;  
 RX MEDLINE=97262071; PubMed=9108485;  
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
 RA Luthy R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,  
 RA Dorsey M., Elliott R., Colombero A., Tan H.-L., Trall G., Sullivan J.,  
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,  
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
 RA Suggs S., Boyle W.J.;  
 RA "Osteoprotegerin: a novel secreted protein involved in the regulation  
 RT of bone density.";  
 RT Cell 89:309-319(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LUNG FIBROBLAST;  
 RX MEDLINE=98151033; PubMed=9492069;  
 RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,  
 RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,  
 RA Tsuda E., Morinaga T., Higashio K.;  
 RA "Identity of osteoclastogenesis inhibitory factor (OCIF) and  
 RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits  
 RT osteoclastogenesis in vitro.";  
 RL Endocrinology 139:1329-1337(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PLACENTA;  
 RX MEDLINE=98351569; PubMed=9688283;  
 RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;  
 RT "Cloning and characterization of the gene encoding human  
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";  
 RL Eur. J. Biochem. 254:685-691(1998).  
 CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES  
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY  
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO  
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN  
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.  
 CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY  
 CC SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,  
 CC KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN  
 CC A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED IN  
 CC THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC EMBL; AB002146; BAA25910.1; -  
 CC EMBL; AB008822; BAA32076.1; -  
 CC EMBL; AB008821; BAA32076.1; JOINED.  
 CC EMBL; U94332; AAB53709.1; -

HSP; P25942; ICDF.  
 MIM; 602643; -  
 DR InterPro; IPR000488; -  
 DR InterPro; IPR001368; -  
 DR Pfam; PF00020; TNFR\_C6; 3.  
 DR PRODOM; PD000771; - 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 2.  
 DR SMART; SM0005; DEATH; 1.  
 KW Glycoprotein; Repeat; Cytokine; Signal.  
 FT SIGNAL 1 21 BY SIMILARITY.  
 FT CHAIN 22 401 OSTEOPROTEGERIN.  
 FT DOMAIN 23 183 4 X TNFR-CYS.  
 FT REPEAT 23 63 TNFR-CYS 1.  
 FT REPEAT 23 106 TNFR-CYS 2.  
 FT REPEAT 107 143 TNFR-CYS 3.  
 FT REPEAT 144 201 TNFR-CYS 4.  
 FT DOMAIN 306 365 DEATH DOMAIN.  
 FT DISULFID 41 54 BY SIMILARITY.  
 FT DISULFID 44 62 BY SIMILARITY.  
 FT DISULFID 65 80 BY SIMILARITY.  
 FT DISULFID 83 97 BY SIMILARITY.  
 FT DISULFID 87 105 BY SIMILARITY.  
 FT DISULFID 118 142 BY SIMILARITY.  
 FT DISULFID 145 160 BY SIMILARITY.  
 FT CARBOHYD 98 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CONFLICT 263 263 A -> D (IN REF. 2 AND 3).  
 SQ SEQUENCE 401 AA; 45996 MW; EB42FA51C9D7C71E CRC64;

Query Match 31.3%; Score 77; DB 4; Length 401;  
 Best Local Similarity 36.6%; Pred. No. 0.0056;  
 Matches 15; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

OY 2 CASGTFSG--GHEGCHKPWTCTQFGFLTVFPNGKTHNAV 40  
 DB 145 CPDGFSSNETSKAPCRKHTNCSVFGLLLTQKGNATHNIC 185

RESULT 15  
 ID O35305 PRELIMINARY; PRT; 625 AA.  
 AC O35305;  
 DT 01-JAN-1998 (T-EMBLrel. 05, Created)  
 DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)  
 DT 01-MAR-2001 (T-EMBLrel. 16, Last annotation update)  
 DE RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-  
 DE INDUCED CYTOKINE RECEPTOR) (RANK).  
 GN TNFRSF1A OR RANK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER EPITHELIUM;  
 RX MEDLINE=98032977; PubMed=9367155;  
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,  
 RA Tonetsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,  
 RA Galibert L.;  
 RA "A homologue of the TNF receptor and its ligand enhance T-cell growth  
 RT and dendritic-cell function.";  
 RL Nature 390:175-179(1997).  
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC EMBL; AF019046; AAB86810.1; -  
 DR HSP; P25942; ICDF.  
 DR MGD; MGI:1314891; Tnfrsf1a.

DR	SMART; PS00050; TNFR_NGFR_2; 2.
DR	SMART; SM00005; DEATH; 1.
FT	NON_TER 1 1
SO	SEQUENCE 372 AA: 42758 MW: F02527A5CD01CCD3 CRC64:

Search completed: September 4, 2001, 16:14:33  
Job time: 1220 sec

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DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
GN TNFRSF18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Gurney A.L., Masters S.A., Huang A., Pitti R.M., Mark M.,
RA Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,
RA Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;
RT "Identification of a new member of the tumor necrosis factor family
RL Curr. Biol. 0:0-0(1999).
DR EMBL: AF125304; AAD22635.1; -.
DR InterPro: IPR001368; -.
DR SMART: SM00208; TNFR; 1.
SQ SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7E82CBE CRC64;

Query Match 100.0%; Score 252; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 4.6e-26;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVOPEFHCGDPCCTTCRRHHPGPGVGQSGKFSFGFCI 40
DB 74 CVOPEFHCGDPCCTTCRRHHPGPGVGQSGKFSFGFCI 113

RESULT 3
ID Q9NYJ9 PRELIMINARY; PRT; 255 AA.
AC Q9NYJ9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE GTR-D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Mastrodicasa E., Riccardi C.;
RT "Identification of a soluble human GTR splicing (hGTR-D).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF241229; AAF63506.1; -.
SQ SEQUENCE 255 AA; 26827 MW; C986652AC97AF2CC CRC64;

Query Match 100.0%; Score 252; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. No. 4.9e-26;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVOPEFHCGDPCCTTCRRHHPGPGVGQSGKFSFGFCI 40
DB 74 CVOPEFHCGDPCCTTCRRHHPGPGVGQSGKFSFGFCI 113

RESULT 4
ID Q9JKR1 PRELIMINARY; PRT; 132 AA.
AC Q9JKR1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GTR-D.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL: AF229434; AAF61568.1; -.
DR InterPro: IPR000561; -.
DR SMART: SM00181; EGF; 1.
SQ SEQUENCE 132 AA; 14106 MW; F586A540B1DFEDE CRC64;

Query Match 66.7%; Score 168; DB 11; Length 132;
Best Local Similarity 62.5%; Pred. No. 4.2e-15;
Matches 25; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 CVOPEFHCGDPCCTTCRRHHPGPGVGQSGKFSFGFCI 40
DB 62 CVTPEVHCDDPCKICKHYPCQPGQVRVESQGDIVFGRCV 101

RESULT 5
ID Q9JKR2 PRELIMINARY; PRT; 222 AA.
AC Q9JKR2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GTR-C.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL: AF229433; AAF61567.1; -.
DR InterPro: IPR000561; -.
DR SMART: SM00181; EGF; 1.
SQ SEQUENCE 222 AA; 24450 MW; 594932BA425A79CA CRC64;

Query Match 66.7%; Score 168; DB 11; Length 222;
Best Local Similarity 62.5%; Pred. No. 6.5e-15;
Matches 25; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 CVOPEFHCGDPCCTTCRRHHPGPGVGQSGKFSFGFCI 40
DB 62 CVTPEVHCDDPCKICKHYPCQPGQVRVESQGDIVFGRCV 101

RESULT 6
ID Q35714 PRELIMINARY; PRT; 228 AA.
AC Q35714;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.
GN TNFRSF18 OR GTR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:14:32 ; Search time 133.1 Seconds  
(without alignments)  
39.761 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_74\_113

Perfect score: 252

Sequence: 1 CVQPEFHGDCPCTTCRHHPCPGQGVQSGKFSFGFCI 40

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_16.\*

1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phase.\*

10: sp\_plant.\*

11: sp\_rodent.\*

12: sp\_unclassified.\*

13: sp\_vertebrate.\*

14: sp\_virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	252	100.0	234	4	O95851 homo sapien
2	252	100.0	241	4	O9Y5U5 homo sapien
3	252	100.0	255	4	O9NVJ9 homo sapien
4	168	66.7	132	11	O9JKR1 mus musculus
5	168	66.7	222	11	O9JKR2 mus musculus
6	168	66.7	228	11	O35714 mus musculus
7	168	66.7	294	11	O9JKR3 mus musculus
8	72	28.6	1574	11	O88281 rattus norv
9	66.5	26.4	107	11	O9JKE0 rattus norv
10	64	25.4	473	11	O9SESO rattus norv
11	64	25.4	643	11	O9ERV6 mus musculus
12	64	25.4	655	11	O9WVF5 mus musculus
13	64	25.4	1210	11	O9EP98 mus musculus
14	63	25.0	62	5	O77419 ascaris suu
15	63	25.0	283	4	O92956 homo sapien
16	63	25.0	404	4	O9UM65 homo sapien
17	62.5	24.8	1077	3	O74853 schizosacch
18	62.5	24.8	1283	4	O95451 homo sapien
19	62.5	24.8	1594	4	O9HC84 homo sapien

20 61.5 24.4 4123 4 075851  
21 61 24.2 2319 11 09RI72  
22 60.5 24.0 216 13 09PSN7  
23 60.5 24.0 850 4 014425  
24 60.5 24.0 1300 11 09WTL4  
25 60.5 24.0 1373 4 075372  
26 60.5 24.0 4547 5 09W343  
27 60 23.8 405 4 092795  
28 60 23.8 628 4 09H2C9  
29 60 23.8 657 4 014226  
30 60 23.8 705 4 09GZX1  
31 60 23.8 1209 11 09QX70  
32 59.5 23.6 62 6 09TUI5  
33 59.5 23.6 152 4 043831  
34 59.5 23.6 809 5 09U3W7  
35 59.5 23.6 4601 5 09V383  
36 59 23.4 266 10 043391  
37 59 23.4 267 6 002764  
38 59 23.4 527 13 090836  
39 59 23.4 599 13 09PSH2  
40 59 23.4 745 4 09P2N8  
41 59 23.4 814 11 09QYL2  
42 58.5 23.2 1321 4 095291  
43 58.5 23.2 1851 11 09ESP3  
44 58 23.0 1114 11 09JKW7  
45 57.5 22.8 410 11 063720

#### ALIGNMENTS

RESULT 1

ID O95851 PRELIMINARY; PRT; 234 AA.  
AC O95851;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
ON NCBI\_TaxID=9606;  
RX MEDLINE=99156876; Pubmed=10037686;  
RA Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L., Liu D., Wang S.X., Kwon B.S.;  
RT "Identification of a novel activation-inducible protein of the tumor necrosis factor receptor superfamily and its ligand.";  
RL J. Biol. Chem. 274:6056-6061(1999).  
DR EMBL; AF117297; AAD19694.1; -;  
DR InterPro; IPR001368; -;  
DR SMART; SM00208; TNFR; 1.  
KW Receptor.  
SQ SEQUENCE 234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;

Query Match 100.0%; Score 252; DB 4; Length 234;  
Best Local Similarity 100.0%; Pred. No. 4.5e-26;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHGDCPCTTCRHHPCPGQGVQSGKFSFGFCI 40  
|||||  
Db 74 CVQPEFHGDCPCTTCRHHPCPGQGVQSGKFSFGFCI 113  
|||||

RESULT 2

O9Y5U5  
ID O9Y5U5 PRELIMINARY; PRT; 241 AA.  
AC O9Y5U5;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

```

FT NON_TER      1      1
SQ NON_TER     107    107
SQ SEQUENCE   107 AA: 11819 MW: 55BFF8327A0933B2 CRC64;

Query Match      26.4%; Score 66.5; DB 11; Length 107;
Best Local Similarity 54.5%; Pred. No. 0.11;
Matches 13; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

Qy 7 HCGDPCCTC-RHHPCPPGQGV 27
II I I I I I I I I I I
Db 48 HCAKCECTCAQHRCPGPGFGV 69

RESULT 10
Q9ESEO
ID Q9ESEO PRELIMINARY; PRT; 473 AA.
AC Q9ESEO;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE EPIDERMAL GROWTH FACTOR RECEPTOR RELATED PROTEIN.
GN ERP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-GASTRO-DUODENAL MUCOUS;
RA Yu Y., Moshier J.A., Majumdar A.P.N.;
RT "Cloning of a novel EGFR-related peptide: A putative negative
RL regulator of EGFR.";
DR EMBL; AF187818; AAG17037.1; -
KW Receptor.
SQ SEQUENCE 473 AA: 52903 MW: 4E0D7C3074F28973 CRC64;

Query Match      25.4%; Score 64; DB 11; Length 473;
Best Local Similarity 34.2%; Pred. No. 0.86;
Matches 13; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 3 QPEFHCGDPCCTCRHHPCPPGQGVQSGKFSFGQCI 40
I I I I I I I I I I I I I I I I
Db 255 QDEATCKDTCPLMLYNPTTYQMDVNPGEKYSFGATCV 292

RESULT 11
Q9ERV6
ID Q9ERV6 PRELIMINARY; PRT; 643 AA.
AC Q9ERV6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE EPIDERMAL GROWTH FACTOR RECEPTOR ISOFORM 2.
GN EGFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/101, 129/SVJ, 129/SVEVITAC;
RA Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
RA Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
RA Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
RA Maible N.J.;
RT "Comparative genomic sequence analysis and isolation of human and
RT mouse alternative Egr transcripts encoding truncated receptor
RT isoforms.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF275366; AAG28046.1; -
DR EMBL; AF275366; AAG28047.1; -
DR EMBL; AF275366; AAG28047.1; JOINED.
DR EMBL; AF275365; AAG28047.1; JOINED.
DR InterPro; IPR000494; -
DR InterPro; IPR002174; -
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR SMART; SM00261; FU; 1.
KW Receptor.
SQ SEQUENCE 643 AA: 72906 MW: 6B34063B1BC928CB CRC64;

Query Match      25.4%; Score 64; DB 11; Length 655;
Best Local Similarity 34.2%; Pred. No. 1.1;
Matches 13; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 3 QPEFHCGDPCCTCRHHPCPPGQGVQSGKFSFGQCI 40
I I I I I I I I I I I I I I I I
Db 255 QDEATCKDTCPLMLYNPTTYQMDVNPGEKYSFGATCV 292

RESULT 13
Q9EP98

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DR EMBL; AF275364; AAG28046.1; JOINED.
DR EMBL; AF275365; AAG28046.1; JOINED.
KW Receptor.
SQ SEQUENCE 643 AA: 71477 MW: DEF22002C84911B1 CRC64;

Query Match      25.4%; Score 64; DB 11; Length 643;
Best Local Similarity 34.2%; Pred. No. 1.1;
Matches 13; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 3 QPEFHCGDPCCTCRHHPCPPGQGVQSGKFSFGQCI 40
I I I I I I I I I I I I I I I I
Db 255 QDEATCKDTCPLMLYNPTTYQMDVNPGEKYSFGATCV 292

RESULT 12
Q9WVF5
ID Q9WVF5 PRELIMINARY; PRT; 655 AA.
AC Q9WVF5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE EPIDERMAL GROWTH FACTOR RECEPTOR (EPIDERMAL GROWTH FACTOR RECEPTOR
GN ISOFORM 3).
DE EGFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=LIVER;
RA Reiter J.L., Threadgill D.W., Danielsen A.J., Schell C.,
RA Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R.,
RA Maible N.J.;
RT "Alternative transcripts from the Human and Mouse EGFR Genes Encode
RT Carboxy-Terminal Truncated Receptors.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/101, 129/SVJ, AND 129/SVEVITAC;
RA Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
RA Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
RA Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
RA Maible N.J.;
RT "Comparative genomic sequence analysis and isolation of human and
RT mouse alternative Egr transcripts encoding truncated receptor
RT isoforms.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF124513; AAD44149.1; -
DR EMBL; AF275366; AAG28047.1; -
DR EMBL; AF275366; AAG28047.1; -
DR EMBL; AF275364; AAG28047.1; JOINED.
DR EMBL; AF275365; AAG28047.1; JOINED.
DR InterPro; IPR000494; -
DR InterPro; IPR002174; -
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR SMART; SM00261; FU; 1.
KW Receptor.
SQ SEQUENCE 655 AA: 72906 MW: 6B34063B1BC928CB CRC64;

Query Match      25.4%; Score 64; DB 11; Length 655;
Best Local Similarity 34.2%; Pred. No. 1.1;
Matches 13; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 3 QPEFHCGDPCCTCRHHPCPPGQGVQSGKFSFGQCI 40
I I I I I I I I I I I I I I I I
Db 255 QDEATCKDTCPLMLYNPTTYQMDVNPGEKYSFGATCV 292

RESULT 13
Q9EP98

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ID Q9EP98 PRELIMINARY; PRT; 1210 AA.
AC Q9EP98;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE EPIDERMAL GROWTH FACTOR RECEPTOR ISOFORM 1.
GN EGFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/101, 129/SVJ, 129/SVEV7AC;
RA Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
RA Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
RA Balasubramanian S., Crossley T.O., Magnuson T.R., James C.D.,
RA Mahle N.J.;
RT "Comparative genomic sequence analysis and isolation of human and
RT mouse alternative Egr transcripts encoding truncated receptor
RT isoforms."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
RA Schehl C., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
RA Balasubramanian S., Crossley T.O., Magnuson T.R., James C.D.,
RA Mahle N.J.;
RT "Comparative genomic sequence analysis and isolation of human and
RT mouse alternative Egr transcripts encoding truncated receptor
RT isoforms."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF275366; AAG28045.1; -.
DR EMBL: AF275364; AAG28045.1; JOINED.
DR EMBL: AF275365; AAG28045.1; JOINED.
DR EMBL: AF275367; AAG24386.1; -.
KW Receptor.
SQ SEQUENCE 1210 AA; 134841 MW; 62CD021C9DE32E18 CRC64;

Query Match 25.4%; Score 64; DB 11; Length 1210;
Best Local Similarity 34.2%; Pred. No. 1.9;
Matches 13; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 3 QPEFHCGDPCCTTCRHHPCPPGGVQSOGKFSFGFCI 40
DB 255 QDEATCKDTCPLMLNPTTYQMDVNPGEKYSFGATCV 292

RESULT 14
O77419 PRELIMINARY; PRT; 62 AA.
AC O77419;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE CHYMOTRYPSIN/ELASTASE INHIBITOR-1 (FRAGMENT).
GN ASC/E-1.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98297373; PubMed=9635450;
RA Lu C.C., Nguyen T., Morris S., Hill D., Sakanari J.A.;
RA "Anisakis simplex: mutational bursts in the reactive site centers of
RT serine protease inhibitors from an ascarid nematode."
RL Exp. Parasitol. 89:257-261(1998).
DR EMBL: U94499; AAC61300.1; -.
DR HSSP: P07851; 1EAI.
DR InterPro: IPR002919; -.
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DR Pfam: PF01826; TIL; 1.
FT NON_TER 1
FT NON_TER 62
SQ SEQUENCE 62 AA; 6794 MW; 154CE25A375E0B2C CRC64;

Query Match 25.0%; Score 63; DB 5; Length 62;
Best Local Similarity 36.2%; Pred. No. 0.21;
Matches 17; Conservative 4; Mismatches 18; Indels 8; Gaps 3;

QY 1 CVQPEFHCGD---PCCTTCRHH--PCPPGGVQ--SOGKFSFGFCQ 39
DB 14 CTGCEMKCGDPENTPCPLMCRPSCSPGRGMRRTNDGKCIPASQC 60

RESULT 15
Q92956 PRELIMINARY; PRT; 283 AA.
AC Q92956;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE HERPESVIRUS ENTRY MEDIATOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97053782; PubMed=8898196;
RA Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
RA "Herpes simplex virus-1 entry into cells mediated by a novel member of
RT the TNF/NGF receptor family."
RL Cell 87:427-436(1996).
DR EMBL: U70321; AAB58354.1; -.
DR HSSP: P25942; ICDF.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_C6; 3.
DR ProDom: PD000771; -.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS00050; TNFR_NGFR_2; 2.
DR SMART: SM00208; TNFR; 1.
SQ SEQUENCE 283 AA; 30420 MW; DFCE146E4E024F4B CRC64;

Query Match 25.0%; Score 63; DB 4; Length 283;
Best Local Similarity 25.5%; Pred. No. 0.75;
Matches 14; Conservative 3; Mismatches 22; Indels 16; Gaps 1;

QY 1 CVQPEFHCGDPCCTTCRH-----HPCPPGGVQSOGKFSFGFCQ 39
DB 42 CKDEYPVGSECCPKCSPGYRVKACGELTGTVCPCPPGTYIAHLNGLSKLQC 96

Search completed: September 4, 2001, 16:14:33
Job time: 1220 sec
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DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
GN TNFRSF18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,
RA Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,
RA Goddard A.D., Wood W.L., Baker K.P., Godowski P.J., Ashkenazi A.;
RT "Identification of a new member of the tumor necrosis factor family
RT and its receptor, a human ortholog of mouse GTR.";
RL Curr. Biol. 0:0-0(1999).
DR EMBL: AF125304; AAD22635.1; -.
DR InterPro: IPR001369; -.
DR SMART: SM00208; TNFR; 1.
DR SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7E82CBE CRC64;
SQ SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7E82CBE CRC64;

Query Match 100.0%; Score 255; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.7e-26;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41
Db 33 GCGPGRLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 73

RESULT 3
ID Q9NVJ9 PRELIMINARY; PRT; 255 AA.
AC Q9NVJ9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE GTR-D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Bartoli A., Ronchetti S., Mastroiaca E., Riccardi C.;
RT "Identification of a soluble human GTR splicing (hGTR-D).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF241229; AAF63506.1; -.
DR SEQUENCE 255 AA; 26827 MW; C986652AC97AF2CC CRC64;

Query Match 100.0%; Score 255; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41
Db 33 GCGPGRLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 73

RESULT 4
ID Q9JKR1 PRELIMINARY; PRT; 132 AA.
AC Q9JKR1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GTR-D.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL: AF229434; AAF61568.1; -.
DR InterPro: IPR000561; -.
DR SMART: SM00181; EGF; 1.
DR SEQUENCE 132 AA; 14106 MW; F586A5404B1DFEDE CRC64;
SQ SEQUENCE 132 AA; 14106 MW; F586A5404B1DFEDE CRC64;

Query Match 34.3%; Score 87.5; DB 11; Length 132;
Best Local Similarity 36.6%; Pred. No. 0.00023;
Matches 15; Conservative 9; Mismatches 10; Indels 7; Gaps 1;

QY 1 GCGPGRLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41
Db 28 GCGPGRLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 61

RESULT 5
ID Q9JKR2 PRELIMINARY; PRT; 222 AA.
AC Q9JKR2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GTR-C.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL: AF229433; AAF61567.1; -.
DR InterPro: IPR000561; -.
DR SMART: SM00181; EGF; 1.
DR SEQUENCE 222 AA; 24450 MW; 594932BA425A79CA CRC64;
SQ SEQUENCE 222 AA; 24450 MW; 594932BA425A79CA CRC64;

Query Match 34.3%; Score 87.5; DB 11; Length 222;
Best Local Similarity 36.6%; Pred. No. 0.00036;
Matches 15; Conservative 9; Mismatches 10; Indels 7; Gaps 1;

QY 1 GCGPGRLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41
Db 28 GCGPGRLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 61

RESULT 6
ID Q35714 PRELIMINARY; PRT; 228 AA.
AC Q35714;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.
GN TNFRSF18 OR GTR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:14:32 ; Search time 133.1 Seconds  
(without alignments)  
40.755 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_33\_73

Perfect score: 255

Sequence: 1 GCGPGRLLLTGTTCRCRV.....TTRCCRDYVGECCSEWDCM 41

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_16:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_unclassified:\*
- 13: sp\_vertebrate:\*
- 14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	255	100.0	234	4	O95851
2	255	100.0	241	4	O9Y5U5
3	255	100.0	255	4	O9NYJ9
4	87.5	34.3	132	11	O9JKR1
5	87.5	34.3	222	11	O9JKR2
6	87.5	34.3	228	11	O35714
7	87.5	34.3	294	11	O9JKR3
8	66	25.9	416	10	O04507
9	65.5	25.7	423	4	O9NZV2
10	65.5	25.7	423	4	O9NS68
11	64.5	25.3	788	5	O22631
12	63.5	24.9	164	5	O22048
13	63	24.7	152	5	O9VXV3
14	62	24.3	1056	4	O9H3R0
15	62	24.3	1100	4	O94877
16	61.5	24.1	68	13	O9PTM3
17	61.5	24.1	150	11	O9JLL2
18	61.5	24.1	188	11	O70148
19	61.5	24.1	214	11	O9JHF1

20	61.5	24.1	348	11	O9QXW7
21	61.5	24.1	416	11	O9JLL3
22	61.5	24.1	416	11	O9JCH6
23	61.5	24.1	434	11	O922R8
24	61.5	24.1	559	11	O9QX30
25	61.5	24.1	1116	13	O73791
26	61	23.9	188	5	O18238
27	60.5	23.7	177	4	O07627
28	59.5	23.3	122	11	O70149
29	59.5	23.3	200	10	O9XFF4
30	59.5	23.3	200	10	O9XFF3
31	59.5	23.3	200	10	O9XFF2
32	59.5	23.3	200	10	O9SBW5
33	59	23.1	152	6	O29620
34	58.5	22.9	175	4	O07628
35	58.5	22.9	4135	6	O18977
36	58	22.7	103	10	O9SBW9
37	58	22.7	182	6	O29619
38	58	22.7	331	14	O69581
39	58	22.7	506	5	O9VVP5
40	57.5	22.5	126	10	O9S9F4
41	57.5	22.5	138	5	O96100
42	57.5	22.5	138	5	O9U8P9
43	57.5	22.5	243	5	O9NL90
44	57.5	22.5	2174	5	O9GQR0
45	57.5	22.5	2910	11	O55225

#### ALIGNMENTS

RESULT 1

ID O95851 PRELIMINARY; PRT; 234 AA.  
AC O95851;  
DT 01-MAY-1999 (TREMBlrel. 10, Created)  
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99156876; PubMed=10037686;  
RA Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L.,  
RA Liu D., Wang S.X., Kwon B.S.;  
RT "Identification of a novel activation-inducible protein of the tumor  
RT necrosis factor receptor superfamily and its ligand.";  
RL J. Biol. Chem. 274:6056-6061(1999).  
DR EMBL; AF117297; AAD19694.1; -;  
DR InterPro; IPR001368; -;  
DR SMART; SM00208; TNFR; 1.  
KW Receptor.  
SQ SEQUENCE 234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;

Query Match 100.0%; Score 255; DB 4; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.7e-26;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGPGRLLLTGTTCRCRVHTTCCRDYVGECCSEWDCM 41  
|||||  
DB 33 GCGPGRLLLTGTTCRCRVHTTCCRDYVGECCSEWDCM 73

RESULT 2

ID O9Y5U5 PRELIMINARY; PRT; 241 AA.  
AC O9Y5U5;  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

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DR PFam: PF00020: TNFR_C6; 2
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
SQ SEQUENCE 423 AA; 46071 MW; BB7C9917132A4B2F CRC64;

Query Match      25.7%; Score 65.5; DB 4; Length 423;
Best Local Similarity 39.1%; Pred. No. 0.55;
Matches 18; Conservative 5; Mismatches 9; Gaps 3;

QY 2 CGPGRLL-----LGTGTDARC--CRVHTTRCCRDYPGEECCSEWDC 40
      |||| | | | | | | | | | | | | | | | | | | | |
Db 52 CGPGMELSKCGFGYGEDAQCVACRLH--RPKEDWGFKCKPCLDC 95

RESULT 10
Q9NS68
ID Q9NS68 PRELIMINARY; PRT; 423 AA.
AC Q9NS68
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE HTROY.
GN HTROY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20347167; PubMed-10764796;
RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Senba E., Kitamura T.;
RT "TROY, a newly identified member of the tumor necrosis factor receptor
RT superfamily, exhibits a homology with Edar and is expressed in
RT embryonic skin and hair follicles.";
RL J. Biol. Chem. 275:20742-20747(2000).
DR EMBL: AB040434; BAB03269.1; -
DR InterPro: IPR001368; -
DR PFam: PF00020; TNFR_C6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
DR SEQUENCE 423 AA; 46015 MW; B5891CEA9ED45361 CRC64;

Query Match      25.7%; Score 65.5; DB 4; Length 423;
Best Local Similarity 39.1%; Pred. No. 0.55;
Matches 18; Conservative 5; Mismatches 9; Gaps 3;

QY 2 CGPGRLL-----LGTGTDARC--CRVHTTRCCRDYPGEECCSEWDC 40
      |||| | | | | | | | | | | | | | | | | | | | |
Db 52 CGPGMELSKCGFGYGEDAQCVACRLH--RPKEDWGFKCKPCLDC 95

RESULT 11
Q22631
ID Q22631 PRELIMINARY; PRT; 788 AA.
AC Q22631
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE T21B6.3 PROTEIN.
GN T21B6.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX Cottage A.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

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```

RX MEDLINE-94150718; PubMed-7906398;
RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
DR EMBL: Z68011; CAA92014.1; -
DR InterPro: IPR000884; -
DR InterPro: IPR002965; -
DR InterPro: IPR003609; -
DR PFam: PF00090; tsp_1; 6.
DR PRINTS; PR01217; PRICHEXTENS.
DR SMART; SM00473; PAN_AP; 1.
SQ SEQUENCE 788 AA; 88727 MW; BB0DD9F1D29BD961 CRC64;

Query Match      25.3%; Score 64.5; DB 5; Length 788;
Best Local Similarity 39.6%; Pred. No. 1.3;
Matches 19; Conservative 4; Mismatches 10; Indels 15; Gaps 5;

QY 2 CGPG-----RLILG-TGTDARCCR---VHTTRCCRDYPGEECC--SEW 38
      |||| | | | | | | | | | | | | | | | | | | | |
Db 667 CGPGQRTTRGCLGPNQGEATTQGPSIETLIC----EQGCCCNWSEW 710

RESULT 12
Q22048
ID Q22048 PRELIMINARY; PRT; 164 AA.
AC Q22048
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE T01B7.8 PROTEIN.
GN T01B7.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Sims M.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-94150718; PubMed-7906398;
RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
DR EMBL: Z66499; CAA91301.1; -
DR InterPro: IPR000561; -
DR InterPro: IPR001007; -
DR InterPro: IPR001271; -
DR InterPro: IPR001450; -
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS00269; DEFENSIN; UNKNOWN_1.

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RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEN;
RX MEDLINE=97322352; PubMed=9177197;
RA Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,
RA Moraca R., Migliorati G., Riccardi C.;
RT "A new member of the tumor necrosis factor/nerve growth factor
RT receptor family inhibits T cell receptor-induced apoptosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
RA Migliorati G., Riccardi C.;
RT "Gene structure and chromosomal assignment of GTR, a mouse member of
RT the tumor necrosis factor/nerve growth factor receptor family.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: U82534; AAB81243.1; -.
DR EMBL: AF109216; AAF14231.1; -.
DR MGD: MGI:894675; Tnfrsf18.
DR InterPro: IPR000561; -.
DR SMART: SM00181; EGF; 1.
KW Signal; Receptor.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 228 GLUCOCORTICOID INDUCED TNFR FAMILY
FT RELATED PROTEIN.
SQ SEQUENCE 228 AA; 25334 MW; 50B8C275D9C56259 CRC64;

Query Match 34.3%; Score 87.5; DB 11; Length 228;
Best Local Similarity 36.6%; Pred. No. 0.00037;
Matches 15; Conservative 9; Mismatches 10; Indels 7; Gaps 1;

QY 1 GCGPRLILGTGDARCCRVHTRCCRDYPGECCESEWDCM 41
|||||: |:|: |||: |:|: |:|: |:|: |:|: |:|:
DB 28 GCGPKVQVNGSNNTRCCSLYA-----PGKEDCPKRCI 61

RESULT 7
Q9JKR3 PRELIMINARY; PRT; 294 AA.
ID Q9JKR3
AC Q9JKR3
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GTR-B.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL: AF229432; AAF61566.1; -.
DR InterPro: IPR000561; -.
DR SMART: SM00181; EGF; 1.
SQ SEQUENCE 294 AA; 32658 MW; FE0D4AE6A007BA9A CRC64;

Query Match 34.3%; Score 87.5; DB 11; Length 294;
Best Local Similarity 36.6%; Pred. No. 0.00046;
Matches 15; Conservative 9; Mismatches 10; Indels 7; Gaps 1;

QY 1 GCGPRLILGTGDARCCRVHTRCCRDYPGECCESEWDCM 41
|||||: |:|: |||: |:|: |:|: |:|: |:|: |:|:
DB 28 GCGPKVQVNGSNNTRCCSLYA-----PGKEDCPKRCI 61

RESULT 8

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004507
ID 004507 PRELIMINARY; PRT; 416 AA.
AC 004507;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE SIMILARITY TO DIANTHUS CYSTEINE PROTEINASE.
GN F21MI2.24.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV COLUMBIA;
RA Vysotskaia V.S., Osborne B.I., Toriumi M., Yu G., Oji O., Shen Y.K.,
RA Araujo R., Au M., Buehler E., Conway A.B., Conway A.R., Dewar K.,
RA Feng J., Kim C., Kurtz D., Li Y., Shinn P., Sun H., Davis R.W.,
RA Ecker J.R., Federspiel N.A., Theologis A.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC000132; AAB60738.1; -.
DR HSP; P07711; ICJL.
DR Mendel; 15355; Arath; I134; I5355.
DR InterPro: IPR000118; -.
DR InterPro: IPR000169; -.
DR InterPro: IPR000668; -.
DR InterPro: IPR000834; -.
DR InterPro: IPR002086; -.
DR Pfam: PF00112; Peptidase_C1; 1.
DR Pfam: PF00396; granulin; 1.
DR PRINTS; PR00705; PAPAIN.
DR PROSITE; PS00070; ALDEHYDE DEHYD. CYS; UNKNOWN_1.
DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
DR PROSITE; PS00640; THIOL_PROTEASE_ASH; 1.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
DR SMART; SM00277; GRAN; 1.
KW Hydrolase; Thiol protease.
SQ SEQUENCE 416 AA; 45684 MW; 15BCB47F5430F922 CRC64;

Query Match 25.9%; Score 66; DB 10; Length 416;
Best Local Similarity 35.3%; Pred. No. 0.47;
Matches 12; Conservative 4; Mismatches 16; Indels 2; Gaps 1;

QY 2 CGPGRLLILGTGDARCCRVHTRCCRDYPGEECC 35
| | | | | : | | : | | : | | | | |
DB 367 CCCARELFLGCLFSWKCEIESAVCKD--GRHCC 398

RESULT 9
Q9NZV2 PRELIMINARY; PRT; 423 AA.
ID Q9NZV2
AC Q9NZV2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE TAJ-ALPHA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20270246; PubMed=10809768;
RA Eby M.T., Jasmijn A., Kumar A., Sharma K., Chaudhary P.M.;
RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-
RT Independent Cell Death.";
RL J. Biol. Chem. 275:15336-15342(2000).
DR EMBL: AF167555; AAF71828.1; -.
DR InterPro: IPR001368; -.

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Search completed: September 4, 2001, 16:14:32  
Job time: 1219 sec

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DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE	GASC-1 PROTEIN.
GN	GASC-1.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX	NCBI_TaxID=9606;
[1]	RN
RP	SEQUENCE FROM N.A.
FX	MEDLINE=20441562; PubMed=10987278;
RA	Yang Z., Imoto I., Fukuda Y., Pimkhaokham A., Shimada Y., Imamura M.,
RA	Sugano S., Nakamura Y., Inazawa J.;
RT	"Identification of a Novel Gene, GASC1, within an Amplicon at 9p23-24"
RT	Frequently Detected in Esophageal Cancer Cell Lines.";
RL	Cancer Res. 60:4735-4739(2000).
DR	EMBL; AB037901; BAB16102.1;-;
DQ	SEQUENCE 1056 AA; 120023 MW; 8FC6A8BBBC458F8F1 CRC64;
Query Match            24.3%; Score 62; DB 4; Length 1056;	
Best Local Similarity   37.2%; Pred.No. 3.6;	
Matches 16; Conservative   2; Mismatches 17; Indels 8; Gaps	
QY	4 PGRLLGTGTD-----ARCC-RVHTTRCCRDYPGECECSWDC 40           :           :
DB	703 PNAFLLEDGTSLLISCAKCCVRVHAS--CYGIPSHETCDGWLC 743           :           :
RESULT 15	
ID	O94877 PRELIMINARY; PRT; 1100 AA.
AC	O94877;
DT	01-MAY-1999 (TrEMBLrel. 10, Created)
DT	01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE	KIAA00780 PROTEIN (FRAGMENT).
GN	KIAA00780.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX	NCBI_TaxID=9606;
[1]	RN
RP	SEQUENCE FROM N.A.
RC	TISSUP-BRAIN;
RX	MEDLINE=99087487; PubMed=9872452;
RA	Nagase T., Ishikawa K., Suyama M., Kikuno R., Miyajima N., Tanaka A.,
RA	Kotani H., Nomura N., Ohara O.;
RT	"Prediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
RL	DNA Res. 5:277-286(1998).
DR	EMBL; AB018323; BAA34500.1; -;
DR	InterPro; IPR002999; -;
DR	InterPro; IPR003347; -;
DR	InterPro; IPR003349; -;
DR	Pfam; PF02373; jmjC; 1.
DR	Pfam; PF02375; jmjN; 1.
DR	SMART; SM00333; TUDOR; 1.
FT	NON_TER 1
SQ	SEQUENCE 1100 AA; 123998 MW; 2651BC5D5DFCF9B5 CRC64;
Query Match            24.3%; Score 62; DB 4; Length 1100;	
Best Local Similarity   37.2%; Pred.No. 3.7;	
Matches 16; Conservative   2; Mismatches 17; Indels 8; Gaps	
QY	4 PGRLLGTGTD-----ARCC-RVHTTRCCRDYPGECECSWDC 40           :           :
DB	756 PNAFLLEDGTSLLISCAKCCVRVHAS--CYGIPSHETCDGWLC 796           :           :

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RESULT 2
Q9Y5U5 ID Q9Y5U5 PRELIMINARY; PRT; 241 AA.
AC Q9Y5U5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
GN TNFRSF18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,
RA Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,
RA Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;
RT "Identification of a new member of the tumor necrosis factor family
RT and its receptor, a human ortholog of mouse GTR.";
RL Curr. Biol. 0:0-0(1999);
DR EMBL; AF125304; AAD22635.1; -.
DR InterPro; IPR001369; -.
DR SMART; SM00208; TNFR; 1.
SQ SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7B82CBE CRC64;

Query Match 100.0%; Score 753; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. NO. 1.2e-77;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLGTGTDCRCRVHTTCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTCRHH 60
DB 33 GCGPGRLLGTGTDCRCRVHTTCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTCRHH 92
QY 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCWPWTDC 120
DB 93 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCWPWTDC 152
QY 121 CV 122
DB 153 CV 154

RESULT 3
Q9NYJ9 ID Q9NYJ9 PRELIMINARY; PRT; 255 AA.
AC Q9NYJ9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE GTR-D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Bartoli A., Ronchetti S., Mastrodicasa E., Ricciardi C.;
RA "Identification of a soluble human GTR splicing (hGTR-D).";
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF241229; AAF63506.1; -.
SQ SEQUENCE 255 AA; 26827 MW; C986652AC97AF2CC CRC64;

Query Match 85.3%; Score 642; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. NO. 4.5e-65;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 GCGPGRLLGTGTDCRCRVHTTCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTCRHH 60
DB 33 GCGPGRLLGTGTDCRCRVHTTCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTCRHH 92
QY 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCWPWTDC 102
DB 93 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCWPWTDC 134

RESULT 4
Q9JKR2 ID Q9JKR2 PRELIMINARY; PRT; 222 AA.
AC Q9JKR2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GTR-C.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Ricciardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229433; AAF61567.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 222 AA; 24450 MW; 594932BA425A79CA CRC64;

Query Match 59.2%; Score 445.5; DB 11; Length 222;
Best Local Similarity 57.4%; Pred. NO. 6.9e-43;
Matches 70; Conservative 21; Mismatches 24; Indels 7; Gaps 1;

QY 1 GCGPGRLLGTGTDCRCRVHTTCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTCRHH 60
DB 28 GCGPGRLLGTGTDCRCRVHTTCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTCRHH 80
QY 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCWPWTDC 120
DB 81 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCWPWTDC 140
QY 121 CV 122
DB 141 CV 142

RESULT 5
Q35714 ID Q35714 PRELIMINARY; PRT; 228 AA.
AC Q35714;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.
GN TNFRSF18 OR GTR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEN;
RX MEDLINE=97322352; PubMed=9177197;
RA Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,
RA Moraca R., Migliorati G., Ricciardi C.;
RT "A new member of the tumor necrosis factor/nerve growth factor
RT receptor family inhibits T cell receptor-induced apoptosis.";
```



Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	753	100.0	234	4	Q95851		Q95851 homo sapien
2	753	100.0	241	4	Q9Y5U5		Q9Y5U5 homo sapien
3	642	85.3	255	4	Q9NYJ9		Q9NYJ9 homo sapien
4	445.5	59.2	222	11	Q9JKR2		Q9JKR2 mus musculus
5	445.5	59.2	228	11	Q35714		Q35714 mus musculus
6	445.5	59.2	294	11	Q9JKR3		Q9JKR3 mus musculus
7	332.5	44.2	132	11	Q9JKR1		Q9JKR1 mus musculus
8	152.5	20.3	267	6	Q02764		Q02764 oryctolagus
9	145	19.3	300	4	Q95407		Q95407 homo sapien
10	140	18.6	401	11	Q08727		Q08727 rattus norv
11	139	18.5	276	13	Q9DD52		Q9DD52 gallus gall
12	139	18.5	401	11	Q08712		Q08712 mus musculus
13	133	17.7	372	4	Q9UHP4		Q9UHP4 homo sapien
14	133	17.7	401	4	Q00300		Q00300 homo sapien
15	128.5	17.1	655	4	Q75509		Q75509 homo sapien
16	122.5	16.3	685	11	Q9EP05		Q9EP05 mus musculus
17	122	16.2	107	11	Q9JKR0		Q9JKR0 rattus norv
18	121	16.1	616	4	Q9Y606		Q9Y606 homo sapien
19	121	16.1	625	11	Q35305		Q35305 mus musculus

DR HSP; P25942; 1CDF.  
DR InterPro: IPR000561; -;  
DR InterPro: IPR001368; -;  
DR Pfam: PF000020; TNFR\_C6; 4.  
DR ProDom: PD000771; -; 1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
KW Receptor.  
SQ SEQUENCE 300 AA; 32679 MW; F90AEE33718449AF CRC64;

Query Match 19.3%; Score 145; DB 4; Length 300;  
Best Local Similarity 27.7%; Pred. No. 9.2e-09;  
Matches 41; Conservative 12; Mismatches 61; Indels 34; Gaps

QY 2 CGRGLLLGTGDARCCRVHITTCRRDYPCEECSEWDCM--CVQPEFHCGD-----PC 53  
| | | | | : | | | | | : | | | |  
Db 52 CPPGTFFV-----ORPCRDSPTTGCPPRHVTQFMNLYLCRYCNVLCGEREREERAC 105  
| | | | | : | | | | | : | | | |  
QY 54 CTT-----CR-----HHPCPQQGVQSOGKSFQCIDCASGTSGGGHEG- 94  
| | | | | : | | | | | : | | | |  
Db 106 HATHNRACRCRTGEFAHAAGCLSEHASCPPGAGVIAGTPSQNTQCQCPPGTFESASSSS 165  
| | | | | : | | | | | : | | | |  
QY 95 -HCKPWTDCTQFGFLTVFPGNKTHNAV 121  
| | | | | : | | | | | : | | | |  
Db 166 EQCOPHRNCTALGLALNVPGSSSHDTLC 193  
| | | | | : | | | | | : | | | |

RESULT 10  
CO8727 PRELIMINARY; PRT; 401 AA.

ID CO8727 PRELIMINARY; PRT; 401 AA.  
AC CO8727;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE OSTEOPOTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR) (OCIF).  
DE GN  
OS TNFRSF11B OR OPG.  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_Taxid=101116;  
RN [1]  
RS SEQUENCE FROM N.A.  
RP TISSUE=INTESTINE;  
RX MEDLINE=97262071; PubMed=9108485;  
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G. A.  
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trall G., Sullivan J. J.  
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W. C.  
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., Suggs S., Boyle W.J.;  
RT "Osteoprotegerin: a novel secreted protein involved in the regulation of bone density.";  
RL Cell 89:309-319,(1997).

CC CC - FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGE  
CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY  
CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO  
CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN  
CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.  
CC CC SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY  
CC SIMILARITY).  
CC CC SUBCELLULAR LOCATION: EXTRACELLULAR.  
CC CC - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
CC ENMBL; U94330; AAB53707.1; -.  
DR HSP; P25942; 1CDF.  
DR InterPro: IPR000488; -;  
DR InterPro: IPR001368; -;  
DR Pfam; PF000020; TNFR\_C6; 4.  
DR ProDom; PD000771; -; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.

Db	81	PCPQQRVESQGDIVFGRCVACAMGTF	SAGRDGHCRLTNC	SQFGFLTMFP	GNKTHNAV	140
Qy	121	CV	122			
Db	141	CI	142			
RESULT	7					
Q9JKR1						
ID	Q9JKR1	PRELIMINARY;	PRT;	132	AA.	
AC	Q9JKR1					
DT	01-OCT-2000	(TREMBLrel. 15, Created)				
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)				
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)				
GN	GTR-D.					
GN	TNFRSF18.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa;	Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;					
OX	NCBI_TaxID=10090;					
[1]						
RP	SEQUENCE FROM N.A.					
RC	TISSUE=THYMUS;					
RA	Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,					
RA	Migliorati G., Riccardi C.;					
RT	*Identification of three novel mRNA splice variants of GTR.*;					
RL	Cell death differ. 0:0-0(2000).					
DR	EMBL; AF229434; AAF61568.1; -.					
DR	InterPro; IPR000561; -.					
DR	SMART; SM00181; EGF; 1.					
SQ	SEQUENCE 132 AA; 14106 MW; F586A5404BIDFEDE CRC64;					
Query Match	44.28;	Score 332.5;	DB 11;	Length 132;		
Best Local Similarity	52.08;	Pred. NO. 2.7e-30;				
Matches	52;	Conservative 17;	Mismatches 24;	Indels 7;	Gaps	
Qy	1	CGCGPRLLLGTGDARCCRVHTRCCRDYDPGECCSEWDCMCVQPEFHCGDPCQCTTCRHH	60			
Db	28	CGCGPKVQSGNTRCCSLYA-----FGKEDCPKRCICVTPEYHCGDPOCKICKHY	80			
Qy	61	PCPQQRVQSGQKFSFGQCIDCASGTFSGGHEGCHKPWT 100				
Db	81	PCPQQRVESQGDIVFGRCVACAMGTF	SAGRDGHCRLWT 120			
RESULT	8					
O02764						
ID	O02764	PRELIMINARY;	PRT;	267	AA.	
AC	O02764;					
DT	01-JUL-1997	(TREMBLrel. 04, Created)				
DT	01-JUL-1997	(TREMBLrel. 04, Last sequence update)				
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)				
DE	OX40 PRECURSOR (FRAGMENT).					
OC	Oryctolagus cuniculus (Rabbit).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.					
OX	NCBI_TaxID=9986;					
[1]						
RP	SEQUENCE FROM N.A.					
RC	STRAIN=CHBB;HM;					
RA	Isono T., Seto A.;					
RL	Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.					
DR	EMBL; AB003911; BAA20059.1; -.					
DR	HSSP; P19438; TEXT.					
DR	InterPro; IPR001368; -.					
DR	Pfam; PF00020; TNFR_c6; 3.					
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.					
DR	PROSITE; PSS0050; TNFR_NGFR_2; 2.					
DR	SMART; SM00208; TNFR; 1.					
KW	Signal.					
FT	NON_TER					

```
DR SMART: SM00005; DEATH: 1.
KW Glycoprotein; Repeat; Cytokine; Signal.
FT SIGNAL 1 21
FT CHAIN 22 401
FT DOMAIN 23 201
FT REPEAT 23 63
FT REPEAT 23 63
FT REPEAT 64 106
FT REPEAT 107 143
FT REPEAT 144 201
FT DOMAIN 306 365
FT DISULFID 41 54
FT DISULFID 44 62
FT DISULFID 65 80
FT DISULFID 83 97
FT DISULFID 87 105
FT DISULFID 118 142
FT DISULFID 145 160
FT CARBOHYD 98 98
FT CARBOHYD 165 165
FT CARBOHYD 178 178
FT CARBOHYD 289 289
FT VARIANT 138 138
FT VARIANT 161 161
FT VARIANT 161 161
FT VARIANT 165 165
FT VARIANT 288 288
FT VARIANT 296 296
FT VARIANT 296 296
SQ SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;

Query Match 18.5%; Score 139; DB 11; Length 401;
Best Local Similarity 26.4%; Pred. No. 5.6e-08;
Matches 39; Conservative 10; Mismatches 65; Indels 34; Gaps 5;

QY 2 CGPGRLLGTGDARCCRVHTTRCCRDYPGEECCSEW-----DCMCVQP-----EPHC 49
DB 44 CAPGTYL-----KHQTVRRKTLVCPDHSYDTSWHTSDCYVCSVPCKELQSVKQEC 97
QY 50 GDCPCCTTC-----RHHPCPPGGVQSOGKFSFGFCIDCASCTFSG--GHE 93
DB 98 NRTHNRYCEGEGRYLEIEFCLKHRSPPGGVQAGTPERTNTVCKKCPDGFSSNETSS 157
QY 94 GHCKPWTDCQFGFLTVFPNGKTHNAV 121
DB 158 APCIKHTNCSTFGLLLQKGNATHDNC 185

RESULT 13
QYUHP4 PRELIMINARY; PRT; 372 AA.
AC QYUHP4
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE OSTEOPROTEGERIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA He 2.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT "Cloning and Expression of Osteoprotegerin from Homo sapiens.";
RL Sheng Wu Hua Hsueh Yu Sheng Wu Li Hsueh Pao 31:680-684(1999).
DR EMBL: AF134187; AAF20168.1;
DR HSSP: P25942; 1CDF.
DR InterPro: IPR000488;
DR InterPro: IPR001368;

Query Match 17.7%; Score 133; DB 4; Length 372;
Best Local Similarity 24.2%; Pred. No. 2.5e-07;
Matches 36; Conservative 14; Mismatches 51; Indels 48; Gaps 6;

QY 21 HTTRCCRDYPG-----ECCSEWDCMCV-----QPEFHCGRPCC--CT----- 55
DB 16 HQLLCKPPTGTYLKQHKTKWKTCAPCPDHYHSDTSDECLYCSVPCKELQYVKQE 75
QY 56 -----TC-----RHHPCPPGGVQSOGKFSFGFCIDCASCTFSG--GH 92
DB 76 CNRTNRYCEKEGRYLEIEFCLKHRSPPGGVQAGTPERTNTVCKKCPDGFSSNETSS 135
QY 93 BGHCKPWTDCQFGFLTVFPNGKTHNAV 121
DB 136 KAPCRKHTNCSTFGLLLQKGNATHDNC 164

RESULT 14
QYUHP4 PRELIMINARY; PRT; 401 AA.
AC QYUHP4
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
DE (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
GN TNFRSF11B OR OPG OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Farpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
of bone density.";
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG FIBROBLAST;
RA MEDLINE=98151033; Pubmed=9492069;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA Tsuda E., Morinaga T., Higashio K.;
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
osteoclastogenesis in vitro.";
RL Endocrinology 139:1329-1337(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA MEDLINE=98351569; Pubmed=9688283;
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT "Cloning and characterization of the gene encoding human
osteoprotegerin/osteoclastogenesis-inhibitory factor.";
RL Eur. J. Biochem. 254:685-691(1998).
CC CC
-!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
```

DR SMART; SMO0005; DEATH; 1.  
KW Glycoprotein; Repeat; Cytokine; Signal.  
FT SIGNAL 1 21 BY SIMILARITY.  
FT CHAIN 22 401 OSTEOPROTEGERIN.  
FT DOMAIN 23 201 4 X TNFR-CYS.  
FT REPEAT 23 63 TNFR-CYS 1.  
FT REPEAT 64 106 TNFR-CYS 2.  
FT REPEAT 107 143 TNFR-CYS 3.  
FT REPEAT 144 201 TNFR-CYS 4.  
FT DOMAIN 306 365 DEATH DOMAIN.  
FT DISULFID 41 54 BY SIMILARITY.  
FT DISULFID 44 62 BY SIMILARITY.  
FT DISULFID 65 80 BY SIMILARITY.  
FT DISULFID 83 97 BY SIMILARITY.  
FT DISULFID 87 105 BY SIMILARITY.  
FT DISULFID 118 142 BY SIMILARITY.  
FT DISULFID 145 160 BY SIMILARITY.  
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 401 AA; 46192 MW; F6C6A31F1D4E573A CRC64;

Query Match 18.6%; Score 140; DB 11; Length 401;  
Best Local Similarity 28.0%; Pred. No. 4.3e-08;  
Matches 42; Conservative 11; Mismatches 59; Indels 38; Gaps 7;

Qy 2 CGPGRLLGTGDARCCRVHTTRC---CRDY-----PGEE-----CSEWD----- 39  
Db 44 CAPGYTL-----KHQCTVRKRLCVPCPYSYDTSWHTSDECVYCSFVKELQTVKQECN 98  
Qy 40 -----CMCVQPEHFHCGDPCCTTCRHHPGPPGOGVQSGKFSFGFCIDCASGTFSG--G 91  
Db 99 RTHNRVCECEERYLEFC-----LKHRSPPGLGLVQLQAGTPERTVCKRCPDGFSGSETS 155

Qy 92 HGHCCKPMTDCTQFGFLVFPGNKTHNAV 121  
Db 156 SKAPCRKHTNCSSGLLLQKGNATHDNVC 185

RESULT 11  
ID Q9DD2 PRELIMINARY; PRT; 276 AA.  
AC Q9DD2:  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DE HUMAN CD40-HOMOLOGUE.  
GN TNFSF5.  
OC Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tregaskes C.A.;  
RL Thesis (2001); University of Reading, Reading, UNITED KINGDOM.  
DR EMBL; AJ293700; CAC20218.1; -.  
SQ SEQUENCE 276 AA; 30009 MW; 4040B7E0DB82454E CRC64;

Query Match 18.5%; Score 139; DB 13; Length 276;  
Best Local Similarity 26.1%; Pred. No. 4.1e-08;  
Matches 46; Conservative 10; Mismatches 58; Indels 62; Gaps 9;

Qy 7 LLLGTGT--DARCCR---VHTTRCC-RDYPGEECCSE-----WD 39  
Db 13 LLGGCGGDVNCSDKQYEHKGRCCNRCQPKKLASECNDTSDSVCTPCENGQYQHSWT 72  
Qy 40 -----CMCVQPEHFHCGDPCCTTC-RHHPCPGQG-- 67

Db 73 KERHCTPHEICEDNAGLIVKRGHGNATHNTVCQC-RAGMHCSDASCQTCVNEPCKQGRGF 131  
Qy 68 VQSGKFSFGFCIDCASGTFPS--GGHGHCKPWTDTCTQFGFLVFPGNKTHNAV 121  
Db 132 VAAMAEARMTSPCEPCAGTFPSNVSSKTEPCHFWTSCEKGLVVKVKGKTNSTDVIC 187

RESULT 12  
ID O08712 PRELIMINARY; PRT; 401 AA.  
AC O08712: 070202.  
DT 01-JUL-1997 (TREMBlrel. 04, Created)  
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)  
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR) (OCIF).  
GN TNFRSF11B OR OPG.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C; TISSUE=KIDNEY;  
RC MEDLINE=97262071; PubMed=9108485;  
RA Simonet W.S.; Lacey D.L.; Dunstan C.R.; Kelley M.; Chang M.-S.;  
RA Luethy R.; Nguyen H.Q.; Woodson S.; Bennett L.; Boone T.; Shimamoto G.;  
RA Darose M.; Elliott R.; Colombero A.; Tan H.-L.; Trail G.; Sullivan J.;  
RA Davy E.; Bucay N.; Renshaw-Gegg L.; Hughes T.M.; Hill D.; Pattison W.;  
RA Campbell P.; Sander S.; Van G.; Tarpley J.; Derby P.; Lee R.;  
RA Suggs S.; Boyle W.J.;  
RT "Osteoprotegerin: a novel secreted protein involved in the regulation  
of bone density.";  
RL Cell 89:309-319(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/OLA, AND NIH SWISS;  
RC MEDLINE=98382527; PubMed=9714833;  
RA Mizuno A.; Murakami A.; Nakagawa N.; Yasuda H.; Tsuda E.; Morinaga T.;  
RA Higashio K.;  
RT "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)  
gene and its expression in embryogenesis.";  
RL Gene 215:339-343(1998).  
CC -I- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES  
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY  
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO  
OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN  
STROMAL CELLS AND OSTEOCLAST PROGENITORS.  
CC -I- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).  
CC -I- SUBCELLULAR LOCATION: EXTRACELLULAR.  
CC -I- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,  
BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND  
PLACENTA. NOT DETECTED IN SPLEEN.  
CC -I- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT  
DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY  
15 TO DAY 17.  
CC -I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
DR EMBL; U94331; AAB33708.1; -.  
DR EMBL; AB013898; BAA28269.1; -.  
DR EMBL; AB013903; BAA33388.1; -.  
DR EMBL; AB013899; BAA33388.1; JOINED.  
DR EMBL; AB013900; BAA33388.1; JOINED.  
DR EMBL; AB013901; BAA33388.1; JOINED.  
DR EMBL; AB013902; BAA33388.1; JOINED.  
DR HSSP; P25942; 1CDF.  
DR MGD; MGI:109587; Tnfrsf11b.  
DR InterPro; IPR000488; -.  
DR InterPro; IPR001368; -.  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR ProDom; PD000771; -; 1.  
DR PROSITE; PS00017; DEATH\_DOMAIN; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.



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Query Match      17.7%; Score 133; DB 4; Length 401;
Best Local Similarity 24.2%; Pred. NO. 2.7e-07;
Matches 36: Conservative 14; Mismatches 51; Indels 48; Gaps 6;

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RESULT	15
O75509	
ID	075509
AC	075509;
DT	01-NOV-1998
DT	(TREMBlrei). 08, Created)
DT	01-NOV-1998
DT	(TREMBlrei). 08, Last sequence update)
DT	01-MAR-2001
DT	(TREMBlrei). 16, Last annotation update)

Query Match	17.1%;	Score 128.5;	DB 4;	Length 655;
Best Local Similarity	27.3%;	Pred. No. 1.3e-06;		
Matches	39: Conservative	12: Mismatches	57: Indels	35: Gaps

Search completed: September 4, 2001, 16:14:32  
Job time: 1219 sec

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ID Q9Y5U5 PRELIMINARY; PRT; 241 AA.
AC Q9Y5U5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
GN TNFRSF18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,
RA Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,
RA Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;
RT "Identification of a new member of the tumor necrosis factor family
RT and its receptor, a human ortholog of mouse GTR."
RL Curr. Biol. 0:0-0(1999).
DR EMBL: AF125304; AAD22635.1; -.
DR InterPro: IPR001368; -.
DR SMART: SM00208; TNFR: 1.
DR SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7E82CBE CRC64;

Query Match 100.0%; Score 737; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DARCCRVHTTRCCRDYPGECCSEWDCMCVQPEFHCGDPCCCTCRHHPCPPGQVQSOGK 60
DB 46 DARCCRVHTTRCCRDYPGECCSEWDCMCVQPEFHCGDPCCCTCRHHPCPPGQVQSOGK 105
QY 61 FSGFQCIDCASGTFSGGHEGHCXPTDCTQFGTLTVPFGNKTNAVCPGSPPAEPLG 119
DB 106 FSGFQCIDCASGTFSGGHEGHCXPTDCTQFGTLTVPFGNKTNAVCPGSPPAEPLG 164

RESULT 3
Q9NYJ9 PRELIMINARY; PRT; 255 AA.
ID Q9NYJ9;
AC Q9NYJ9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE GTR-D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Bartoli A., Ronchetti S., Mastrodicasa E., Riccardi C.;
RT "Identification of a soluble human GTR splicing (hGTR-D).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF241229; AAF63506.1; -.
DR SEQUENCE 255 AA; 26827 MW; C986652AC97AF2CC CRC64;

Query Match 77.7%; Score 573; DB 4; Length 255;
Best Local Similarity 67.4%; Pred. No. 6.2e-56;
Matches 97; Conservative 2; Mismatches 9; Indels 36; Gaps 2;

QY 1 DARCCRVHTTRCCRDYPGECCSEWDCMCVQPEFHCGDPCCCTCRHHPCPPGQVQSOGK 60
DB 46 DARCCRVHTTRCCRDYPGECCSEWDCMCVQPEFHCGDPCCCTCRHHPCPPGQVQSOGK 105
QY 61 FSGFQCIDCASGTFSGGHEGHCXPTDCTQFGTLTVPFGNKTNAVCPGSPPAEPLG 119
DB 106 FSGFQCIDCASGTFSGGHEGHCXPTDCTQFGTLTVPFGNKTNAVCPGSPPAEPLG 165

us-09-512-363-2_copy_46_164.rspt
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QY 94 FLTVPFGNKTNAVCPGSPPAEP 117
DB 166 WET-----CGCEPGRPPGPP 180

RESULT 4
Q9JKR2 PRELIMINARY; PRT; 222 AA.
ID Q9JKR2;
AC Q9JKR2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GTR-C.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL: AF229433; AAF61567.1; -.
DR InterPro: IPR000561; -.
DR SMART: SM00181; EGF: 1.
DR SEQUENCE 222 AA; 24450 MW; 594932BA425A79CA CRC64;

Query Match 57.7%; Score 425.5; DB 11; Length 222;
Best Local Similarity 61.1%; Pred. No. 1.2e-39;
Matches 69; Conservative 16; Mismatches 27; Indels 1; Gaps 1;

QY 8 HTTRCCRDY-PGECCSEWDCMCVQPEFHCGDPCCCTCRHHPCPPGQVQSOGKFSFGQ 66
DB 40 NNTRCCSLYAPGKDCPKERCICVTPEYHCGDPQCKICKHYPCQQRVESQGDIVGFR 99
QY 67 CIDCASGTFSGGHEGHCXPTDCTQFGTLTVPFGNKTNAVCPGSPPAEPLG 119
DB 100 CVACAMGTFSGAGDHGCHRLWNTNCSQFGFLTMFGNKTNAVCIPEPLPTEQVG 152

RESULT 5
Q35714 PRELIMINARY; PRT; 228 AA.
ID Q35714;
AC Q35714;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.
GN TNFRSF18 OR GTR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEN;
RX MEDLINE=97322352; PubMed=9177197;
RA Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,
RA Moraca R., Migliorati G., Riccardi C.;
RT "A new member of the tumor necrosis factor/nerve growth factor
RT receptor family inhibits T cell receptor-induced apoptosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
RA Migliorati G., Riccardi C.;
RT "Gene structure and chromosomal assignment of GTR, a mouse member of
RT the tumor necrosis factor/nerve growth factor receptor family.";
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2001, 16:14:31 ; Search time 133.1 Seconds  
(without alignments)  
118.289 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_46\_164

Perfect score: 737

Sequence: 1 DARCCRVHTTRCCRDYPGEE.....GNKTHNAVVCVPGSPAEPLG 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_16:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_unclassified:\*
- 13: sp\_vertebrate:\*
- 14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	737	100.0	234	4	O95851
2	737	100.0	241	4	O9Y5U5
3	573	77.7	255	4	O9NYJ9
4	425.5	57.7	222	11	O9JKR2
5	425.5	57.7	228	11	O35714
6	425.5	57.7	294	11	O9JKR3
7	295.5	40.1	132	11	O9JKR1
8	147.5	20.0	267	6	O02764
9	145	19.7	300	4	O95407
10	137	18.6	372	4	O9UHP4
11	137	18.6	401	4	O00300
12	131	17.8	401	11	O08712
13	131	17.8	616	4	O9Y6Q6
14	130.5	17.7	401	11	O08727
15	130	17.6	276	13	O9DDD2
16	128	17.4	655	4	O75509
17	123	16.7	625	11	O35305
18	122	16.6	107	11	O9JKE0
19	120.5	16.4	459	11	O62327

20	120.5	16.4	482	11	O88734
21	120	16.3	655	11	O9EP05
22	117	15.9	439	4	Q16042
23	116	15.7	302	13	O9PUS0
24	110	14.9	1371	11	O9QVW4
25	108	14.7	1574	11	O88281
26	107	14.5	4601	5	O9V383
27	101.5	13.8	1537	5	O9VAI2
28	100.5	13.6	126	10	O9S9F4
29	99	13.4	1764	11	O35806
30	99	13.4	1833	11	O08999
31	98.5	13.4	351	14	O57117
32	97.5	13.2	176	14	O68396
33	97.5	13.2	176	14	O9PZQ7
34	97.5	13.2	176	14	O9PX59
35	97.5	13.2	176	14	O9PX08
36	97	13.2	1637	6	O9XSU8
37	97	13.2	2319	11	O9RI72
38	96.5	13.1	176	14	O9PZR9
39	96.5	13.1	176	14	O9PZR8
40	96.5	13.1	176	14	O9PWX6
41	96.5	13.1	757	5	O9VZF2
42	96	13.0	1308	5	O9GPN8
43	96	13.0	1792	13	O57484
44	95.5	13.0	814	11	O9QYL2
45	95.5	13.0	851	13	O42507

#### ALIGNMENTS

RESULT 1

ID O95851 PRELIMINARY; PRT; 234 AA.  
AC O95851;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99156876; PubMed=10037686;  
RA Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L.,  
RA Liu D., Wang S.X., Kwon B.S.;  
RT "Identification of a novel activation-inducible protein of the tumor  
RT necrosis factor receptor superfamily and its ligand.";  
RL J. Biol. Chem. 274:6056-6061(1999).  
DR EMBL; AF117297; AAD19694.1; -  
DR InterPro; IPR001368; -  
DR SMART; SM00208; TNFR; 1.  
KW Receptor.  
SQ SEQUENCE 234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;

Query Match 100.0%; Score 737; DB 4; Length 234;

Best Local Similarity 100.0%; Pred. No. 3.9e-74;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHC	GDPCCTTTRHHPCPPGQVQSGK 60
DB	46	DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHC	GDPCCTTTRHHPCPPGQVQSGK 105
QY	61	FSFGQCIDCASGTFSGSGHEGCHKPWT	DCTQFGFLTVPFGNKTNAVCPGSPAEPLG 119
DB	106	FSFGQCIDCASGTFSGSGHEGCHKPWT	DCTQFGFLTVPFGNKTNAVCPGSPAEPLG 164

RESULT 2

O9Y5U5



GN	TNFRSFL8.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=THYMUS;
RA	Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA	Migliorati G., Ricciardi C.;
RT	"Identification of three novel mRNA splice variants of GTR.";
RL	Cell Death Differ. 0:0-0(2000).
DR	EMBL; AF229434; AAF61568.1; -;
DR	InterPro; IPR000561; -;
DR	SMART; SM00181; EGF; 1.
SQ	SEQUENCE 132 AA; 14106 MW; F586A5404BDFEDE CRC64;
Query Match	40.1%; Score 295.5; DB 11; Length 132;
Best Local Similarity	58.0%; Pred. No. 1.9e-25;
Matches	47; Conservative 12; Mismatches 21; Indels 1; Gaps 1;
Qy	8 HTTCCRDY-PGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPGPGVOSQKFSFGQ 66
Db	40 NNTCCSLYAPGKEDPKERCICITPEYHCGDPQCKICKHYPCQPGQGVESQGDIVFGR 99
Qy	.67 CIDCASGTFSGHGCHCKPWT 87
Db	100 CVACAMGTFSGRGGHRLWT 120
RESULT	8
002764	PRELIMINARY; PRT; 267 AA.
AC	002764
DT	01-JUL-1997 (TrEMBLrel. 04, Created)
DT	01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE	OX40 PRECURSOR (FRAGMENT).
OS	Oryctolagus cuniculus (Rabbit).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX	NCBI_TaxID=9986;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	SRAIN-CHBB.HM;
RA	Isono T., Seto A.;
RL	Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AB003911; BAA20059.1; -;
DR	HSP; P19438; 1EXT.
DR	InterPro; IPR001368; -;
DR	Pfam; PF00020; TNFR_c6; 3.
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.
DR	PROSITE; PS50050; TNFR_NGFR_2; 2.
DR	SMART; SM00208; TNFR; 1.
KW	Signal.
FT	NON_TER 1 1
FT	SIGNAL <1 18 POTENTIAL.
FT	CHAIN 19 267 OX40.
SQ	SEQUENCE 267 AA; 28489 MW; A8B4CD3173C9500B CRC64;
Query Match	20.0%; Score 147.5; DB 6; Length 267;
Best Local Similarity	25.8%; Pred. No. 8.7e-09;
Matches	41; Conservative 11; Mismatches 48; Indels 59; Gaps 6;
Qy	12 CCRD-YPECCSEWDCMCVQPEF---HCGDPCCTTCRHHPCPG----- 52
Db	25 CVGDTYGGDR-----CLECPGGMVSRNCRSODTIC--HPCEPGFYNAVYQACKPC 78
Qy	53 -----OGVOSQKFSFGQICDASGTFSGHGHCCKPW 86
Db	79 TONRRSGSEPOOEFTTTRDTVCRCRGTOPLNGYKGVDCAPCPGCHFSFGNNRACRPW 138



OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=KIDNEY;  
 RX MEDLINE=97262071; PubMed=9108485;  
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
 RA Luehry R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,  
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trill G., Sullivan J.,  
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,  
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
 RA Suggs S., Boyle W.J.;  
 FT "Osteoprotegerin: a novel secreted protein involved in the regulation  
 RT of bone density.";  
 RL Cell 89:309-319(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LUNG FIBROBLAST;  
 RX MEDLINE=98151033; PubMed=9492069;  
 RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,  
 RA Sato Y., Goto M., Yanaguchi K., Kuriyama M., Kanno T., Murakami A.,  
 RA Tsuda E., Morinaga T., Higashio K.;  
 FT "Identity of osteoclastogenesis inhibitory factor (OCIF) and  
 RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits  
 RT osteoclastogenesis in vitro.";  
 RL Endocrinology 139:1329-1337(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PLACENTA;  
 RX MEDLINE=98351569; PubMed=9688283;  
 RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;  
 FT "Cloning and characterization of the gene encoding human  
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";  
 RL Eur. J. Biochem. 254:685-691(1998).  
 CC -!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES  
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY  
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO  
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN  
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.  
 CC -!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY  
 CC SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,  
 CC KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN  
 CC A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED IN  
 CC THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.  
 CC -!- SIMILARITY: CONTAINS A LA-NGER/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL; AB002146; BAA25910.1; -;  
 DR EMBL; AB008822; BAA32076.1; -;  
 DR EMBL; AB008821; BAA32076.1; JOINED.  
 DR EMBL; U94332; AAB53709.1; -;  
 DR HSP; P25942; ICDP.  
 DR MIM; 602643; -;  
 DR InterPro; IPR000488; -;  
 DR InterPro; IPR001368; -;  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR ProDom; PD000771; -; 1.  
 DR ProSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
 DR ProSITE; PS00050; TNFR\_NGFR\_2; 2.  
 DR SMART; SM00005; DEATH; 1.  
 KW Glycoprotein; Repeat; Cytokine; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 401  
 FT DOMAIN 23 183  
 FT REPEAT 23 63  
 FT REPEAT 64 106  
 FT REPEAT 107 143  
 FT REPEAT 144 201  
 FT REPEAT 306 365  
 FT DOMAIN 41 54  
 FT DISULFID 44 62  
 FT DISULFID 65 80  
 FT DISULFID 83 97  
 FT DISULFID 87 105

FT DISULFID 118 142  
 FT DISULFID 145 160  
 FT CARBOHYD 98  
 FT CARBOHYD 152 152  
 FT CARBOHYD 165 165  
 FT CARBOHYD 178 178  
 FT CARBOHYD 289 289  
 FT CONFLICT 263 263  
 SQ SEQUENCE 401 AA; 45996 MW; EB42FA51C9D7C71E CRC64;  
 Query Match 18.68; Score 137; DB 4; Length 401;  
 Best Local Similarity 23.8%; Pred. No. 1.8e-07;  
 Matches 38; Conservative 15; Mismatches 59; Indels 48; Gaps 6;  
 QY 8 HTTCCRDYPG-----EECCSEWDCMV-----QPEFHGDCPC--CT----- 42  
 DB 37 HQLLCKDCKPPGTYLKQCTAKWTKVACPCPDHYTDSWHTSDECLYCSPVCKELQYVQKE 96  
 QY 43 -----TC-----RRHPCPPGQGGVQSGKFSFGQICDASGTFSG--GH 79  
 DB 97 CNRTHNRVCECKEGRYLEIEFCLHRSCPPGFGVVGAGTPERTVTKRCPDGFSENETSS 156  
 QY 80 EGHCKPMTDCTQFGFLTVFPGNKTHNAVCPGSPPAEPLG 119  
 DB 157 KAPCRKHTNCVSFGLLLTKQGNATHDNICSGNSESTOKCG 196  
 RESULT 12  
 O08712 PRELIMINARY; PRT; 401 AA.  
 AC O08712; O70202;  
 DT 01-JUL-1997 (T-EMBLrel. 04, Created)  
 DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)  
 DT 01-MAR-2001 (T-EMBLrel. 16, Last annotation update)  
 DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)  
 DE (OCIF).  
 GN TNFRSF11B OR OPG.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=KIDNEY;  
 RX MEDLINE=97262071; PubMed=9108485;  
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
 RA Luehry R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,  
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trill G., Sullivan J.,  
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,  
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
 RA Suggs S., Boyle W.J.;  
 RT "Osteoprotegerin: a novel secreted protein involved in the regulation  
 RT of bone density.";  
 RL Cell 89:309-319(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/OLA, AND NIH SWISS;  
 RX MEDLINE=98382527; PubMed=9714833;  
 RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,  
 RA Higashio K.;  
 FT "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)  
 RT gene and its expression in embryogenesis.";  
 RL Gene 215:1339-1343(1998).  
 CC -!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES  
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY  
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO  
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN  
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.  
 CC -!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).  
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,  
 CC BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND



RESULT	14
008727	
ID	008727 PRELIMINARY; PRT; 401 AA.
AC	008727;
DT	01-JUL-1997 (Tremblrel_04, Created)
DT	01-JUL-1997 (Tremblrel_04, Last sequence update)
DT	01-MAR-2001 (Tremblrel_16, Last annotation update)
DE	OSTEOPTERGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR) (OCIF).
DE	GN TNFRSF11B OR OPG.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=101116;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=INTESTINE;
RC	MEDLINE=97262071; PubMed=9108485;
RA	Lumet M.W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA	Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA	Derosé M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA	Davy E., Bucay N., Renshaw-Clegg L., Hughes T.M., Pattison W.,
RA	Campbell P., Sander S., Van G.G., Tarpley J.J., Derby P., Lee R.,
RA	Suggs S., Boyle W.J.;
RT	"Osteoprotegerin: a novel secreted protein involved in the regulation
RL	of bone density.";
RL	Cell 89:309-319(1997).
CC	-1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
CC	OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
CC	SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
CC	OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
CC	STROMAL CELLS AND OSTEOCLAST PROGENITORS.
CC	-1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
CC	SIMILARITY).
CC	-1- SUBCELLULAR LOCATION: EXTRACELLULAR.
DR	EMBL: U94330; AAB53707.1; -
DR	HSP; P25942; ICDF.
DR	InterPro: IPR000488; -
DR	InterPro: IPR001368; -
DR	Pfam: PF00020; TNFR_c6; 4.
DR	ProDom: PD000771; -; 1.
DR	PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR	PROSITE: PS00050; TNFR_NGFR_2; 2.
DR	SMART: SM00005; DEATH; 1.
KW	Glycoprotein; Repeat; Cytokine; Signal.
FT	SIGNAL 1 21 BY SIMILARITY.
FT	CHAIN 22 401 OSTEOPTERGERIN.
FT	DOMAIN 23 201 4 X TNFR-CYS.
FT	REPEAT 23 63 TNFR-CYS 1.
FT	REPEAT 64 106 TNFR-CYS 2.
FT	REPEAT 107 143 TNFR-CYS 3.
FT	REPEAT 144 201 TNFR-CYS 4.
FT	DOMAIN 306 365 DEATH DOMAIN.
FT	DISULFID 41 54 BY SIMILARITY.
FT	DISULFID 44 62 BY SIMILARITY.
FT	DISULFID 65 80 BY SIMILARITY.
FT	DISULFID 83 97 BY SIMILARITY.
FT	DISULFID 87 105 BY SIMILARITY.
FT	DISULFID 118 142 BY SIMILARITY.
FT	DISULFID 145 160 BY SIMILARITY.
FT	CARBOHYD 98 98 N-LINKED (GLCNAC... ) (POTENTIAL).
FT	CARBOHYD 165 165 N-LINKED (GLCNAC... ) (POTENTIAL).
FT	CARBOHYD 178 178 N-LINKED (GLCNAC... ) (POTENTIAL).
FT	CARBOHYD 289 289 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ	SEQUENCE 401 AA; 46192 MW; FEC6A31FD4E573A CRC64;

Best Local Similarity	75.1%	Freq. NO. 35-76,
Matches 142;	Conservative	2; Mismatches 9; Indels 36; Gaps 2;



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:14:33 ; Search time 133.1 Seconds  
(without alignments)  
163.020 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_1\_164

Perfect score: 979

Sequence: 1 MAQHGMGAFRALCGLLALC.....GNKTHNAVCPGSPPAEPLG 164

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_16:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phase:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_unclassified:\*

13: sp\_vertebrate:\*

14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	979	100.0	234	4	O95851
2	979	100.0	241	4	O9Y5U5
3	815	83.2	255	4	O9NYJ9
4	510	52.1	222	11	O9JKR2
5	510	52.1	228	11	O35714
6	510	52.1	224	11	O9JKR3
7	380	38.8	132	11	O9JKR1
8	171.5	17.5	267	6	O02764
9	154.5	15.8	276	13	O9DDD2
10	153	15.6	300	4	O95407
11	141.5	14.5	401	11	O08727
12	139.5	14.2	401	11	O08712
13	138.5	14.1	616	4	O9Y6Q6
14	137	14.0	372	4	O9UHP4
15	137	14.0	401	4	O00300
16	129.5	13.2	655	4	O75509
17	125	12.8	655	11	O9EP05
18	123	12.6	625	11	O35305
19	122	12.5	107	11	O9JKE0

20	121	12.4	302	13	O9PUS0
21	120.5	12.3	459	11	O62327
22	120.5	12.3	482	11	O88734
23	119	12.2	439	4	O16042
24	117.5	12.0	1587	4	O00508
25	116.5	11.9	1511	4	O75412
26	115.5	11.8	1371	11	O9QVW4
27	114.5	11.7	2906	11	O9WUH9
28	112	11.4	152	5	O9XVX3
29	112	11.4	1637	6	O9XSV8
30	111.5	11.4	1764	11	O35806
31	111	11.3	1111	5	O9XWD6
32	111	11.3	1792	13	O57484
33	110.5	11.3	1687	11	O61204
34	110	11.2	1522	5	O22685
35	110	11.2	1698	5	O94438
36	109.5	11.2	164	5	O22048
37	109.5	11.2	4601	5	O9V383
38	109	11.1	1574	11	O88281
39	107.5	11.0	1833	11	O08999
40	107	10.9	1308	5	O9GPM8
41	107	10.9	3680	5	O9VR08
42	106.5	10.9	870	6	O02660
43	105	10.7	188	5	O18238
44	105	10.7	2009	5	O9VXM0
45	105	10.7	2319	11	O9R172

## ALIGNMENTS

RESULT 1

O95851  
ID O95851 PRELIMINARY; PRT; 234 AA.  
AC O95851;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99156876; PubMed=10037686;  
RA KWON B., YU K.Y., NI J., YU G.L., JANG I.K., KIM Y.J., XING L.,  
RA LIU D., WANG S.X., KWON B.S.;  
RT "Identification of a novel activation-inducible protein of the tumor  
RT necrosis factor receptor superfamily and its ligand."  
RL J. Biol. Chem. 274:6056-6061(1999).  
DR EMBL; AF117297; AAD19694.1; -  
DR InterPro; IPR001368; -  
DR SMART; SM00208; TNFR; 1.  
KW Receptor.  
SQ SEQUENCE 234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;

Query Match 100.0%; Score 979; DB 4; Length 234;

Best Local Similarity 100.0%; Pred. No. 2.8e-95;

Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMGAFRALCGLLALCALSGLQRPPTGGCGPGRLLLTGTDTARCCRVHTTCCRD 60  
DB 1 MAQHGMGAFRALCGLLALCALSGLQRPPTGGCGPGRLLLTGTDTARCCRVHTTCCRD 60  
QY 61 YGEECCSEWDCMCVQPEHFCGDPCCCTTCRHPPCPGQVQSGKFSFGQICDASGTF 120  
DB 61 YGEECCSEWDCMCVQPEHFCGDPCCCTTCRHPPCPGQVQSGKFSFGQICDASGTF 120  
QY 121 SGGHGHCKPWTDCQFGFLTVPFGNKNTHNAVCPGSPPAEPLG 164  
DB 121 SGGHGHCKPWTDCQFGFLTVPFGNKNTHNAVCPGSPPAEPLG 164

RC	STRAIN=CHBB:HM;
RL	Isono T., Seto A.;
RR	Submitted (MAY-1997) to the EMBL/GenBank/DDBB databases.
RA	EMBL; AB003911; BAA20059.1; -
DR	HSSP; P19438; 1EXT.
DR	InterPro; IPR001368; -. 1.
DR	Fram; PF00020; TNFR_C6; 3.
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.
DR	PROSITE; PS50050; TNFR_NGFR_2; 2.
DR	SMART; SM00208; TNFR; 1.
KW	Signal.
FT	1
FT	NON_TER
FT	SIGNAL
FT	<1
FT	CHAIN
FT	19
FT	267
SO	SOURCE
SO	267 AA; 28489 MW; ARB4CD3173C9500B CRC64:
	OX40.
	POTENTIAL.

Query Match 17.5%; Score 171.5; DB 6; Length 267;  
Best Local Similarity 32.6%; Pred. NO. 2e-10;  
Matches 59; Conservative 11; Mismatches 74; Indels 37; Gaps 10;

Qy	12	ALCGLA-LLCALS	LGRPTGGPGC-----GPRLLL----	-GTGTDARCCRVHTRCCRD	60
Db	4	AALGALLLL	LLGLLGAEP--PCVGDTPYGGDRCCLCPGVGMVSRNCRNSQDTICHP	61	
Qy	61	YPG--EECGSEWDCM-CVQ-----PEFHGDGPCCTTCRHHPCPPGGVGVSQKGFSG	109		
Db	62	EPGYNEAVNYQACKPCTOCNRSSSEPQQECTHTRTDTCR---CRP--GTQLNGYKHG	116		
Qy	110	FQCIDCASGTFSGHGHBCKPWTDCTQGFLTVFPGNKTHNAV	-----VPGSPPAE	161	
Db	117	VDCAPCPQHGFSEGNRACRPNTNCITLAGKRITQPASSISDAVEDRSSLATQPNETPSA	176		

Qy 162 P 162  
—  
Db 177 P 177

RESULT	9	
Q9DDDD2	Q9DDDD2	
ID	PRELIMINARY;	PRT; 276 AA.
AC	Q9DDDD2;	
DT	01-MAR-2001 (TREMBLrel. 16, Created)	
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)	
DE	HUMAN CD40-HOMOLOGUE.	
GN	TNFSF5.	
OS	Gallus gallus (Chicken).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	
OC	Gallus.	
OX	NCBI_TaxID=9031;	
RN	[1]	
RA	SEQUENCE FROM N.A.	
RA	Tregaskes C.A.;	
RL	Thesis (2001), University of Reading, Reading, UNITED KINGDOM.	
DR	EMBL; AJ293700; CAC20218.1; -.	
SQ	SEQUENCE 276 AA; 30009 MW; 4040B7E0DB82454E CRC64;	

Query Match 15.88; Score 154.5; DB 13; Length 276;  
Best Local Similarity 26.88; Pred. NO. 1.2e-08;  
Matches 53; Conservative 10; Mismatches 58; Indels 77; Gaps 11;

**QY** 16 LALLCALSLGQRPTGGPGCG-PGRLLLTGTGDARCCR-----VHTTRCC-RDYPGECCSE 69  
| | | | | | | | | | | | | | | | | | | | | |  
**Dd** 7 LGSLCALLL-----GCOPG-----DAVNCSDKOYEHGKRCNRCOPGKKLASE 50  
| | | | | | | | | | | | | | | | | | | | | |

Qy 70 -----WD-----CMCVQPEF 79  
Db 51 CNDTEDSYCTPCENGOYOHSWTKERHCTPHETCEDNAGLIVKPHGNATHNTVCOC-RAGM 109

QV 80 HCGDPCC<sup>TT</sup>C-RHHPCPGG-VOSQKFSFGFOCIDCASG<sup>TF</sup>S--GGHEGCHCKPWT<sup>DC</sup>T 135

Db	110	HCSDASCOTC	VENEPCKQGF	GFVAAAEARMT	SPCEPFAEGTFSN	SSKTEPCHF	WTSC	169
Qy	136	QFGFLT	VEPGNKTH	NAVC	153			
Db	170	EKGLV	VVKGTNT	SDVIC	187			
RESULT	10							
Q95407								
ID	Q95407		PRELIMINARY;		PRT;	300	AA.	
AC	Q95407;							
DT	01-MAY-1999	(TEMBLrel. 10, Created)						
DT	01-MAY-1999	(TEMBLrel. 10, Last sequence update)						
DT	01-MAR-2001	(TEMBLrel. 16, Last annotation update)						
DE	DCOY RECEPTOR 3 (M68)	(M68C) (M68E) (DJ583P15.1.1).						
GN	DCR3 OR TR6 OR TNRSF6B.							
OS	Homo sapiens (Human).							
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;							
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
OX	NCBI_TaxID=9606;							
PN	111							

RP SEQUENCE FROM N.A.  
RX MEDLINE=99087326; PubMed=9872321;  
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,  
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,  
RA Godowski P.J., Wood W.J., Gurney A.L., Hillan K.J., Cohen R.L.,  
RA Goddard A.D., Botstein D., Ashkenazi A.;  
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and  
RT colon cancer.";  
RT Nature 396:699-703(1998).  
RN [2]  
RN SEQUENCE FROM N.A.  
RN TISSUE=BLOOD;  
RC MEDLINE=99253915; PubMed=10318773;  
RX Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;  
RT "A newly identified member of tumor necrosis factor receptor  
RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";  
RT J. Biol. Chem. 274:13733-13736(1999).  
RN [3]  
RN SEQUENCE FROM N.A.  
RN TISSUE=PANCREAS;  
RC MEDLINE=20122600; PubMed=10655513;  
RX Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,  
RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;  
RT "Overexpression of M69/DCR3 in human gastrointestinal tract tumors  
RT independent of gene amplification and its location in a four-gene  
RT cluster.";  
RN Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).

```

RN      [4]
RP      SEQUENCE FROM N.A.
RA      Matthews L.;
RL      Submitted (NOV-2000) to the EMBL/GenBank/DBDJ databases.
RR
DR      ENBL; AF104419; AAD03056.1; -
DR      ENBL; AF134240; AAD29688.1; -
DR      ENBL; AF217796; AAF35244.1; -
DR      ENBL; AF217793; AAF33685.1; -
DR      ENBL; AF217794; AAF33686.1; -
DR      ENBL; AL121845; CAC03668.1; -
DR      HSSP; P25942; 1CDF.
DR      InterPro; IPR000561; -.
DR      InterPro; IPR001368; -.
DR      Pfam; PF000020; TNFR_c6; 4.
DR      ProDom; PD000771; -; 1
DR      PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR      PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR      PROSITE; PS00050; TNFR_NGFR_2; 2.
DR      PROSITE;
DR      Receptor.
SQ      SEQUENCE 300 AA; 32679 MW; F90AEE33718449AF CRC64;
KW

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Query Match	15.68;	Score 153;	DB 4;	Length 300;
Best Local Similarity	26.38;	Pred. No. 1.9e-08;		

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RN  SEQUENCE FROM N.A.
RP  STRAIN=C3H/HEN;
RX  MDLINE=97322352; PubMed=9177197;
RA  Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,
RA  Moraca R., Migliorati G., Riccardi C.;
RT  "A new member of the tumor necrosis factor/nerve growth factor
RT  receptor family inhibits T cell receptor-induced apoptosis.";
RL  Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BALB/C;
RA  Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
RA  Migliorati G., Riccardi C.;
RT  "Gene structure and chromosomal assignment of GTR, a mouse member of
RT  the tumor necrosis factor/nerve growth factor receptor family.";
RL  Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR  EMBL; U82534; AAB81243.1; -.
DR  EMBL; AF109216; AAF14231.1; -.
DR  MGD; MGI:894675; Tnfrsf18.
DR  InterPro; IPR000561; -.
DR  SMART; SM00181; EGF; 1.
KW  Signal; Receptor.
FT  SIGNAL 1 19 POTENTIAL.
FT  CHAIN 20 228 GLUCOCORTICOID INDUCED TNFR FAMILY
FT  RELATED PROTEIN.
SQ  SEQUENCE 228 AA; 25334 MW; 50D8C275D9C56259 CRC64;

Query Match 52.1%; Score 510; DB 11; Length 228;
Best Local Similarity 54.1%; Pred. No. 4.9e-46;
Matches 86; Conservative 25; Mismatches 40; Indels 8; Gaps 2;

QY 7 MGAFRALCGLLALCALSLGQ-RPTGGPGCGPGRLLLTGTDCRCRVHTTRCCRDYPGEE 65
DB 1 MGAWAMLYGVSMCLVDLQGPSVVEPGGPGKVGQSGNNTCCSLYA-----PGKE 53
QY 66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGQKFSFGFCIDCASGTFSSGHE 125
DB 54 DCPKERCICVTPHYHCGDPQCKICKHYPCQPGQORVESQGDIVGFRVCACAMGTFSSAGRD 113

QY 126 GHCKPWTCTQFGFLTVPFGNKNTHNAVCPGSPPAEPLG 164
DB 114 GHCLRWTCNSQFGFLTMTFPGNKNTHNAVCIPEPLTEQYG 152

RESULT 7
QJUKR1 ID QJUKR1 PRELIMINARY; PRT; 132 AA.
AC QJUKR1;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE GTR-B.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229434; AAF61568.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 132 AA; 14106 MW; F586A5404B1DFEDE CRC64;

Query Match 38.8%; Score 380; DB 11; Length 132;
Best Local Similarity 50.4%; Pred. No. 1.4e-32;
Matches 64; Conservative 21; Mismatches 34; Indels 8; Gaps 2;

QY 7 MGAFRALCGLLALCALSLGQ-RPTGGPGCGPGRLLLTGTDCRCRVHTTRCCRDYPGEE 65
DB 1 MGAWAMLYGVSMCLVDLQGPSVVEPGGPGKVGQSGNNTCCSLYA-----PGKE 53
QY 66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGQKFSFGFCIDCASGTFSSGHE 125
DB 54 DCPKERCICVTPHYHCGDPCQCKICKHYPCQPGQORVESQGDIVGFRVCACAMGTFSSAGRD 113

QY 126 GHCKPWT 132
DB 114 GHCLRW 120

RESULT 8
QJUKR1 ID QJUKR1 PRELIMINARY; PRT; 267 AA.
AC QJUKR1;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE OX40 PRECURSOR (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.

Query Match 52.1%; Score 510; DB 11; Length 294;

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Best Local Similarity 54.1%; Pred. No. 6.1e-46;
Matches 86; Conservative 25; Mismatches 40; Indels 8; Gaps 2;

QY 7 MGAFRALCGLLALCALSLGQ-RPTGGPGCGPGRLLLTGTDCRCRVHTTRCCRDYPGEE 65
DB 1 MGAWAMLYGVSMCLVDLQGPSVVEPGGPGKVGQSGNNTCCSLYA-----PGKE 53
QY 66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGQKFSFGFCIDCASGTFSSGHE 125
DB 54 DCPKERCICVTPHYHCGDPCQCKICKHYPCQPGQORVESQGDIVGFRVCACAMGTFSSAGRD 113

QY 126 GHCKPWTCTQFGFLTVPFGNKNTHNAVCPGSPPAEPLG 164
DB 114 GHCLRWTCNSQFGFLTMTFPGNKNTHNAVCIPEPLTEQYG 152

RESULT 7
QJUKR1 ID QJUKR1 PRELIMINARY; PRT; 132 AA.
AC QJUKR1;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE GTR-D.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229434; AAF61568.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 132 AA; 14106 MW; F586A5404B1DFEDE CRC64;

Query Match 38.8%; Score 380; DB 11; Length 132;
Best Local Similarity 50.4%; Pred. No. 1.4e-32;
Matches 64; Conservative 21; Mismatches 34; Indels 8; Gaps 2;

QY 7 MGAFRALCGLLALCALSLGQ-RPTGGPGCGPGRLLLTGTDCRCRVHTTRCCRDYPGEE 65
DB 1 MGAWAMLYGVSMCLVDLQGPSVVEPGGPGKVGQSGNNTCCSLYA-----PGKE 53
QY 66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGQKFSFGFCIDCASGTFSSGHE 125
DB 54 DCPKERCICVTPHYHCGDPCQCKICKHYPCQPGQORVESQGDIVGFRVCACAMGTFSSAGRD 113

QY 126 GHCKPWT 132
DB 114 GHCLRW 120

RESULT 8
QJUKR1 ID QJUKR1 PRELIMINARY; PRT; 267 AA.
AC QJUKR1;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE OX40 PRECURSOR (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.

Query Match 52.1%; Score 510; DB 11; Length 294;

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CC -|- SUBCELLULAR LOCATION: EXTRACELLULAR.  
CC -|- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,  
CC BRAIN, HEART, KIDNEY, STOMACH, INTESINE, SKIN, CALVARIA AND  
CC PLACENTA. NOT DETECTED IN SPLEEN.  
CC -|- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT  
CC DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY  
CC 15 TO DAY 17.  
CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
DR EMBL; U94331; AB53708.1; -.  
DR EMBL; AB013898; BAA28269.1; -.  
DR EMBL; AB013903; BAA33388.1; -.  
DR EMBL; AB013899; BAA33388.1; JOINED.  
DR EMBL; AB013900; BAA33388.1; JOINED.  
DR EMBL; AB013901; BAA33388.1; JOINED.  
DR EMBL; AB013902; BAA33388.1; JOINED.  
DR HSP; P25942; ICDF.  
DR MGD; MGI:109587; Tnfrsf11b.  
DR InterPro; IPR000488; -.  
DR InterPro; IPR001368; -.  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR ProDom; PD00071; -; 1.  
DR ProSite; PS00171; DEATH\_DOMAIN; 1.  
DR ProSite; PS00652; TNFR\_NGFR\_1; 1.  
DR ProSite; PS00050; TNFR\_NGFR\_2; 2.  
DR SMART; SM00005; DEATH; 1.  
KW Glycoprotein; Repeat; Cytokine; Signal.  
FT SIGNAL 1 21  
FT CHAIN 22 401 OSTEOPROTEGERIN.  
FT DOMAIN 23 201 4 X TNFR-CYS.  
FT REPEAT 23 63 TNFR-CYS 1.  
FT REPEAT 64 106 TNFR-CYS 2.  
FT REPEAT 107 143 TNFR-CYS 3.  
FT REPEAT 144 201 TNFR-CYS 4.  
FT DOMAIN 306 365 DEATH DOMAIN.  
FT DISULFID 41 54 BY SIMILARITY.  
FT DISULFID 44 62 BY SIMILARITY.  
FT DISULFID 65 80 BY SIMILARITY.  
FT DISULFID 83 97 BY SIMILARITY.  
FT DISULFID 87 105 BY SIMILARITY.  
FT DISULFID 118 142 BY SIMILARITY.  
FT DISULFID 145 160 BY SIMILARITY.  
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARIANT 138 138 R -> P (IN STRAINS 129/OLA AND NIH  
FT VARIANT 161 161 I -> R (IN STRAINS 129/OLA AND NIH  
FT VARIANT 165 165 N -> D (IN STRAINS 129/OLA AND NIH  
FT VARIANT 288 288 S -> A (IN STRAINS 129/OLA AND NIH  
FT VARIANT 296 296 L -> R (IN STRAINS 129/OLA AND NIH  
FT SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRG64;

Query Match 14.2%; Score 139.5; DB 11; Length 401;  
Best Local Similarity 25.7%; Pred. No. 6.5e-07;  
Matches 43; Conservative 10; Mismatches 69; Indels 45; Gaps 6;  
QY 15 GLALLCALSILGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGECCESEW---- 70  
DB 36 GHQLLC-----DKACGTYL-----KQHTVTRKTLVCPDHSYDTSNHTSD 78  
QY 71 DCMCVQP-----EFHCGDPCCTTC-----RHHPCPPGQVQSQCKFSF 108  
DB 79 ECVGSPVKELQSVKQECNRTHNRVCECEBGRYLEIFCLKHKRSCPPGSGVYQAGTPR 138  
QY 109 GFQCIDCAGSTFSG--GHEGCHKPWTDCYQFGLTVFPNGKTHNAVY 153  
DB 139 NTVCKKCPDGFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVC 185

RESULT 13  
QY9Y6Q6  
ID Q9Y6Q6 PRELIMINARY; PRT; 616 AA.  
AC Q9Y6Q6;  
DT 01-NOV-1999 (TEMBLrel. 12, Created)  
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)  
DE 01-MAR-2001 (TEMBLrel. 16, Last annotation update)  
DE RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-  
DE INDUCED CYTOKINE RECEPTOR) (RANK).  
GN TNFRSF11A OR RANK.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98032977; PubMed=9367155;  
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,  
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,  
RA Galibert L.  
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth  
RT and dendritic-cell function";  
RL Nature 390:175-179(1997).  
CC -|- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.  
CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).  
CC -|- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN  
CC SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL  
CC GLAND.  
CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
DR EMBL; AF018253; AAB86809.1; -.  
DR HSP; P25942; ICDF.  
DR MIM; 603499; -.  
DR InterPro; IPR001368; -.  
DR Pfam; PF00020; TNFR\_c6; 4.  
DR ProSite; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
DR ProSite; PS00050; TNFR\_NGFR\_2; 1.  
DR SMART; SM0208; TNFR; 1.  
KW Receptor; Glycoprotein; Transmembrane; Signal; Repeat.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 616 RECEPTOR ACTIVATOR OF NF-KAPPA-B.  
FT DOMAIN 24 212 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 213 233 POTENTIAL.  
FT DOMAIN 234 616 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 33 195 4 X TNFR-CYS.  
FT REPEAT 33 69 TNFR-CYS 1.  
FT REPEAT 70 112 TNFR-CYS 2.  
FT REPEAT 113 152 TNFR-CYS 3.  
FT REPEAT 153 195 TNFR-CYS 4.  
FT DISULFID 34 46 BY SIMILARITY.  
FT DISULFID 47 60 BY SIMILARITY.  
FT DISULFID 50 68 BY SIMILARITY.  
FT DISULFID 71 86 BY SIMILARITY.  
FT DISULFID 92 112 BY SIMILARITY.  
FT DISULFID 114 124 BY SIMILARITY.  
FT DISULFID 126 133 BY SIMILARITY.  
FT DISULFID 127 151 BY SIMILARITY.  
FT DISULFID 154 169 BY SIMILARITY.  
FT DISULFID 175 194 BY SIMILARITY.  
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT SEQUENCE 616 AA; 66033 MW; E3DE9A7A08196F81 CRG64;

Query Match 14.1%; Score 138.5; DB 4; Length 616;  
Best Local Similarity 24.1%; Pred. No. 1.2e-06;  
Matches 52; Conservative 14; Mismatches 69; Indels 81; Gaps 10;  
QY 11 RALCGALLCALSILGQRTGPGCGPGRLLLTGTGDARCCR----VHTTRCCR-----DY 61  
DB 9 RPLFALLLLCALL-----ARLQVALQIAPPCTSEKHYEHLGRCCNCKPEPKY 55



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FT DISULFID 118 142 BY SIMILARITY.
FT DISULFID 145 160 BY SIMILARITY.
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 263 263 A -> D (IN REF. 2 AND 3).
SQ SEQUENCE 401 AA; 45996 MW; EB42FA51C9D7C71E CRG64;

Query Match      14.0%; Score 137; DB 4; Length 401;
Best Local Similarity 23.8%; Pred. No. 1.2e-06;
Matches 38; Conservative 15; Mismatches 59; Indels 48; Gaps 6;

Qy 53 HTTRCGRDYPG-----EECCSEWDCMCV-----QPEFHCGDPC--CT----- 87
Db 37 HOLLCDKCPGTYLKQHCTAKWKTVCAPCDPDHYTDSWHTSDECLYCSPVKELQYVQE 96

Qy 88 -----TC-----RHHPCPPGQGVQSGKFSFGFCIDCASGTFSG--GH 124
Db 97 CNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVQAGTPERNTVCKRCPDGFFSNETSS 156

Qy 125 EGHCKPWTCTQFGPLTVPFGNKNTHNAVCPGSPPAEPLG 164
Db 157 KAPCRKHTNCVSFGLLLTQGNATHDNICSGNSESTQKCG 196
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Search completed: September 4, 2001, 16:14:34  
Job time: 1221 sec

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QY 62 PGECCSEWDCMCVQPEFHCG-----DPC----- 85
Db 56 MSSCKTTSDSVCLP-----CGPEYDLSWNEEDKCLLHKVCDTGKALVAVVAGNSTTPRR 111
QY 86 -----CITCRHH-PCPPGQVQSQGKFGFCQICDASGTSGGHEG--HCKP 130
Db 112 CACTAGYHWSODCECCRTECAPGLGAHQHPLQNLKNDIVCKPCLAGYFSDAFSSDTKCRP 171
QY 131 WTDCTQGFGLVFPCKNTHNAV-----VPG-SPAPB 162
Db 172 WTNCTFLGKRVHEHGTGKSDAVCSSSLPARKPPNEP 207

RESULT 14
Q9UHP4 PRELIMINARY; PRT; 372 AA.
AC Q9UHP4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE OSTEOPROTEGERIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT "Cloning and Expression of Osteoprotegerin from Homo sapiens.";
RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684(1999).
DR EMBL; AF134187; AAP20168.1; -.
DR HSSP; P25942; 1CDF.
DR InterPro; IPR000488; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_c6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
DR SMART; SM00005; DEATH; 1.
FT NON_TER 1
SQ SEQUENCE 372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;

Query Match 14.0%; Score 137; DB 4; Length 372;
Best Local Similarity 23.8%; Pred. No. 1.le-06;
Matches 38; Conservative 15; Mismatches 59; Indels 48; Gaps 6;

QY 53 HTTRCRRDYPG-----EECCSEWDCMV-----QPEFHCGDPC--CT----- 87
Db 16 HQLLCRCPGTYLKQHCATKWKTVCAPCPDHYTDSNHTSDECLYCSVPCKELQYVQKE 75
QY 88 -----TC-----RHHPCPPGQVQSQGKFGFCQICDASGTSG--GH 124
Db 76 CNRTHNRVCECKEGRYLEIEFLCHRSPPGPGVVGQAQTPERTNTVCKRCPDGFSSNETSS 135
QY 125 EGHCKPWTDCTQGFGLTVFPCKNTHNAVCPGSPAPBPLG 164
Db 136 KAPCRKHTNCSVFGLLLTQGNATHDNCNSGSESTQKCG 175

RESULT 15
O00300 PRELIMINARY; PRT; 401 AA.
AC O00300; 060236;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
DE (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
GN TNFRSF11B OR OPG OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trill G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin; a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG FIBROBLAST;
RX MEDLINE=98151033; PubMed=9492069;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA Tsuda E., Morinaga T., Higashio K.;
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RT osteoclastogenesis in vitro.";
RL Endocrinology 139:1329-1337(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE=98351569; PubMed=9688283;
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT "Cloning and characterization of the gene encoding human
RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";
RL Eur. J. Biochem. 254:685-691(1998).
CC -!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
CC -!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,
CC KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN
CC A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED IN
CC THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; AB002146; BAA25910.1; -.
DR EMBL; AB008822; BAA32076.1; -.
DR EMBL; AB008821; BAA32076.1; JOINED.
DR EMBL; U94332; AAB53709.1; -.
DR HSSP; P25942; 1CDF.
DR MIM; 602643; -.
DR InterPro; IPR000488; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRODOM; PD000771; -.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
DR SMART; SM00005; DEATH; 1.
KW Glycoprotein; Repeat; Cytokine; Signal.
FT SIGNAL 1 21
FT CHAIN 22 401
FT DOMAIN 23 183
FT REPEAT 23 63
FT REPEAT 64 106
FT REPEAT 107 143
FT REPEAT 144 201
FT DOMAIN 306 365
FT DISULFID 41 54
FT DISULFID 44 62
FT DISULFID 65 80
FT DISULFID 83 97
FT DISULFID 87 105
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RESULT 2
Q9Y5U5
ID Q9Y5U5 PRELIMINARY; PRT; 241 AA.
AC Q9Y5U5;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
GN TNFRSF18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,
RA Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,
RA Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;
RT "Identification of a new member of the tumor necrosis factor family
RT and its receptor, a human ortholog of mouse GITR.";
RL Curr. Biol. 0:0-0(1999);
DR EMBL; AF125304; AAD22635.1; -
DR InterPro; IPR001368; -
DR SMART; SM00208; TNFR; 1.
SQ SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7EB2CBE CRC64;

Query Match 100.0%; Score 841; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.4e-83;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGGCGPGRLLLTGTGTARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
DB 26 QRTGGGCGPGRLLLTGTGTARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 85

QY 61 CTTCTRHHPCCPGQVQSGKFSFGFCIDCASGTFSGGHEGHCCKPWTDC----- 109
DB 86 CTTCTRHHPCCPGQVQSGKFSFGFCIDCASGTFSGGHEGHCCKPWTDCWCRCRRPKTP 145

QY 110 -----TQFGFLTVPFGNKNTHNAVCPGSPPAEP 137
DB 146 EAASSPRKSGASDRQRRRGWET-----CGCEPGRPPGP 180

RESULT 4
Q9JKR2
ID Q9JKR2 PRELIMINARY; PRT; 222 AA.
AC Q9JKR2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GITR-C.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GITR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229433; AAF61567.1; -
DR InterPro; IPR000561; -
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 222 AA; 24450 MW; 594932BA425A79CA CRC64;

Query Match 55.4%; Score 465.5; DB 11; Length 222;
Best Local Similarity 56.9%; Pred. No. 6.2e-43;
Matches 74; Conservative 21; Mismatches 28; Indels 7; Gaps 1;

QY 7 PCGPGPGRLLLTGTGTARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTCRH 66
DB 27 PCGPGPGRLLLTGTGTARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTCRH 79

QY 67 HPCPPGQVQSGKFSFGFCIDCASGTFSGGHEGHCCKPWTDCQTQFGFLTVPFGNKNTHNA 126
DB 80 YPCQPQRVESQGDIVFGFRVCACAMGTFESAGRDGHCRLWNTNCSQFGFLTVPFGNKNTHNA 139

QY 127 VCVPGSPPAE 136
DB 140 VCIPEPLPTE 149

RESULT 5
Q35714
ID Q35714 PRELIMINARY; PRT; 228 AA.
AC Q35714;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.
GN TNFRSF18 OR GITR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEN;
RX MEDLINE=97322352; PubMed=9177197;

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Query Match 81.7%; Score 687; DB 4; Length 255;
Best Local Similarity 71.3%; Pred. No. 7e-67;
Matches 117; Conservative 2; Mismatches 9; Indels 36; Gaps 2;

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2001, 16:14:30 ; Search time 133.1 Seconds  
(without alignments)  
136.182 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_26\_162  
Perfect score: 841  
Sequence: 1 QRTGGGCGGPRLLLTGT.....PFGKTHNAVCPGSPPAEP 137

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_16.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_unclassified.\*  
13: sp\_vertebrate.\*  
14: sp\_virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	841	100.0	234	4 Q95851	Q95851 homo sapien
2	841	100.0	241	4 Q9V5U5	Q9V5U5 homo sapien
3	687	81.7	255	4 Q9NVJ9	Q9NVJ9 homo sapien
4	465.5	55.4	222	11 Q9JKR2	Q9JKR2 mus musculus
5	465.5	55.4	228	11 Q95714	Q95714 mus musculus
6	465.5	55.4	294	11 Q9JKR3	Q9JKR3 mus musculus
7	339.5	40.4	132	11 Q9JKR1	Q9JKR1 mus musculus
8	154.5	18.4	267	6 O02764	O02764 oryctolagus
9	150.5	17.9	300	4 Q95407	Q95407 homo sapien
10	140	16.6	401	11 Q08727	Q08727 rattus norv
11	139	16.5	276	13 Q9DD02	Q9DD02 gallus gall
12	139	16.5	401	11 Q08712	Q08712 mus musculus
13	133	15.8	372	4 Q9UHP4	Q9UHP4 homo sapien
14	133	15.8	401	4 Q00300	Q00300 homo sapien
15	131	15.6	616	4 Q9Y6Q6	Q9Y6Q6 homo sapien
16	129.5	15.4	655	4 Q75509	Q75509 homo sapien
17	123	14.6	625	11 Q03505	Q03505 mus musculus
18	122.5	14.6	655	11 Q9EP05	Q9EP05 mus musculus
19	122	14.5	107	11 Q9JKE0	Q9JKE0 rattus norv

20	120.5	14.3	459	11 Q62327	Q62327 mus musculus
21	120.5	14.3	482	11 Q88734	Q88734 mus musculus
22	119	14.1	439	4 Q16042	Q16042 homo sapien
23	116.5	13.9	302	13 Q9PUS0	Q9PUS0 salvelinus
24	112	13.3	152	5 Q9XVX3	Q9XVX3 caenorhabdi
25	112	13.3	1637	6 Q9XSV8	Q9XSV8 bos taurus
26	111	13.2	1371	11 Q9QVW4	Q9QVW4 rattus sp.
27	109.5	13.0	4601	5 Q9V383	Q9V383 drosophila
28	109	13.0	1574	11 Q88281	Q88281 rattus norv
29	109	13.0	2906	11 Q9WUH9	Q9WUH9 rattus norv
30	107	12.7	164	5 Q22048	Q22048 caenorhabdi
31	107	12.7	1308	5 Q9GPM8	Q9GPM8 caenorhabdi
32	106.5	12.7	1698	5 Q94438	Q94438 chironomus
33	104.5	12.4	1587	4 Q00508	Q00508 homo sapien
34	104	12.4	1522	5 Q22685	Q22685 caenorhabdi
35	103.5	12.3	126	10 Q9S9F4	Q9S9F4 phytolacca
36	103.5	12.3	1511	4 Q75412	Q75412 homo sapien
37	103	12.2	1242	4 Q9NS15	Q9NS15 homo sapien
38	103	12.2	1382	4 Q9H7K2	Q9H7K2 homo sapien
39	103	12.2	1764	11 Q35806	Q35806 rattus norv
40	103	12.2	1833	11 Q08999	Q08999 mus musculus
41	103	12.2	1963	6 Q28019	Q28019 bos taurus
42	102.5	12.2	188	5 Q18238	Q18238 caenorhabdi
43	102.5	12.2	283	6 Q9XS28	Q9XS28 cercopithec
44	102.5	12.2	870	6 Q02660	Q02660 bos taurus
45	102.5	12.2	1792	13 Q57484	Q57484 gallus gall

## ALIGNMENTS

RESULT 1

ID Q95851 PRELIMINARY; PRT; 234 AA.  
AC Q95851;  
DT 01-MAY-1999 (TREMREL. 10, Created)  
DT 01-MAY-1999 (TREMREL. 10, Last sequence update)  
DT 01-MAR-2001 (TREMREL. 16, Last annotation update)  
DE TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99156876; Pubmed=10037686;  
RA Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L.,  
RA Liu D., Wang S.X., Kwon B.S.;  
RT "Identification of a novel activation-inducible protein of the tumor  
RT necrosis factor receptor superfamily and its ligand";  
RL J. Biol. Chem. 274:6056-6061(1999).  
RL EMBL; AF117297; AAD19694.1; -;  
DR InterPro; IPR001368; -;  
DR SMART; SM00208; TNFR; 1.  
KW Receptor.  
SQ SEQUENCE 234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;

Query Match 100.0%; Score 841; DB 4; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.4e-83;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	QRTGGGCGGPRLLLTGTGTTCRCRDYPCGECCESEWDCMCVPEHFCGDP	60
Db	26	QRTGGGCGGPRLLLTGTGTTCRCRDYPCGECCESEWDCMCVPEHFCGDP	85
QY	61	CTTCRRHPCPGQVQSGQKFSFGQICDASGTFSGSGHEGCKPWTDTCTGFLTVPPG	120
Db	86	CTTCRRHPCPGQVQSGQKFSFGQICDASGTFSGSGHEGCKPWTDTCTGFLTVPPG	145
QY	121	NKTHNAVCPGSPPAEP	137
Db	146	NKTHNAVCPGSPPAEP	162

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DR EMBL; AF217796; AAF35244.1; -
DR EMBL; AF217793; AAF33685.1; -
DR EMBL; AF217794; AAF33686.1; -
DR EMBL; AL121845; CAC03668.1; -
DR HSSP; P25942; ICDF.
DR InterPro; IPR000561; -
DR InterPro; IPR001368; -
DR Pfam; PF00020; TNFR_C6; 4.
DR ProDom; PD000771; -; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 300 AA; 32679 MW; F90AEE33718449AF CRC64;

Query Match 17.9%; Score 150.5; DB 4; Length 300;
Best Local Similarity 26.9%; Pred. No. I.I.e-08;
Matches 45; Conservative 13; Mismatches 64; Indels 45; Gaps

QY 9 CGPRLLLGTGDARCCRVHTTRCCRDYPCGECCSEWDCM--CVQPEFHCGD-----PC 60
DB 52 CPGETFV-----QRCRRDSPTTCGCPPRHRYTQFWNYLERCRYCNVLCGEEREARAC 105
QY 61 CTT-----CR-----HHPCPPGGVQSGKSFQGCIDCASGTSGGHEG- 101
DB 106 HATHNRCRCRTGFFAHAGFCLHASCPCGAGVIAPCTPSQNTQCPCPGTFSASSSS 165
QY 102 -HCKPWTDCTOFGELVFPKNTKTHAVC-----VPGSPPEA 136
DB 166 EQCPHRNCTALGALNVPGSSSHDTLTCTSGTGFPLSTRVPGAEECE 212

RESULT 10
00872 PRELIMINARY; PRT; 401 AA.

ID AC AC 008727;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR) (OCIF).
DE (OCIF).
GN TNFRSF11B OR OPG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
[1]
SEQUENCE FROM N.A.
TISSUE=INTESTINE;
MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.
RA Daroese M., Elliott R., Colombo A., Tan H.-L., Trail G., Sullivan J.
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.,
RA "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGE
CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; U94330; AAB33707.1; -
DR HSSP; P25942; ICDF.
DR InterPro; IPR000488; -
DR InterPro; IPR001368; -

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RA Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,  
 RA Moraca R., Migliorati G., Riccardi C.;  
 RT "A new member of the tumor necrosis factor/nerve growth factor  
 RT receptor family inhibits T cell receptor-induced apoptosis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BAUB/C;  
 RA Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,  
 RA Migliorati G., Riccardi C.;  
 RT "Gene structure and chromosomal assignment of GTR, a mouse member of  
 RT the tumor necrosis factor/nerve growth factor receptor family.";  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U82534; AAB81243.1; -;  
 DR MGD; AF109216; AAF14231.1; -;  
 DR MGI:894675; Tnfrsf18.  
 DR InterPro: IPR000561; -;  
 DR SMART; SM00181; EGF; 1.  
 KW Signal; Receptor.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 228 GLUCOCORTICOID INDUCED TNFR FAMILY  
 FT RELATED PROTEIN.  
 SQ SEQUENCE 228 AA; 25334 MW; 50D8C275D9C56259 CRC64;  
 Query Match 55.4%; Score 465.5; DB 11; Length 228;  
 Best Local Similarity 56.9%; Pred. No. 6.3e-43;  
 Matches 74; Conservative 21; Mismatches 28; Indels 7; Gaps 1;  
 QY 7 PCGPGRLLLGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHGCDPCCTTCRH 66  
 DB 27 PCGPGKVGQSGNNTRCCSLYA-----PGKEDCPKERCICVTPEYHCGDPQCKICKH 79  
 QY 67 HPCPPGQGVQSGKFGFCIDCASGTFSGGHEGCHKPWTDCQFGFLTVPFGNKTHNA 126  
 DB 80 YPCQPGQGVQSGDIVFGFRCVACAMGTFSGAGRDGCHRLWNTNCSQFGFLTVPFGNKTHNA 139  
 QY 127 VCVPGSPPAE 136  
 DB 140 VCIPEPLPTE 149  
 Query Match 55.4%; Score 465.5; DB 11; Length 228;  
 Best Local Similarity 56.9%; Pred. No. 7.9e-43;  
 Matches 74; Conservative 21; Mismatches 28; Indels 7; Gaps 1;  
 QY 7 PCGPGRLLLGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHGCDPCCTTCRH 66  
 DB 27 PCGPGKVGQSGNNTRCCSLYA-----PGKEDCPKERCICVTPEYHCGDPQCKICKH 79  
 QY 67 HPCPPGQGVQSGKFGFCIDCASGTFSGGHEGCHKPWTDCQFGFLTVPFGNKTHNA 126  
 DB 80 YPCQPGQGVQSGDIVFGFRCVACAMGTFSGAGRDGCHRLWNTNCSQFGFLTVPFGNKTHNA 139  
 QY 127 VCVPGSPPAE 136  
 DB 140 VCIPEPLPTE 149  
 Query Match 55.4%; Score 465.5; DB 11; Length 294;  
 Best Local Similarity 56.9%; Pred. No. 7.9e-43;  
 Matches 74; Conservative 21; Mismatches 28; Indels 7; Gaps 1;  
 QY 7 PCGPGRLLLGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHGCDPCCTTCRH 66

DB 27 PCGPGKVGQSGNNTRCCSLYA-----PGKEDCPKERCICVTPEYHCGDPQCKICKH 79  
 QY 67 HPCPPGQGVQSGKFGFCIDCASGTFSGGHEGCHKPWTDCQFGFLTVPFGNKTHNA 126  
 DB 80 YPCQPGQGVQSGDIVFGFRCVACAMGTFSGAGRDGCHRLWNTNCSQFGFLTVPFGNKTHNA 139  
 QY 127 VCVPGSPPAE 136  
 DB 140 VCIPEPLPTE 149  
 RESULT 7  
 Q9JKR1 ID Q9JKR1 PRELIMINARY; PRT; 132 AA.  
 AC Q9JKR1;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE GTR-B.  
 GN TNFRSF18.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=THYMUS;  
 RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,  
 RA Migliorati G., Riccardi C.;  
 RT "Identification of three novel mRNA splice variants of GTR.";  
 RL Cell Death Differ. 0:0-0(2000).  
 DR EMBL; AF229434; AAF61566.1; -;  
 DR InterPro: IPR000561; -;  
 DR SMART; SM00181; EGF; 1.  
 SQ SEQUENCE 132 AA; 14106 MW; F586A5404B1DFEDE CRC64;  
 Query Match 40.4%; Score 339.5; DB 11; Length 132;  
 Best Local Similarity 52.5%; Pred. No. 1.8e-29;  
 Matches 53; Conservative 17; Mismatches 24; Indels 7; Gaps 1;  
 QY 7 PCGPGRLLLGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHGCDPCCTTCRH 66  
 DB 27 PCGPGKVGQSGNNTRCCSLYA-----PGKEDCPKERCICVTPEYHCGDPQCKICKH 79  
 QY 67 HPCPPGQGVQSGKFGFCIDCASGTFSGGHEGCHKPWT 107  
 DB 80 YPCQPGQGVQSGDIVFGFRCVACAMGTFSGAGRDGCHRLWT 120  
 RESULT 8  
 Q02764 ID Q02764 PRELIMINARY; PRT; 267 AA.  
 AC Q02764;  
 DT 01-JUL-1997 (TREMBlrel. 04, Created)  
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE OX40 PRECURSOR (FRAGMENT).  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CHB:HM;  
 RA Isono T., Seto A.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB003911; BAA20059.1; -;  
 DR HSSP; P19438; 1EXT.  
 DR InterPro: IPR001368; -;  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.

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DR PRODOM; PD000771; -. 1.
DR PROSITE; PSS0017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
DR SMART; SM00005; DEATH; 1.
KW Glycoprotein; Repeat; Cytokine; Signal.
FT SIGNAL 1 21
FT CHAIN 22 401 OSTEOPTROTGERIN.
FT DOMAIN 23 201 4 X TNFR-CYS.
FT REPEAT 23 63 TNFR-CYS 1.
FT REPEAT 64 106 TNFR-CYS 2.
FT REPEAT 107 143 TNFR-CYS 3.
FT REPEAT 144 201 TNFR-CYS 4.
FT DOMAIN 306 365 DEATH DOMAIN.
FT DISULFID 41 54 BY SIMILARITY.
FT DISULFID 44 62 BY SIMILARITY.
FT DISULFID 65 80 BY SIMILARITY.
FT DISULFID 83 97 BY SIMILARITY.
FT DISULFID 87 105 BY SIMILARITY.
FT DISULFID 118 142 BY SIMILARITY.
FT DISULFID 145 160 BY SIMILARITY.
FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 138 138 R -> P (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 161 161 I -> R (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 165 165 N -> D (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 288 288 S -> A (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 296 296 L -> R (IN STRAINS 129/OLA AND NIH SWISS).
SQ SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;

Query Match 16.5%; Score 139; DB 11; Length 401;
Best Local Similarity 26.4%; Pred. No. 2.4e-07;
Matches 39; Conservative 10; Mismatches 65; Indels 34; Gaps 5;

OY 9 CGGRLLLGTGTCRCRVHTTCRRYPGECCSEW-----RHHPGPGGQVQSGKFSFGFCIDCAGTFSG--CHE 100
DB 44 CAPGTYL-----KHCTVRRKTLCPDHSYTDWHTSDCYVCSVCKELQSVKQEC 97
OY 57 GDPCTTC-----RHHPGPGGQVQSGKFSFGFCIDCAGTFSG--CHE 100
DB 98 NRTHNRVCEEGRYLEIEFCLKHRSCTPPGSGVQAGTPERTVCKKCPDGFSSNETSS 135
OY 101 GHCKPWTDCQTFGLTFVFPNGKTHNAV 128
DB 158 APCIKHTNCTFGLLLTKGNATHDNIC 164

Query Match 15.8%; Score 133; DB 4; Length 372;
Best Local Similarity 24.2%; Pred. No. 1e-06;
Matches 36; Conservative 14; Mismatches 51; Indels 48; Gaps 6;

OY 28 HTRCCRDYPG-----EECCSEWDCMCV-----OPEPHCGDPC--CT----- 62
DB 16 HQLLCDKCPGTYLKQHCYAKWKTVCAPCDPHYHYDWSHTSDCYVCSVCKELQVVKQE 75
OY 63 -----TC-----RHHPGPGGQVQSGKFSFGFCIDCAGTFSG--GH 99
DB 76 CNRTHNRVCEEGRYLEIEFCLKHRSCTPPGSGVQAGTPERTVCKKCPDGFSSNETSS 135
OY 100 EGHCKPWTDCQTFGLTFVFPNGKTHNAV 128
DB 136 KAPCRKHTNCSVFGLLLTQKGNATHDNIC 164

RESULT 14
O00300 PRELIMINARY; PRT: 401 AA.
AC O00300; O60236;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE OSTEOPTROTGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR) (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
DE GN TNFRSF11B OR OPG OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luethy R., Nguyen H.-Q., Wooden S., Bennett L., Boone T., Shimamoto G., Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., Suggs S., Boyle W.J.;
RA "Osteoprotegerin: a novel secreted protein involved in the regulation of bone density.";
RT Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG FIBROBLAST;
RX MEDLINE=98151033; PubMed=9492069;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N., Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A., Tsuda E., Morinaga T., Higashio K.;
RA "Identity of osteoclastogenesis inhibitory factor (OCIF) and osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits osteoclastogenesis in vitro.";
RT Endocrinology 139:1329-1337(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE=98351569; PubMed=9688283;
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RA "Cloning and characterization of the gene encoding human

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Db 158 YFSDAFSSTDKCRPWTNCTFLGKRVEHHGTEKSDAVCSSLPARKPPNEP 207

Search completed: September 4, 2001, 16:14:30  
Job time: 1217 sec

RT osteoprotegerin/osteoclastogenesis-inhibitory factor." ;  
RL Eur. J. Biochem. 254:1683-691(1998).  
CC -!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES  
CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY  
CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO  
CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN  
CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.  
CC -!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY  
CC SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.  
CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,  
CC KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN  
CC A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED IN  
CC THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.  
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
DR EMBL; AB002146; BAA32076.1; -.  
DR EMBL; AB008822; BAA32076.1; -.  
DR EMBL; AB008821; BAA32076.1; JOINED.  
DR EMBL; U94332; AAB53709.1; -.  
DR HSSP; P25942; ICDF.  
DR MIM; 602643; -.  
DR InterPro; IPR000488; -.  
DR InterPro; IPR001368; -.  
DR Pfam; PF00020; TNFR\_C6; 3.  
DR ProDom; PD000771; -. 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
DR PROSITE; PS00505; TNFR\_NGFR\_2; 2.  
DR SMART; SM00005; DEATH; 1.  
KW Glycoprotein; Repeat; Cytokine; Signal.  
FT SIGNAL 1 21 BY SIMILARITY.  
FT CHAIN 22 401 OSTEOPROTEGERIN.  
FT DOMAIN 23 183 4 X TNFR-CYS.  
FT REPEAT 23 63 TNFR-CYS 1.  
FT REPEAT 64 106 TNFR-CYS 2.  
FT REPEAT 107 143 TNFR-CYS 3.  
FT REPEAT 144 201 TNFR-CYS 4.  
FT DOMAIN 306 365 DEATH DOMAIN.  
FT DISULFID 41 54 BY SIMILARITY.  
FT DISULFID 44 62 BY SIMILARITY.  
FT DISULFID 65 80 BY SIMILARITY.  
FT DISULFID 83 97 BY SIMILARITY.  
FT DISULFID 87 105 BY SIMILARITY.  
FT DISULFID 118 142 BY SIMILARITY.  
FT DISULFID 145 160 BY SIMILARITY.  
FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 178 178 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CONFLICT 263 263 A -> D (IN REF. 2 AND 3).  
SQ SEQUENCE 401 AA; 45996 MW; EB42FA51C9D7C71E CRC64;

Query Match 15.8%; Score 133; DB 4; Length 401;  
Best Local Similarity 24.2%; Pred. No. 1.1e-06;  
Matches 36; Conservative 14; Mismatches 51; Indels 48; Gaps 6;  
QY 28 HTTRCCRDYPG-----ECCSEWDCMCV-----QPEFHCGRDPC-CT----- 62  
DB 37 HOLLCDKCPGPGTYLKQCHTAKWKTCAPCPDHYTDSWHTSDCELYCSPVCKELQYVKQE 96  
QY 63 -----TC-----RHHCPPGGGVQSGQKFSFGFCIDCAGSFSG--GH 99  
DB 97 CNRTHNRVCECKEGRYLETEFLCKHRSPPGGVQVQAGTPERNVTCVKRCPDGFNETSS 156  
QY 100 EGHCKPWTDCDTQFGFLTVPGNKTHNAV 128  
DB 157 KAPCRKHTNCSVFGLLLTQKGNATHDNIC 185

RESULT 15  
QY9Y606 PRELIMINARY; PRT; 616 AA.  
ID QY9Y606

AC Q9Y606;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-  
DE INDUCED CYTOKINE RECEPTOR) (RANK).  
OS TNFRSF11A OR RANK.  
GN Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98032977; PubMed=9367155;  
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,  
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,  
RA Galibert L.;  
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth  
RT and dendritic-cell function." ;  
RL Nature 390:175-179(1997).  
CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).  
CC -!- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN  
CC SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL  
CC GLAND.  
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
DR EMBL; AF018253; AAB86809.1; -.  
DR HSSP; P25942; ICDF.  
DR MIM; 603499; -.  
DR InterPro; IPR001368; -.  
DR Pfam; PF00020; TNFR\_C6; 4.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
DR PROSITE; PS00505; TNFR\_NGFR\_2; 1.  
DR SMART; SM00208; TNFR; 1.  
KW Receptor; Glycoprotein; Transmembrane; Signal; Repeat.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 616 RECEPTOR ACTIVATOR OF NF-KAPPA-B.  
FT DOMAIN 24 212 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 213 233 POTENTIAL.  
FT DOMAIN 234 616 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 33 195 4 X TNFR-CYS.  
FT REPEAT 70 112 TNFR-CYS 1.  
FT REPEAT 113 152 TNFR-CYS 2.  
FT REPEAT 153 195 TNFR-CYS 3.  
FT REPEAT 153 195 TNFR-CYS 4.  
FT DISULFID 34 46 BY SIMILARITY.  
FT DISULFID 47 60 BY SIMILARITY.  
FT DISULFID 50 68 BY SIMILARITY.  
FT DISULFID 71 86 BY SIMILARITY.  
FT DISULFID 92 112 BY SIMILARITY.  
FT DISULFID 114 124 BY SIMILARITY.  
FT DISULFID 126 133 BY SIMILARITY.  
FT DISULFID 127 151 BY SIMILARITY.  
FT DISULFID 154 169 BY SIMILARITY.  
FT DISULFID 175 194 BY SIMILARITY.  
FT CARBOHYD 105 105 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 174 174 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 616 AA; 66033 MW; E3DE9A7A08196F81 CRC64;

Query Match 15.6%; Score 131; DB 4; Length 616;  
Best Local Similarity 24.1%; Pred. No. 2.6e-06;  
Matches 41; Conservative 13; Mismatches 52; Indels 64; Gaps 8;  
QY 28 HTTRCCRC-----DYPGECCSEWDCMCVQPEFHCG-----DPC----- 60  
DB 42 HLGRCCKCEPGKYMSSKCTTSDSVCLP---CGPDEYLDWSNEEDKLLHKKVCDTGA 97  
QY 61 -----CTTCRHH--PCPPGGGVQSGQKFSFGFCIDCAGS 93  
DB 98 LVAVVAGNSTTPRRCACTAGYHWSQDCGCCRRNTECAPGLGAQHPLQLNKDTVKPCLAG 157  
QY 94 TFSGGHEG--HCKPWTDCDTQFGFLTVPGNKTHNAV---VPG-SPPAEP 137

```

RESULT 2
Q9Y5U5 ID Q9Y5U5 PRELIMINARY; PRT; 241 AA.
AC Q9Y5U5;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.
GN TNFRSF18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,
RA Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,
RA Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;
RT "Identification of a new member of the tumor necrosis factor family
RT and its receptor, a human ortholog of mouse GITR.";
RL Curr. Biol. 0:0-0(1999).
DR EMBL; AF125304; AAD22635.1; -.
DR InterPro; IPR001368; -.
DR SMART; SM00208; TNFR; 1.
SQ SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7E82CBE CRC64;

Query Match 100.0%; Score 969; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.6e-94;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAMGAFRALCGLALLCALSIGORPTGGCGPGRLLLTGTGDARCCRVHTTRCCRD 60
DB 1 MAQHGAMGAFRALCGLALLCALSIGORPTGGCGPGRLLLTGTGDARCCRVHTTRCCRD 60

QY 61 YPGECCSEWDCMCVQPFHCGPCCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTF 120
DB 61 YPGECCSEWDCMCVQPFHCGPCCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTF 120

QY 121 SGGHEGCHKPWTDC-----TQFGFLTVPFGNKTHNAV 153
DB 121 SGGHEGCHKPWTDC-----TQFGFLTVPFGNKTHNAV 153

QY 121 SGGHEGCHKPWTDC-----TQFGFLTVPFGNKTHNAV 153
DB 121 SGGHEGCHKPWTDC-----TQFGFLTVPFGNKTHNAV 153

QY 154 VPGSPPAEP 162
DB 154 VPGSPPAEP 162

QY 172 EPGRPDPGP 180
DB 172 EPGRPDPGP 180

RESULT 4
Q9JKR2 ID Q9JKR2 PRELIMINARY; PRT; 222 AA.
AC Q9JKR2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GITR-C.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GITR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229433; AAF61567.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 222 AA; 24450 MW; 594932BA425A79CA CRC64;

Query Match 52.2%; Score 506; DB 11; Length 222;
Best Local Similarity 54.5%; Pred. No. 8.6e-46;
Matches 85; Conservative 25; Mismatches 38; Indels 8; Gaps 2;

QY 7 MGAFRALCGLALLCALSIGQ-RPTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEE 65
DB 1 MGAWAMLYGVSMCLVLDLQGPSVVEEPGCGPGKVGQSGNNTCCSLYA-----PGKE 53

QY 66 CCSEWDCMCVQPFHCGPCCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTFSGGHE 125
DB 54 DCPKERCICVTEYHCGDPCCKICKHYPCQPGQGVQSGDIVFGFCVACAMGTFSGAGRD 113

QY 126 GHCKPWTDCQFGFLTVPFGNKTHNAVCPGSPPAE 161
DB 114 GHCLWTNCSQFGFLTVPFGNKTHNAVCIPEPLPTE 149

RESULT 5
Q35714 ID Q35714 PRELIMINARY; PRT; 228 AA.
AC Q35714;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.
GN TNFRSF18 OR GITR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

```



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2001, 16:14:30 ; Search time 133.1 Seconds  
(without alignments)  
161.032 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_1\_162

Perfect score: 969

Sequence: 1 MAQHGAMGAFRALCGLALLC.....FPGNKTHNAVCPGSPPAEP 162

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_16.\*

1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phase.\*

10: sp\_plant.\*

11: sp\_rodent.\*

12: sp\_unclassified.\*

13: sp\_vertebrate.\*

14: sp\_virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	969	100.0	234	4	Q95851
2	969	100.0	241	4	Q9V5U5
3	815	84.1	255	4	Q9NVJ9
4	506	52.2	222	11	Q9JKR2
5	506	52.2	228	11	Q35714
6	506	52.2	294	11	Q9JKR3
7	380	39.2	132	11	Q9JKR1
8	171.5	17.7	267	6	O02764
9	154.5	15.9	276	13	Q9DD22
10	153	15.8	300	4	Q93407
11	141.5	14.6	401	11	O08727
12	139.5	14.4	401	11	O08712
13	138.5	14.3	616	4	Q9V6Q6
14	133	13.7	372	4	Q9UHP4
15	133	13.7	401	4	O00300
16	129.5	13.4	655	4	O73509
17	125	12.9	655	11	Q9EPUS
18	123	12.7	625	11	O35305
19	122	12.6	107	11	Q9JKE0

20	121	12.5	302	13	Q9PUS0
21	120.5	12.4	459	11	O62327
22	120.5	12.4	482	11	O88734
23	119	12.3	439	4	Q16042
24	115.5	11.9	1371	11	Q9QVW4
25	114.5	11.8	1587	4	O00508
26	114.5	11.8	2906	11	Q9WUH9
27	113.5	11.7	1511	4	O75412
28	112	11.6	152	5	Q9XVX3
29	112	11.6	1637	6	Q9XSV8
30	111.5	11.5	1764	11	Q35806
31	111	11.5	1111	5	Q3XWD6
32	111	11.5	1792	13	O57484
33	110.5	11.4	1687	11	O61204
34	110	11.4	1522	5	O22685
35	110	11.4	1698	5	O94438
36	109.5	11.3	164	5	O22048
37	109.5	11.3	4601	5	Q9V383
38	109	11.2	1574	11	O88281
39	107.5	11.1	1833	11	O08999
40	107	11.0	1308	5	O9GPN8
41	107	11.0	3680	5	Q9VR08
42	106.5	11.0	870	6	O02660
43	105	10.8	188	5	Q18238
44	105	10.8	2009	5	Q9VXM0
45	105	10.8	2319	11	Q9R172

## ALIGNMENTS

RESULT 1

ID Q95851 PRELIMINARY; PRT; 234 AA.

AC Q95851;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-99156876; Pubmed-10037686;

RA Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L.,

RA Liu D., Wang S.X., Kwon B.S.;

RT "Identification of a novel activation-inducible protein of the tumor

RT necrosis factor receptor superfamily and its ligand.";

RL J. Biol. Chem. 274:6056-6061(1999).

DR EMBL; AF117297; AAD19694.1; -.

DR InterPro; IPR001368; -.

DR SMART; SM00208; TNFR; 1.

KW Receptor.

SQ SEQUENCE 234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;

Query Match

Best Local Similarity 100.0%; Score 969; DB 4; Length 234;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAMGAFRALCGLALLCALSIGQRTGGPGGPGRLILGTGTDARCCRVHTRCCRD 60

|||||

DB 1 MAQHGAMGAFRALCGLALLCALSIGQRTGGPGGPGRLILGTGTDARCCRVHTRCCRD 60

|||||

QY 61 YPGEECCSEWDCMCQVEFHCGDPCCTTCRHPCPPGGVGQSGKFSFGFCIDCASGTF 120

|||||

DB 61 YPGEECCSEWDCMCQVEFHCGDPCCTTCRHPCPPGGVGQSGKFSFGFCIDCASGTF 120

|||||

QY 121 SGGHEGCKPWTDCDTQFGTLTVFPNGKTHNAVCPGSPPAEP 162

|||||

DB 121 SGGHEGCKPWTDCDTQFGTLTVFPNGKTHNAVCPGSPPAEP 162

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RC STRAIN-CHBB:HM;
RA Isono T., Seto A.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003911; BAA20059.1; -
DR HSSP; P19438; 1EXT.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_c6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
DR SMART; SM00208; TNFR; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 18
FT CHAIN 19 267
FT CHAIN OX40.
SQ SEQUENCE 267 AA; 28489 MW; ABB4CD3173C9500B CRC64;

Query Match 17.7%; Score 171.5; DB 6; Length 267;
Best Local Similarity 32.6%; Pred. No. 1.7e-08;
Matches 59; Conservative 11; Mismatches 74; Indels 37; Gaps 10;

QY 12 ALCGLA-LLCALSLGQRTPGPGC-----GPRLL-----GTGTDARCCRVHTTRCCRD 60
DB 4 AALGLALLLLGLLGAEP--PDCVGDTPGDRCLCPCQPGYGVSRNRSQDTICHP 61
QY 61 YPG--EECCSEWDCM-CVQ-----PEFHCGDPCCTTCRHHPCPPGQVQSQGKFSFG 109
DB 62 EPGFVNEAVNYOACKPCTQCNRRSSGSEPOQECTHTRDTVCR---CRP--GTQPLNGYKHG 116
QY 110 FQCIDCASGTFSGHEGCKPWTCTQCGFLTVFGNTHNAV-----VPCSPPAE 161
DB 117 VDCAPCPQGHFSEGNRACRPWTNCTLAGKRTLPASSISAVDCEDRSLSLATQPWETPSA 176
QY 162 P 162
DB 177 P 177

RESULT 9
Q9DDD2 PRELIMINARY; PRT; 276 AA.
AC Q9DDD2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE HUMAN CD40-HOMOLOGUE.
GN TNFSF5.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Tregaskes C.A.;
RL Thesis (2001), University of Reading, Reading, UNITED KINGDOM.
DR EMBL; AJ293700; CAC20218.1; -
SQ SEQUENCE 276 AA; 30009 MW; 4040B7E0DB8245AE CRC64;

Query Match 15.9%; Score 154.5; DB 13; Length 276;
Best Local Similarity 26.8%; Pred. No. 1.1e-08;
Matches 53; Conservative 10; Mismatches 58; Indels 77; Gaps 11;

QY 16 LALLCALSLGQRTPGPGCG-PGRLLLTGTGDARCC-----VHTTRCC-RYPGEECCSE 69
DB 7 LGLLCALL-----GCGPG-----DAVNCSDKQYEHKRCRCNCPGKKLASE 50
QY 70 -----ND-----CMCVQPEF 79
DB 51 CNDTDSVCTPCENGQYOHSTKERCHPHEICEDNAGLIVKRHGNATHNTVQC-RAGM 109
QY 80 HCGDPCCTTC-RHHPCPPGQG-VOSQGFSGFGQICDASGTF--GGHEGCKPWTDTCT 135
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Db 110 HCSDAQCTCVENEPCKQGFVAAAEARMTSPCEPCAGTFSNVSSKTEPCHFWTSCB 169
QY 136 QFGFLTVFPGNKTHNAV 153
DB 170 EKGLVVVKVKGNTSDVIC 187

RESULT 10
Q95407 PRELIMINARY; PRT; 300 AA.
AC Q95407;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE DECOY RECEPTOR 3 (M68) (M68C) (M68E) (DJ583P15.1.1).
GN DCR3 OR TR6 OR TNFRSF6B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99087326; PubMed=9872321;
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
RA Goddard A.D., Bolstein D., Ashkenazi A.;
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
RT colon cancer.";
RL Nature 396:699-703(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD.
RX MEDLINE=99253915; PubMed=10318773;
RA Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT "A newly identified member of tumor necrosis factor receptor
RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
RL J. Biol. Chem. 274:13733-13736(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=PANCREAS;
RX MEDLINE=20122600; PubMed=10655513;
RA Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,
RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
RT "Overexpression of M68/Dcr3 in human gastrointestinal tract tumors
RT independent of gene amplification and its location in a four-gene
RT cluster.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF104419; AAD03056.1; -
DR EMBL; AF134240; AAD29688.1; -
DR EMBL; AF217796; AAF35244.1; -
DR EMBL; AF217793; AAF33685.1; -
DR EMBL; AF217794; AAF33686.1; -
DR EMBL; AL121845; CAC03668.1; -
DR HSSP; P25942; ICDF.
DR InterPro; IPR000561; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; -.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 300 AA; 32679 MW; F90AEB33718449AF CRC64;

Query Match 15.8%; Score 153; DB 4; Length 300;
Best Local Similarity 26.3%; Pred. No. 1.7e-08;
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RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C3H/HEN;
RX  MEDLINE=97322352; PubMed=9177197;
RA  Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,
RT  Miglioni G., Riccardi C.;
RA  Moraca R., Miglioni G., Riccardi C.;
RT  "A new member of the tumor necrosis factor/nerve growth factor
RT  receptor family inhibits T cell receptor-induced apoptosis.";
RL  Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BALB/C;
RA  Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
RA  Miglioni G., Riccardi C.;
RT  "Gene structure and chromosomal assignment of GTR, a mouse member of
RT  the tumor necrosis factor/nerve growth factor receptor family.";
RL  Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR  EMBL; U82534; AAB81243.1; -.
DR  EMBL; AF109216; AAF14231.1; -.
DR  MGD; MGI:894675; Tnfrsf18.
DR  InterPro; IPR000561; -.
DR  SMART; SM00181; EGF; 1.
KW  Signal; Receptor.
FT  SIGNAL 1 19 POTENTIAL.
FT  CHAIN 20 228 GLUCOCORTICOID INDUCED TNFR FAMILY
FT  RELATED PROTEIN.
FT  SEQUENCE 228 AA; 25334 MW; 50D8C275D9C56259 CRC64;

Query Match 52.2%; Score 506; DB 11; Length 228;
Best Local Similarity 54.5%; Pred. No. 8.8e-46;
Matches 85; Conservative 25; Mismatches 38; Indels 8; Gaps 2;

QY 7 MGAFRALCGALLCALSLGQ-RPTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEE 65
DB 1 MGAWAMLYGVSMCLVLDLQGPVSVEEPGCGPGKVGQSGNNTGCCSLYA-----PGKE 53
QY 66 CCSEWDCMCVQPEFHCGDPCCCTTCRHHPCPPGQVQSGKFSFGQCIDCASGTFSGGHE 125
DB 54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQVRVESQGDIVFGFRVCACAMGTFSGARD 113
QY 126 GHCKPWTCTQFGFLTFVPGNKTHNAVCPGSPPAE 161
DB 114 GHCLWLTNCSQFGFLTFMPGNKTHNAVCIPEPLPTE 149

RESULT 6
QYJRK3 ID Q9JKR3 PRELIMINARY; PRT; 294 AA.
AC Q9JKR3;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE GTR-B.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Miglioni G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229432; AAF61566.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 294 AA; 32658 MW; FE0D4E6A007BA9A CRC64;

Query Match 52.2%; Score 506; DB 11; Length 294;
Best Local Similarity 54.5%; Pred. No. 8.8e-46;
Matches 85; Conservative 25; Mismatches 38; Indels 8; Gaps 2;

QY 7 MGAFRALCGALLCALSLGQ-RPTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEE 65
DB 1 MGAWAMLYGVSMCLVLDLQGPVSVEEPGCGPGKVGQSGNNTGCCSLYA-----PGKE 53
QY 66 CCSEWDCMCVQPEFHCGDPCCCTTCRHHPCPPGQVQSGKFSFGQCIDCASGTFSGGHE 125
DB 54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQVRVESQGDIVFGFRVCACAMGTFSGARD 113
QY 126 GHCKPWTCTQFGFLTFVPGNKTHNAVCPGSPPAE 161
DB 114 GHCLWLTNCSQFGFLTFMPGNKTHNAVCIPEPLPTE 149

RESULT 7
QYJRK3 ID Q9JKR3 PRELIMINARY; PRT; 132 AA.
AC Q9JKR3;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE GTR-D.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Miglioni G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR.";
RL Cell Death Differ. 0:0-0(2000).
DR EMBL; AF229434; AAF61568.1; -.
DR InterPro; IPR000561; -.
DR SMART; SM00181; EGF; 1.
SQ SEQUENCE 132 AA; 14106 MW; F586A5A04B1DFEDE CRC64;

Query Match 39.2%; Score 380; DB 11; Length 132;
Best Local Similarity 50.4%; Pred. No. 1e-32;
Matches 64; Conservative 21; Mismatches 34; Indels 8; Gaps 2;

QY 7 MGAFRALCGALLCALSLGQ-RPTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEE 65
DB 1 MGAWAMLYGVSMCLVLDLQGPVSVEEPGCGPGKVGQSGNNTGCCSLYA-----PGKE 53
QY 66 CCSEWDCMCVQPEFHCGDPCCCTTCRHHPCPPGQVQSGKFSFGQCIDCASGTFSGGHE 125
DB 54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQVRVESQGDIVFGFRVCACAMGTFSGARD 113
QY 126 GHCKPWT 132
DB 114 GHCLWLT 120

RESULT 8
QYJRK3 ID Q02764 PRELIMINARY; PRT; 267 AA.
AC Q02764;
DT 01-JUL-1997 (TremBLrel. 04, Created)
DT 01-JUL-1997 (TremBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE OX40 PRECURSOR (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.

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CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,
CC BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND
CC PLACENTA. NOT DETECTED IN SPLEEN.
CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT
CC DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
CC 15 TO DAY 17.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; U94331; AAB53708.1; -.
DR EMBL; AB013898; BAA28269.1; -.
DR EMBL; AB013903; BAA33388.1; -.
DR EMBL; AB013899; BAA33388.1; JOINED.
DR EMBL; AB013900; BAA33388.1; JOINED.
DR EMBL; AB013901; BAA33388.1; JOINED.
DR EMBL; AB013902; BAA33388.1; JOINED.
DR HSSP; P25942; ICDF.
DR MGD; MGI:109587; Tnfsl1b.
DR InterPro; IPR000488; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 3.
DR ProDom; PD000771; -.
DR PROSITE; PS00017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
DR SMART; SM00005; DEATH; 1.
DR Glycoprotein; Repeat; Cytokine; Signal.
FT SIGNAL 1 21
FT CHAIN 22 401 OSTEOPROTEGERIN.
FT DOMAIN 23 201 4 X TNFR-CYS.
FT REPEAT 23 63 TNFR-CYS 1.
FT REPEAT 64 106 TNFR-CYS 2.
FT REPEAT 107 143 TNFR-CYS 3.
FT REPEAT 144 201 TNFR-CYS 4.
FT DOMAIN 306 365 DEATH DOMAIN.
FT DISULFID 41 54 BY SIMILARITY.
FT DISULFID 44 62 BY SIMILARITY.
FT DISULFID 65 80 BY SIMILARITY.
FT DISULFID 83 97 BY SIMILARITY.
FT DISULFID 87 105 BY SIMILARITY.
FT DISULFID 118 142 BY SIMILARITY.
FT DISULFID 145 160 BY SIMILARITY.
FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 138 138 R -> P (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 161 161 I -> R (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 165 165 N -> D (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 288 288 S -> A (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 296 296 L -> R (IN STRAINS 129/OLA AND NIH SWISS).
SQ SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;

Query Match 14.48; Score 139.5; DB 11; Length 401;
Best Local Similarity 25.78; Pred. No. 5.8e-07;
Matches 43; Conservative 10; Mismatches 69; Indels 45; Gaps 6;

QY 15 GLALLCALSLGORTGGCGPGRLLLTGTGDARCRVHTTRCCRDYGPGECCSEW---- 70
DB 36 GHQLLC-----DKCAPGTVL-----KQCTVRRKTLVCPDPSHSDSHWTS 78
QY 71 DCMCVQP-----EFHCGDPCCPTC-----RHPCPPGQGVQSGKFSF 108
DB 79 ECVYCSPVCKELQSVKQCNTRNVRVCEEGRYLEIEFLKHKRSCPPGSGVVQAGTPDR 138
QY 109 GFQCIDCASCTFSG--GHEGCHKPMTDCTQCGFLTVFGNKNTHNVC 153
DB 139 NTVCKKCPDGFSGFSETSSKAPCIKHTNCSTFGLLLIQGNATHDNVC 185
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RESULT 13
QY606
ID QY606; PRELIMINARY; PRT; 616 AA.
AC QY606;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-
DE INDUCED CYTOKINE RECEPTOR) (RANK).
GN TNFRSF11A OR RANK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheraia; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function.";
RL Nature 390:175-179(1997).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN
CC SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL
CC GLAND.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC EMBL; AF018253; AAB86809.1; -.
CC HSSP; P25942; ICDF.
CC MIM; 603499; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
DR SMART; SM00208; TNFR; 1.
DR Receptor; Glycoprotein; Transmembrane; Signal; Repeat.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 616 RECEPTOR ACTIVATOR OF NF-KAPPA-B.
FT DOMAIN 24 212 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 213 233 POTENTIAL.
FT DOMAIN 234 616 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 33 195 4 X TNFR-CYS.
FT REPEAT 33 69 TNFR-CYS 1.
FT REPEAT 70 112 TNFR-CYS 2.
FT REPEAT 113 152 TNFR-CYS 3.
FT REPEAT 153 195 TNFR-CYS 4.
FT DISULFID 34 46 BY SIMILARITY.
FT DISULFID 47 60 BY SIMILARITY.
FT DISULFID 50 68 BY SIMILARITY.
FT DISULFID 71 86 BY SIMILARITY.
FT DISULFID 92 112 BY SIMILARITY.
FT DISULFID 114 124 BY SIMILARITY.
FT DISULFID 126 133 BY SIMILARITY.
FT DISULFID 127 151 BY SIMILARITY.
FT DISULFID 154 169 BY SIMILARITY.
FT DISULFID 175 194 BY SIMILARITY.
FT CARBOHYD 105 105 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 616 AA; 66033 MW; E3DE9A7A08196F81 CRC64;
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Query Match 14.38; Score 138.5; DB 4; Length 616;
Best Local Similarity 24.18; Pred. No. 1.1e-06;
Matches 52; Conservative 14; Mismatches 69; Indels 81; Gaps 10;

QY 11 RALCGLLALCALSLGORTGGCGPGRLLLTGTGDARCCR----VHTTRCCR----DY 61
DB 9 RPLFALLLLCALL-----ARLQVALQIAPPCTSEKHVHLGRCCNKCEPGKY 55
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FT	DISULFID	41	54		BY SIMILARITY.
FT	DISULFID	44	62		BY SIMILARITY.
FT	DISULFID	65	80		BY SIMILARITY.
FT	DISULFID	83	97		BY SIMILARITY.
FT	DISULFID	87	105		BY SIMILARITY.
FT	DISULFID	118	142		BY SIMILARITY.
FT	DISULFID	145	160		BY SIMILARITY.
FT	CARBOHYD	98	98		N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	165	165		N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	178	178		N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	289	289		N-LINKED (GLCNAC. .) (POTENTIAL).
SQ	SEQUENCE	401 AA;	46192 MW;	FEC6A31FD4E573A CRC64;	
 Query Match            14.6%; Score 141.5; DB 11; Length 401; Best Local Similarity   27.2%; Pred. No. 3.6e-07; Matches     46; Conservative   11; Mismatches   63; Indels     49; Gaps					
QY	15	GUALICALSGRPTGGCGGPRLLLTGTGDARCRCRVHTTRC--CRDY-----PCEE GS			
DB	36	GROQLLC-----DKCAPGYLV-----KQHCTVRRKTLCPCDPYSDTDSWHTSDE 79			
QY	66	C-----CSEWD-----CMCVPEFHCGDPCCCTTCRHPCPGQGVSOGKF 106			
DB	80	CVCSPVKELQTVKQECNRTHNVCEEGERYLELEFC-----LHRSPPGLGVLAQTTP 130			
QY	107	SFGFCIDCASGTFSG--GHGCHCKPWDTQGFGLTVFPGNKTHNAVNC 153			
DB	137	ERNVTCKRCPDGFFSGETSSRKAPCRKHNTCSSLGILLIKGNATHDNVC 185			
 RESULT     12					
ID	O08712	PRELIMINARY;	PRT;	401 AA.	
AC	O08712:	O70202;			
DT	01-JUL-1997	(TREMBLrel. 04, Created)			
DT	01-JUL-1997	(TREMBLrel. 04, Last sequence update)			
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)			
DE	OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR) (OCIF).				
DE	OCIF).				
GN	TNFRSF11B OR OPG.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BALB/C; TISSUE=KIDNEY;				
RX	MEDLINE=97262071; PubMed=9108485;				
RA	Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,				
RA	Lumelyota, Metaxoa; Woodson S., Bennett L., Boone T., Shimamoto G.				
RA	Derose M., Elliott R., Colombero A., Tan H.-L., Trill G., Sullivan J.				
RA	Davay E., Bucsay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.				
RA	Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,				
RA	Sudgs S., Boyle W.J.;				
RT	"Osteoprotegerin: a novel secreted protein involved in the regulation				
RT	of bone density."				
RL	Cell 89:309-319(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=129/Ola, AND NIH SWISS:				
RX	MEDLINE=98382527; PubMed=9714833;				
RA	Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.				
RA	Higashio K.;				
RT	"Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)				
RT	gene and its expression in embryogenesis.";				
RL	Gene 215:339-343(1998).				
CC	-!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGE				
CC	OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY				
CC	SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO				
CC	OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN				
CC	STROMAL CELLS AND OSTEOCLAST PROGENITORS.				
CC	-!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).				

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FT DISULFID 118 142 BY SIMILARITY.
FT DISULFID 145 160 BY SIMILARITY.
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 263 263 A -> D (IN REF. 2 AND 3).
SQ SEQUENCE 401 AA; 45996 MW; EB42FA51C9D7C71E CRC64;

Query Match 13.7%; Score 133; DB 4; Length 401;
Best Local Similarity 24.2%; Pred. No. 2.8e-06;
Matches 36; Conservative 14; Mismatches 51; Indels 48; Gaps 6;

Qy 53 HTRCCRDYPG---EECCSEWDCMCV-----QPEFHCGDPC--CT----- 87
Db 37 HQLLCDKCPPTYLKQHCTAKWTVCACPDPHYTDSWHTSDECLYCSVPCKELQYVQKE 96

Qy 88 -----TC-----RHHPCPPGGVQSQKSFSGFQCIDCAGTFSG--GH 124
Db 97 CNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERTNTVCKRCPDGFSSNETSS 156

Qy 125 ECHCKPHTDCTQFGFLTVFPCKNTHNVC 153
Db 157 KAPCRKHTNCSVFGLLLTQKGNATHDNC 185
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Search completed: September 4, 2001, 16:14:30  
Job time: 1217 sec

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QY 62 PGECCSEWDCMCVQPEFHG-----DPC----- 85
Db 56 MSSKCTTTSDSVCLP-----CGPEYLDWSNEEDKLLHKVCDTGKALVAVVAGNSTTPRR 111
QY 86 -----CTTCRHH-PCPPGQGVQSQGKFSFGFCIDCASGTFSGHEG--HCKP 130
Db 112 CACTAGYHNSQDCECCRRNTECAPGLGAQHPLQNLKNDTVCKPCLAGYFSDAFSSTDRCRP 171
QY 131 WTDCTQFGFLTVPFGNKTNAV-----VPG-SPPAEP 162
Db 172 WTNCFLGRVHGHEKSDAVCSSLPARKPPNEP 207

RESULT 14
Q9UHP4
ID Q9UHP4 PRELIMINARY; PRT; 372 AA.
AC Q9UHP4;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE OSTEOPROTEGERIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA He 2.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT "Cloning and Expression of Osteoprotegerin from Homo sapiens.";
RL Sheng Wu Hua Hsueh Yu Sheng Wu Li Hsueh Pao 31:680-684(1999).
DR EMBL; AF134187; AAF20168.1; -
DR HSP; P25942; ICDF.
DR InterPro; IPR000488; -
DR InterPro; IPR001368; -
DR Pfam; PF00020; TNFR_C6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS0050; TNFR_NGFR_2; 2.
DR SMART; SM00005; DEATH; 1.
FT NON_TER 1
SQ SEQUENCE 372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;

Query Match 13.7%; Score 133; DB 4; Length 372;
Best Local Similarity 24.2%; Pred. No. 2.6e-06;
Matches 36; Conservative 14; Mismatches 51; Indels 48; Gaps 6;

QY 53 HTRCRDYPG-----BECSEWDCMCV-----QPEFHGCDPC--CT----- 87
Db 16 HQLLCKDCPPGTVLKHCHTAKWKTVCAPCPDHYYTDSWHTSDCLYCSPPVCHELQYVQKE 75
QY 88 -----TC-----RHHPCPPGQGVQSQGKFSFGFCIDCASGTFSG--GH 124
Db 76 CNRTHNRVCECKRGYLEIFCLKHSRCPGPGFGVQAGTPERNTVCKRCPDGFSTSS 135
QY 125 ECHCKPWTDTQFGFLTVPFGNKTNAV 153
Db 136 KAPCRHNTCSVFGLLLTOKGNATHDNIC 164

RESULT 15
O00300
ID O00300 PRELIMINARY; PRT; 401 AA.
AC O00300; O60236;
DT 01-JUL-1997 (TremBLrel. 04, Created)
DT 01-JUL-1997 (TremBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
DE (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
GN TNFRSF11B OR OPB OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG FIBROBLAST;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA Tsuda E., Morinaga T., Higashio K.;
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RT osteoclastogenesis in vitro.";
RL Endocrinology 139:1329-1337(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT "Cloning and characterization of the gene encoding human
RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";
RL Eur. J. Biochem. 254:685-691(1998).
CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,
CC KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN
CC A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED IN
CC THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; AB002146; BAA25910.1; -
DR EMBL; AB008822; BAA32076.1; -
DR EMBL; AB008821; BAA32076.1; JOINED.
DR EMBL; U94332; AAB53709.1; -
DR HSP; P25942; ICDF.
DR MIM; 602643; -
DR InterPro; IPR000488; -
DR InterPro; IPR001368; -
DR Pfam; PF00020; TNFR_C6; 3.
DR PRODOM; PD000771; -; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS0050; TNFR_NGFR_2; 2.
DR SMART; SM00005; DEATH; 1.
KW Glycoprotein; Repeat; Cytokine; Signal.
FT SIGNAL 1 21 BY SIMILARITY
FT CHAIN 22 401 OSTEOPROTEGERIN.
FT DOMAIN 23 183 4 X TNFR-CYS.
FT REPEAT 23 63 TNFR-CYS 1.
FT REPEAT 64 106 TNFR-CYS 2.
FT REPEAT 107 143 TNFR-CYS 3.
FT REPEAT 144 201 TNFR-CYS 4.
FT DOMAIN 306 365 DEATH DOMAIN.
FT DISULFID 41 54 BY SIMILARITY.
FT DISULFID 44 62 BY SIMILARITY.
FT DISULFID 65 80 BY SIMILARITY.
FT DISULFID -83 97 BY SIMILARITY.
FT DISULFID 87 105 BY SIMILARITY.
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2001, 09:46:14 ; Search time 12.35 Seconds  
(without alignments)  
390.133 Million cell updates/sec

Title: US-09-512-363-2

Perfect score: 234

Sequence: 1 MAQHGMGAMFALCGIALLC.....EEGRGSAEKGRLGLDW 234

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 197339 seqs, 20590346 residues

Word size : 0

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	193	82.5	241	3	US-08-911-423-4
3	187	79.9	311	3	US-08-911-423-8
4	99	42.3	232	3	US-08-911-423-7
5	11	4.7	228	3	US-08-911-423-2
6	8	3.4	782	1	US-07-725-083-2
7	8	3.4	782	4	US-08-669-286-10
8	8	3.4	782	4	US-09-469-253-10
9	7	3.0	335	2	US-08-289-699A-4
10	7	3.0	335	2	US-08-878-283-4
11	7	3.0	603	4	US-09-097-889-23
12	7	3.0	713	1	US-08-188-228-62
13	7	3.0	713	1	US-08-332-643-56
14	7	3.0	713	1	US-08-332-638-62
15	7	3.0	751	4	US-09-036-987A-24
16	7	3.0	1010	4	US-08-882-046-7
17	7	3.0	1218	2	US-08-400-159-6
18	7	3.0	1218	3	US-08-611-729A-6
19	7	3.0	1218	4	US-08-882-046-2
20	7	3.0	1219	4	US-08-882-046-5
21	6	2.6	15	4	US-09-077-354B-6
22	6	2.6	15	5	PCT-US93-06751-23
23	6	2.6	16	3	US-08-793-426A-4
24	6	2.6	16	4	US-09-294-565-4
25	6	2.6	29	1	US-08-376-362A-18
26	6	2.6	34	1	US-08-190-802A-165
27	6	2.6	79	6	Patent No. 5284931-7

ALIGNMENTS

RESULT 1  
US-08-911-423-6  
; Sequence 6, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-6

Sequence 191, Appl  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 25, Appl  
Sequence 6, Appli  
Sequence 2, Appli  
Sequence 12, Appl  
Sequence 11, Appl  
Sequence 11, Appl  
Sequence 8, Appli  
Sequence 8, Appli  
Patent No. 5489533  
Sequence 2, Appli  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 1, Appli  
Sequence 52, Appl  
Sequence 360, App

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
;; STREET: 1100 New York Avenue, Suite 600  
;; CITY: Washington  
;; STATE: D.C.  
;; COUNTRY: USA  
;; ZIP: 20005  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; FILING DATE: 03-JUL-1991  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/353,432  
;; FILING DATE: 18-MAY-1989  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Goldstein, Jorge A.  
;; REGISTRATION NUMBER: 29,021  
;; REFERENCE/DOCKET NUMBER: 0609.2170001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 371-2600  
;; TELEFAX: (202) 371-2540  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 782 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-07-725-083-2

Query Match 3.4%; Score 8; DB 1; Length 782;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ALLCALS 24  
Db 9 ALLCALS 16

RESULT 7  
US-08-669-286-10  
; Sequence 10, Application US/08669286  
; Patent No. 6130060  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, SEIJI  
; APPLICANT: NAKURAI, TAKASHI  
; APPLICANT: NEZU JUNI-ICHI  
; TITLE OF INVENTION: GENE ENCODING ADSEVERIN  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP  
; STREET: P.O. Box 747  
; CITY: Falls Church  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY Jr., Gerald M.  
; REGISTRATION NUMBER: 28,977

;; REFERENCE/DOCKET NUMBER: 230-110P  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (703) 205-8000  
;; TELEFAX: (703) 205-8050  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 782 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-669-286-10

Query Match 3.4%; Score 8; DB 4; Length 782;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ALLCALS 24  
Db 9 ALLCALS 16

RESULT 8  
US-09-469-253-10  
; Sequence 10, Application US/09469253  
; Patent No. 6184352  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, SEIJI  
; APPLICANT: SAKURAI, TAKASHI  
; APPLICANT: NEZU, JUNI-ICHI  
; TITLE OF INVENTION: GENE ENCODING ADSEVERIN  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP  
; STREET: P.O. Box 747  
; CITY: Falls Church  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/669,286  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY Jr., Gerald M.  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 230-110P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 782 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-469-253-10

Query Match 3.4%; Score 8; DB 4; Length 782;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MGAFRALCGLLCALSLGQRTGPGGGRLLLTGTDAKCCRVHTTRCCRDYPGEEC 60  
QY 67 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQVQSGKFSFGFQIDCASGTFSGGHEG 126  
Db 61 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQVQSGKFSFGFQIDCASGTFSGGHEG 120  
QY 127 HCKPWTCTQGFGLTVFPGNKTNNVAVCPGPPAPBPLGWLTVVLLAVAAACVLLLTSAQLG 186  
Db 121 HCKPWTCTQGFGLTVFPGNKTNNVAVCPGPPAPBPLGWLTVVLLAVAAACVLLLTSAQLG 180  
QY 187 LHIWQLR 193  
Db 181 LHIWQLR 187

RESULT 4  
US-08-911-423-7  
; Sequence 7, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 232 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-7

Query Match 42.3%; Score 99; DB 3; Length 232;  
Best Local Similarity 100.0%; Pred. No. 3.7e-88;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGAFRALCGLLCALSLGQRTGPGGGRLLLTGTDAKCCRVHTTRCCRDYPGEEC 66  
Db 1 MGAFRALCGLLCALSLGQRTGPGGGRLLLTGTDAKCCRVHTTRCCRDYPGEEC 60

QY 67 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQVQSGK 105  
Db 61 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQVQSGK 99  
RESULT 5  
US-08-911-423-2  
; Sequence 2, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-2

Query Match 4.7%; Score 11; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 0.0045;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 FPGNKTNNVAVC 153  
Db 131 FPGNKTNNVAVC 141

RESULT 6  
US-07-725-083-2  
; Sequence 2, Application US/07725083  
; Patent No. 5407821  
; GENERAL INFORMATION:  
; APPLICANT: Breakfield, Xandra O.  
; APPLICANT: Ozellus, Laurie J.  
; TITLE OF INVENTION: Genetic Diagnosis of Torsion Dystonia  
; NUMBER OF SEQUENCES: 2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 603 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-09-097-889-23

Query Match 3.0%; Score 7; DB 4; Length 603;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 182 SAQLGLH 188  
Db 224 SAQLGLH 230

RESULT 12  
US-08-188-228-62  
; Sequence 62, Application US/08188228  
; Patent No. 5597725  
; GENERAL INFORMATION:  
; APPLICANT: Suzuki, Shintaro  
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS  
; NUMBER OF SEQUENCES: 62  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/188,228  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/049,460  
; FILING DATE: 19 APR 1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/872,643  
; FILING DATE: 17 APR 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5597725and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 31340  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 62:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 713 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-188-228-62

Query Match 3.0%; Score 7; DB 1; Length 713;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 VLLLTSA 183  
Db 16 VLLLTSA 22  
RESULT 13  
US-08-332-643-56  
; Sequence 56, Application US/08332643  
; Patent No. 5639634  
; GENERAL INFORMATION:  
; APPLICANT: Suzuki, Shintaro  
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/332,643  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/872,643  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5639634and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/30795  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 713 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-332-643-56

Query Match 3.0%; Score 7; DB 1; Length 713;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 VLLLTSA 183  
Db 16 VLLLTSA 22

RESULT 14  
US-08-332-638-62  
; Sequence 62, Application US/08332638  
; Patent No. 5646250  
; GENERAL INFORMATION:  
; APPLICANT: Suzuki, Shintaro  
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS  
; NUMBER OF SEQUENCES: 62  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago

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QY 17 ALLCALS 24
      |||||
Db 9 ALLCALS 16

RESULT 9
US-08-289-699A-4
; Sequence 4, Application US/08289699A
; Patent No. 5695993
; GENERAL INFORMATION:
; APPLICANT: Fukudome, Kenji
; APPLICANT: Esmon, Charles T.
; TITLE OF INVENTION: Cloning and Regulation of an Endothelial
; TITLE OF INVENTION: Cell Protein C/Activated Protein C Receptor
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 West Peachtree
; STREET: Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30306-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/289,699A
; FILING DATE: 12-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMR152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)873-8794
; TELEFAX: (404)873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-289-699A-4

Query Match 3.0%; Score 7; DB 1; Length 335;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 GPGRLLL 41
      |||||
Db 216 GPGRLLL 222

RESULT 10
US-08-878-283-4
; Sequence 4, Application US/08878283
; Patent No. 5852171
; GENERAL INFORMATION:
; APPLICANT: Fukudome, Kenji
; APPLICANT: Esmon, Charles T.
; TITLE OF INVENTION: Cloning and Regulation of an Endothelial
; TITLE OF INVENTION: Cell Protein C/Activated Protein C Receptor
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 West Peachtree
; STREET: Street
; CITY: Atlanta

Query Match 3.0%; Score 7; DB 1; Length 335;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 GPGRLLL 41
      |||||
Db 216 GPGRLLL 222

RESULT 11
US-09-097-889-23
; Sequence 23, Application US/09097889
; Patent No. 6218117
; GENERAL INFORMATION:
; APPLICANT: Heirnsstadt, Corrina
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT QUANTITATIVELY ALTER DETECTABLE
; TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA: MITOCHONDRIAL DNA RATIOS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,889
; FILING DATE: 15-JUN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenman Ph.D., Stephen J.
; REGISTRATION NUMBER: 43,058
; REFERENCE/DOCKET NUMBER: 660088.417
```



; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/332,638  
; FILING DATE: 01-NOV-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/872,643  
; FILING DATE: 17 APR 1992  
; APPLICATION NUMBER: US/08/049,460  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5646250and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 31340  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 62:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 713 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-332-638-62

Query Match 3.0%; Score 7; DB 1; Length 713;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 VLLLTSA 183  
|||||||  
DB 16 VLLLTSA 22

RESULT 15  
US-09-036-987A-24  
; Sequence 24, Application US/09036987A  
; Patent No. 6143526  
; GENERAL INFORMATION:  
; APPLICANT: Baltz, Richard H.  
; APPLICANT: Broughton, Mary C.  
; APPLICANT: Crawford, Kathryn P.  
; APPLICANT: Madduri, Krishnamurthy  
; APPLICANT: Merlo, Donald J.  
; APPLICANT: Treadway, Patti J.  
; APPLICANT: Turner, Jan R.  
; APPLICANT: Waldron, Clive  
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dow Agrosciences LLC Patent Department  
; STREET: 9330 Zionsville Road  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: USA  
; ZIP: 46268  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/036,987A

; FILING DATE: 09-MAR-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stuart, Donald R  
; REGISTRATION NUMBER: 28,479  
; REFERENCE/DOCKET NUMBER: 50,608  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317)337-4816  
; TELEFAX: (317)337-4847  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 751 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-036-987A-24

Query Match 3.0%; Score 7; DB 4; Length 751;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 TGGPGCG 35  
|||||||  
DB 364 TGGPGCG 370

Search completed: September 5, 2001, 09:46:36  
Job time: 22 sec

Qy 181 TSAQLGLHIWQLRKTQLLEVPSTEDARSCOFFPEERGERSAEKRGRLGLWV 234  
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Db 181 TSAQLGLHIWQLRKTQLLEVPSTEDARSCOFFPEERGERSAEKRGRLGLWV 234

RESULT 2  
QY505 PRELIMINARY; PRT; 241 AA.  
AC QY505;  
DT 01-NOV-1999 (TReMBLrel. 12, Created)  
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE GLUCOCORTICOID-INDUCED TNFR-RELATED PROTEIN.  
GN TNFRSF18.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BONE MARROW;  
RA Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M.,  
RA Baldwin D.T., Gray A.M., Dowd P., Brush J., Heldens S., Schow P.,  
RA Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.,  
RT "Identification of a new member of the tumor necrosis factor family  
and its receptor, a human ortholog of mouse GITR.";  
RL Curr. Biol. 0:0-0(1999).  
DR EMBL; AF125304; AAD22635.1; -.  
DR InterPro; IPR001368; -.  
DR SMART; SM00208; TNFR; 1.  
SQ SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7E82CBE CRC64;

Query Match 82.5%; Score 193; DB 4; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1.3e-184;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQHGMAGAFRALCGLALLCALSGLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
|||||  
Db 1 MAQHGMAGAFRALCGLALLCALSGLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
Qy 61 YPGECCSEWDCMCVQPEFHCGDPCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
|||||  
Db 61 YPGECCSEWDCMCVQPEFHCGDPCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
Qy 121 SGGHEGCHKPWTDC 193  
|||||  
Db 121 SGGHEGCHKPWTDC 193

RESULT 3  
QY505 PRELIMINARY; PRT; 255 AA.  
AC QY505;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)  
DE GITR-D.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=THYMUS;  
RA Nocentini G., Bartoli A., Ronchetti S., Mastrodicasa E., Riccardi C.,  
RT "Identification of a soluble human GITR splicing (hGITR-D).";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF241229; AAF63506.1; -.  
SQ SEQUENCE 255 AA; 26827 MW; C986652AC97AF2CC CRC64;

Query Match 57.3%; Score 134; DB 4; Length 255;  
Best Local Similarity 100.0%; Pred. No. 1.1e-125;  
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQHGMAGAFRALCGLALLCALSGLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
|||||  
Db 1 MAQHGMAGAFRALCGLALLCALSGLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
Qy 61 YPGECCSEWDCMCVQPEFHCGDPCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
|||||  
Db 61 YPGECCSEWDCMCVQPEFHCGDPCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
Qy 121 SGGHEGCHKPWTDC 134  
|||||  
Db 121 SGGHEGCHKPWTDC 134

RESULT 4  
QY505 PRELIMINARY; PRT; 222 AA.  
AC QY505;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE GITR-C.  
GN TNFRSF18.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=THYMUS;  
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,  
RA Migliorati G., Riccardi C.,  
RT "Identification of three novel mRNA splice variants of GITR.";  
RL Cell Death Differ. 0:0-0(2000).  
DR EMBL; AF229433; AAF61567.1; -.  
DR InterPro; IPR000561; -.  
DR SMART; SM00181; EGF; 1.  
SQ SEQUENCE 222 AA; 24450 MW; 594932BA425A79CA CRC64;

Query Match 4.7%; Score 11; DB 11; Length 222;  
Best Local Similarity 100.0%; Pred. No. 0.007;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 143 FPGNKTHNAV 153  
|||||  
Db 131 FPGNKTHNAV 141

RESULT 5  
QY505 PRELIMINARY; PRT; 228 AA.  
AC QY505;  
DT 01-JAN-1998 (TReMBLrel. 05, Created)  
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE GLUCOCORTICOID INDUCED TNFR FAMILY RELATED PROTEIN PRECURSOR.  
GN TNFRSF18 OR GITR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C3H/HEN;  
RX MEDLINE=97322352; PubMed=9177197;



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2001, 09:46:19 ; Search time 22.44 Seconds  
(without alignments)  
1379.651 Million cell updates/sec

Title: us-09-512-363-2

Perfect score: 234

Sequence: 1 MAQHGMAGAFRALCGLALIC.....EEERGSAAEKXRLGLMW 234

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 425026 seqs, 132305027 residues

Word size : 0

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL16.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_unclassified.\*  
13: sp\_vertebrate.\*  
14: sp\_virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	234	100.0	234	4	Q95851 homo sapien
2	193	82.5	241	4	Q9Y5U5 homo sapien
3	134	57.3	255	4	Q9NYJ9 homo sapien
4	11	4.7	222	11	Q9JKR2 mus musculus
5	11	4.7	228	11	Q35714 mus musculus
6	11	4.7	294	11	Q9JKR3 mus musculus
7	8	3.4	215	5	Q9TZD2 caenorhabdi
8	8	3.4	241	2	O67793 aquifex aeo
9	8	3.4	245	4	O14596
10	8	3.4	260	2	Q9L2D4
11	8	3.4	422	10	Q9LFM8
12	8	3.4	438	14	O39493
13	8	3.4	504	4	O75850
14	8	3.4	509	2	O05457
15	8	3.4	548	2	Q9EWY9
16	8	3.4	829	4	Q9Y5D4
17	8	3.4	932	4	Q9Y5H0
18	7	3.0	69	2	Q9HUV7
19	7	3.0	79	4	Q9Y2Q7 homo sapien

20	7	3.0	93	4	Q9UMM3	Q9umm3 homo sapien
21	7	3.0	106	5	Q9VG89	Q9vg89 drosophila
22	7	3.0	120	2	Q53783	Q53783 streptomyce
23	7	3.0	124	2	Q9FC37	Q9fc37 streptomyce
24	7	3.0	133	1	O58336	O58336 pyrococcus
25	7	3.0	133	1	Q9UYT8	Q9uyt8 pyrococcus
26	7	3.0	144	2	Q91146	Q91146 pseudomonas
27	7	3.0	148	8	Q9G9S8	Q9g9s8 metridia lu
28	7	3.0	172	2	O54470	O54470 serratia ma
29	7	3.0	200	2	Q917A2	Q917a2 pseudomonas
30	7	3.0	204	2	O9X600	O9x6q0 leptospira
31	7	3.0	213	2	O9PSD5	O9psd5 deinococcus
32	7	3.0	222	4	O14569	O14569 homo sapien
33	7	3.0	222	11	Q9WUE3	Q9wue3 mus musculu
34	7	3.0	233	3	Q9HFL8	Q9hfl8 metarhizium
35	7	3.0	242	10	O9LDY4	O9ldy4 oryza sativ
36	7	3.0	256	2	O31618	O31618 bacillus su
37	7	3.0	261	2	Q9LOW0	Q9low0 streptomyce
38	7	3.0	272	2	Q9RS38	Q9rs38 deinococcus
39	7	3.0	287	8	Q9XLV8	Q9xlv8 dipionema p
40	7	3.0	288	2	O9RY11	O9ryy1 deinococcus
41	7	3.0	296	10	O9FWE7	O9fwe7 oryza sativ
42	7	3.0	306	6	O9GKE3	O9gke3 oryctolagus
43	7	3.0	315	5	Q9V738	Q9v738 drosophila
44	7	3.0	320	2	Q9ZBX6	Q9zbx6 streptomyce
45	7	3.0	320	2	Q9X7P6	Q9x7p6 streptomyce

#### ALIGNMENTS

RESULT 1

ID O95851 PRELIMINARY; PRT; 234 AA.

AC O95851;  
DT 01-MAY-1999 (TREMREL. 10, Created)  
DT 01-MAY-1999 (TREMREL. 10, Last sequence update)  
DT 01-MAR-2001 (TREMREL. 16, Last annotation update)  
DE TNF RECEPTOR SUPERFAMILY ACTIVATION-INDUCIBLE PROTEIN.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99156876; PubMed=10037686;

RA Kwon B., Yu K.Y., Ni J., Yu G.L., Jang I.K., Kim Y.J., Xing L.,

RA Liu D., Wang S.X., Kwon B.S.;

RT "Identification of a novel activation-inducible protein of the tumor

RT necrosis factor receptor superfamily and its ligand.";

RL J. Biol. Chem. 274:6056-6061(1999).

DR EMBL; AF117297; AAD19694.1; -.

DR InterPro; IPR001368; -.

DR SMART; SM00208; TNFR; 1.

KW Receptor.

SQ SEQUENCE 234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;

Query Match 100.0%; Score 234; DB 4; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.4e-225;

Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMAGAFRALCGLALICLSLQGRPTGGCGGPRLLLTGTGTCRCRVHTTCCRD 60

Db 1 MAQHGMAGAFRALCGLALICLSLQGRPTGGCGGPRLLLTGTGTCRCRVHTTCCRD 60

QY 61 YPEECCSMDCMQVPEHCPCCTTCRHHPCPGQVQSGKSFQCIDCASGTF 120

Db 61 YPEECCSMDCMQVPEHCPCCTTCRHHPCPGQVQSGKSFQCIDCASGTF 120

QY 121 SGGHEGCHKPWTDCQFGFLTVPFGNKNHVCVPGSPPAEPLGWLTVVLLAAACVLL 180

Db 121 SGGHEGCHKPWTDCQFGFLTVPFGNKNHVCVPGSPPAEPLGWLTVVLLAAACVLL 180

KW Hypothetical protein.  
SQ SEQUENCE 241 AA; 27514 MW; B9432671E3308A77 CRC64;

Query Match 3.4%; Score 8; DB 2; Length 241;  
Best Local Similarity 100.0%; Pred. No. 7.4; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0;

Qy 17 ALLCALSL 24  
| | | | | | | |  
Db 38 ALLCALSL 45

RESULT 9  
O14596 PRELIMINARY; PRT; 245 AA.  
AC O14596;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DE FOLATE BINDING PROTEIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-SALIVARY GLAND;  
RA Verma R.S., Elwood P.C.;  
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF000380; AAB81937.1; -;  
SQ SEQUENCE 245 AA; 26268 MW; BA36B7DB95FC0E20 CRC64;

Query Match 3.4%; Score 8; DB 4; Length 245;  
Best Local Similarity 100.0%; Pred. No. 7.5;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 180 LTSALQL 187  
| | | | | | | |  
Db 177 LTSALQL 184

RESULT 10  
Q9L2D4 PRELIMINARY; PRT; 260 AA.  
AC Q9L2D4;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE HYPOTHETICAL 26.0 KDA PROTEIN.  
GN SC7A8.24C  
OS Streptomyces coelicolor.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A3(2);  
RA Oliver K., Harris D.;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A3(2);  
RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A3(2);  
RX MEDLINE=97000351; PubMed=8843436;  
RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,  
RA Kinashi H., Hopwood D.A.;  
RT "A set of ordered cosmids and a detailed genetic and physical map for

RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";  
RL Mol. Microbiol. 21:77-96(1996).  
DR EMBL; AL137187; CAB69773.1; -;  
DR InterPro: IPR002781; -;  
DR Pfam: PF01925; DUF81; 2.  
KW Hypothetical protein.  
SQ SEQUENCE 260 AA; 25996 MW; DA0F43E1197BACE1 CRC64;

Query Match 3.4%; Score 8; DB 2; Length 260;  
Best Local Similarity 100.0%; Pred. No. 7.9; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0;

Qy 168 VLLAVAA 175  
| | | | | | | |  
Db 112 VLLAVAA 119

RESULT 11  
Q9LFM8 PRELIMINARY; PRT; 422 AA.  
AC Q9LFM8;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE HYPOTHETICAL 48.6 KDA PROTEIN.  
GN F2I11.180.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
OC Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bevan M., Peters S.A., van Staveren M., Dirkse W., Stiekema W.,  
RA Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL360314; CAB96664.1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 422 AA; 48570 MW; 31D1BC828F40BC39 CRC64;

Query Match 3.4%; Score 8; DB 10; Length 422;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 173 VAACVLL 180  
| | | | | | | |  
Db 402 VAACVLL 409

RESULT 12  
O39493 PRELIMINARY; PRT; 438 AA.  
AC O39493;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
DE GLYCOPROTEIN M.  
GN UL10.  
OS Bovine herpesvirus 1.  
OC Viruses; GSDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Varicellovirus.  
OX NCBI\_TaxID=10320;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-JURA;  
RX MEDLINE=95313343; PubMed=7793062;  
RA Vlcek C., Benes V., Lu Z., Kutish G.F., Paces V., Rock D.,

RA Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,  
 RA Moraca R., Migliorati G., Riccardi C.;  
 RT "A new member of the tumor necrosis factor/nerve growth factor  
 RT receptor family inhibits T cell receptor-induced apoptosis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALE/C;  
 RA Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,  
 RA Migliorati G., Riccardi C.;  
 RT "Gene structure and chromosomal assignment of GTR, a mouse member of  
 RT the tumor necrosis factor/nerve growth factor receptor family.";  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U82534; AAB81243.1; -;  
 DR EMBL; AF109216; AAF14231.1; -;  
 DR MGD; MGI:894675; Tnfrsf18.  
 DR InterPro: IPR000561; -;  
 DR SMART; SM00181; EGF; 1.  
 KW SIGNAL 1 19 POTENTIAL.  
 FT SIGNAL 20 228 GLUCOCORTICOID INDUCED TNFR FAMILY  
 FT CHAIN 20 228 RELATED PROTEIN.  
 FT  
 SQ SEQUENCE 228 AA; 25334 MW; 50D8C275D9C56259 CRC64;

Query Match 4.7%; Score 11; DB 11; Length 228;  
 Best Local Similarity 100.0%; Pred. No. 0.0072;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 FPGNKTTHNAVC 153  
 Db 131 FPGNKTTHNAVC 141  
 |||||

RESULT 6  
 Q9JKR3 PRELIMINARY; PRT; 294 AA.  
 AC Q9JKR3;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE GTR-B.  
 GN TNFRSF18.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=THYMUS;  
 RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,  
 RA Migliorati G., Riccardi C.;  
 RT "Identification of three novel mRNA splice variants of GTR.";  
 RL Cell Death Differ. 0:0-0(2000).  
 DR EMBL; AF229432; AAF61566.1; -;  
 DR InterPro: IPR000561; -;  
 DR SMART; SM00181; EGF; 1.  
 SQ SEQUENCE 294 AA; 32658 MW; FE0D4AE6A007BA9A CRC64;

Query Match 4.7%; Score 11; DB 11; Length 294;  
 Best Local Similarity 100.0%; Pred. No. 0.0088;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 FPGNKTTHNAVC 153  
 Db 131 FPGNKTTHNAVC 141  
 |||||

RESULT 7  
 Q9T2D2 PRELIMINARY; PRT; 215 AA.  
 AC Q9T2D2;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE R160.6 PROTEIN.  
 GN R160.6  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RC MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,  
 RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,  
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.; and C.  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans.";  
 RL Nature 368:32-38(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RC Waterston R.;  
 RA Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF099001; AAC68733.1; -;  
 SQ SEQUENCE 215 AA; 24502 MW; 0AAC4FFF7914F65 CRC64;

Query Match 3.4%; Score 8; DB 5; Length 215;  
 Best Local Similarity 100.0%; Pred. No. 6.8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 VLLAVAAC 176  
 Db 24 VLLAVAAC 31  
 |||||

RESULT 8  
 O67793 PRELIMINARY; PRT; 241 AA.  
 ID O67793;  
 AC O67793;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE HYPOTHETICAL 27.5 KDA PROTEIN.  
 GN AQ\_1986.  
 OS Aquifex aeolicus.  
 OC Bacteria; Aquificales; Aquificaceae; Aquifex.  
 OX NCBI\_TaxID=63363;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VF5;  
 RC MEDLINE=98196666; PubMed=9537320;  
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,  
 RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,  
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;  
 RT "The complete genome of the hyperthermophilic bacterium Aquifex  
 RT aeolicus.";  
 RL Nature 392:353-358(1998).  
 DR EMBL; AE000766; AAC07762.1; -;

RT "A set of ordered cosmids and a detailed genetic and physical map for  
RL the 8 Mb Streptomyces coelicolor A3(2) chromosome.";  
RL Mol. Microbiol. 21:77-96(1996).  
DR EMBL; AL445503; CAC13089.1; -  
KW Kinase.  
SQ SEQUENCE 548 AA; 58276 MW; 72F37F817FD5D8E9 CRC64;

Query Match 3.4%; Score 8; DB 2; Length 548;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 VLLAVAA 175  
| | | | |  
Db 24 VLLAVAA 31

Search completed: September 5, 2001, 09:47:57  
Job time: 98 sec

RA Letchworth G.J., Schwyzzer M.;  
 RT "Nucleotide sequence analysis of a 30-kb region of the bovine  
 RT herpesvirus 1 genome which exhibits a colinear gene arrangement with  
 RT the UL21 to UL4 genes of herpes simplex virus.";

RL Virology 210:100-108(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-JURA;  
 RA Schwyzzer M., Paces V., Letchworth G.J., Misra V., Buhk H.J.,  
 RA Lowery D.E., Simard C., Bello L.J., Thiry E., Vitek C.;  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ004801; CA006124.1; -;  
 DR InterPro: IPR000785; -;  
 DR Pfam: PF01528; Herpes\_glycop. 1.  
 DR PRINTS: PR00333; HSVINTEGLMP.  
 SQ SEQUENCE 438 AA; 45517 MW; 4E7C7FA64FAAEFC7 CRC64;

Query Match 3.4%; Score 8; DB 14; Length 438;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 VLLAVAA 175  
 Db 93 VLLAVAA 100  
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RESULT 13  
 OT5850  
 ID 075850 PRELIMINARY; PRT; 504 AA.  
 AC 075850;  
 DT 01-NOV-1998 (TReMBLrel. 08, Created)  
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE WUGSC:HJD0751H13.3 PROTEIN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Leonard S., Graves T., Strommatt C.;  
 RT "The sequence of Homo sapiens PAC clone DJ0751H13.";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Waterston R.H.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Waterston R.;  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
 DR EMBL: AC004877; AAC36300.1; -;  
 DR HSP: P08047; 1SP2.  
 DR InterPro: IPR000822; -;  
 DR Pfam: PF00096; zf-C2H2; 12.  
 DR PRINTS: PR00048; ZINC\_FINGER.  
 DR PROSITE: PS00028; ZINC\_FINGER\_C2H2; 12.  
 DR SMART: SM00355; ZnF\_C2H2; 1.  
 KW DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.  
 SQ SEQUENCE 504 AA; 55490 MW; F9308169B56DA27B CRC64;

Query Match 3.4%; Score 8; DB 4; Length 504;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 GPGCGPG 37  
 Db 317 GPGCGPG 324  
 |||||

RESULT 14

O05457  
 ID 005457 PRELIMINARY; PRT; 509 AA.  
 AC 005457;  
 DT 01-JUL-1997 (TReMBLrel. 04, Created)  
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)  
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
 DE HYPOTHETICAL 53.2 KDA PROTEIN.  
 GN RV3887C OR MTCY15F10.25  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E.,  
 RA Taylor K., Whitehead S., Barrell B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence.";  
 RL Nature 393:537-544(1998).  
 DR EMBL: Z94121; CAB08087.1; -;  
 DR TuberculList; RV3887c; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 509 AA; 53278 MW; 00F961EAF1C4B1B9 CRC64;

Query Match 3.4%; Score 8; DB 2; Length 509;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 VLLAVAA 175  
 Db 205 VLLAVAA 212  
 |||||

RESULT 15  
 Q9EWY9  
 ID Q9EWY9 PRELIMINARY; PRT; 548 AA.  
 AC Q9EWY9;  
 DT 01-MAR-2001 (TReMBLrel. 16, Created)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE PUTATIVE TWO COMPONENT SYSTEM HISTIDINE KINASE.  
 GN 28CG38.30C.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A3(2);  
 RA Saunders D.C., Harris D.;  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A3(2);  
 RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A3(2);  
 RX MEDLINE=97000351; PubMed=8843436;  
 RA Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,  
 RA Kinashi H., Hopwood D.A.;



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2001, 09:46:14 ; Search time 20.66 Seconds  
(without alignments)  
686.641 Million cell updates/sec

Title: US-09-512-363-2

Perfect score: 234

Sequence: 1 MAQHGAMGAFRALGGLALLC.....EERGRSAAEKRLGLDLW 234

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 412676 seqs, 60623988 residues

Word size : 0

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

A\_Geneseq\_0601:\*

1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT:\*

2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT:\*

3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	234	100.0	234	21	AA195879 Human tumour necro
2	234	100.0	234	21	AA195879 Tumour necrosis fa
3	228	97.4	228	19	AA195879 Truncated human 31
4	193	82.5	241	19	AA195879 Amino acid sequenc
5	193	82.5	241	20	AA195879 Human TNF receptor
6	193	82.5	241	21	AA195879 Human protein PRO3
7	193	82.5	241	21	AA195879 Human PRO364 prote
8	193	82.5	241	21	AA195879 Human tumour necro
9	193	82.5	241	21	AA195879 Human PRO364 prote
10	193	82.5	241	21	AA195879 Human PRO364 prote
11	193	82.5	241	22	AA195879 Human Immunostimul

12	193	82.5	241	22	AA195879 Human PRO364. Hom
13	193	82.5	241	22	AA195879 Human PRO364 prote
14	193	82.5	241	22	AA195879 Human angiotensin
15	193	82.5	241	22	AA195879 Human molecule ass
16	187	79.9	235	21	AA195879 Human 312C2 protei
17	187	79.9	311	19	AA195879 Human tumour necro
18	173	73.9	240	21	AA195879 TRILSV2 amino acid
19	173	73.9	240	21	AA195879 PRO364-related EST
20	139	59.4	317	22	AA195879 Polypeptide encode
21	138	59.0	316	22	AA195879 Human tumour necro
22	132	56.4	241	21	AA195879 TRILSV1 amino acid
23	132	56.4	241	21	AA195879 Human 312C2 protei
24	99	42.3	232	19	AA195879 Mouse glucocorticoid
25	11	4.7	222	19	AA195879 Mouse glucocorticoid
26	11	4.7	228	19	AA195879 Amino acid sequenc
27	11	4.7	228	19	AA195879 Mouse glucocorticoid
28	11	4.7	294	19	AA195879 Human 5' EST secre
29	7	3.0	50	20	AA195879 Human 5' EST relat
30	7	3.0	61	21	AA195879 Secreted protein B
31	7	3.0	79	19	AA195879 Secreted protein 1
32	7	3.0	79	20	AA195879 Secreted protein 4
33	7	3.0	79	20	AA195879 Human ORF ORF959
34	7	3.0	120	21	AA195879 CA455 protein. Ze
35	7	3.0	138	13	AA195879 Human COMP/TSP-1 c
36	7	3.0	242	21	AA195879 Renal cancer assoc
37	7	3.0	297	20	AA195879 Murine TANGO 300 e
38	7	3.0	299	22	AA195879 Human COMP/TSP-2 c
39	7	3.0	300	21	AA195879 Zea mays protein f
40	7	3.0	307	21	AA195879 Zea mays protein f
41	7	3.0	312	21	AA195879 TANGO 300 signal p
42	7	3.0	341	22	AA195879 Murine Dendritic C
43	7	3.0	355	22	AA195879 Human secreted pro
44	7	3.0	361	21	AA195879 Human TANGO 300 pr
45	7	3.0	361	22	AA195879 Human TANGO 300 pr

#### ALIGNMENTS

RESULT 1

AA195879

ID AA195879 standard; Protein; 234 AA.

AC AA195879;

DT 20-NOV-2000 (first entry)

DE Human tumour necrosis factor receptor-like protein TR11.

DE TR11; human; tumour necrosis factor receptor-like protein; immunodeficiency; autoimmune disease; rheumatoid arthritis; immunosuppressive; antineoplastic; antiarthritic; haemostatic; dermatological; antiinflammatory; therapy; diagnosis.

OS Homo sapiens.

XX

XX Key Location/Qualifiers

XX Peptide 1..25

XX Protein 26..234

XX Domain 26..162

XX Domain 163..179

XX Domain 180..234

XX Modified-site 146

XX Domain 72..81

XX Domain 84..93

XX Domain 94..100

```

RESULT 4
AAW37839
ID AAW37839 standard; Protein: 241 AA.
XX
AC AAW37839;
XX
DT 28-JUL-1998 (first entry)
XX
DE Amino acid sequence of the human 312C2 T cell protein.
XX
KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
KW antigen-specific T cell proliferation; cytokine production by T-cell;
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;
KW autoimmune disorders.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..726
FT /*tag= a
FT /product= "human 312C2 protein"
XX
PN WO9806842-A1.
XX
PD 19-FEB-1998.
XX
PF 14-AUG-1997; 97WO-US13931.
XX
PR 07-OCT-1996; 96US-0027901.
PR 16-AUG-1996; 96US-0689943.
XX
PA (SCHE ) SCHERING CORP.
XX
PI Gorman DM, Randall TD, Zlotnik A;
XX
DR WPI: 1998-159534/14.
DR N-PSDB; AAV19153.
XX
PT Isolated 312C2 T cell gene - used to develop products for treating,
PT e.g. cancers, auto-immune disorders, transplantation rejection and
PT other T cell disorders
XX
PS Claim 2; Pages 59-60; 71pp; English.
XX
CC This is the amino acid sequence encoding the human 312C2 T cell
CC protein. The 312C2 proteins are expressed in thymus cells and are
CC induced on T cells and spleen cells following activation. Engagement
CC of 312C2 stimulates proliferation of T cell clones, antigen-specific
CC proliferation and cytokine production by T-cells, and potentiates T
CC cell expansion or apoptosis. The products can be used in the
CC treatment of conditions associated with abnormal physiology or
CC development, including abnormal proliferation, e.g. cancerous
CC conditions or degenerative conditions. They can be used in the
CC regulation or development of haematopoietic cells, e.g. lymphoid cells
CC which affect immunological responses, e.g. autoimmune disorders.
XX
SQ Sequence 241 AA;

```

```

Query Match 82.5%; Score 193; DB 19; Length 241;
Best Local Similarity 100.0%; Pred. No. 4.4e-175;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAQHGMGAFRALCGIALCALSLGQRPYGGPCGGPGRLLLTGTARCCRVHTTRCCRD 60
DB 1 maqhgmgafRALCGIALCALSLGQRPYGGPCGGPGRLLLTGTARCCRVHTTRCCRD 60
QY 61 YPGEECCSEWDCMCVPEFHCGDPCCCTTCRHHPCPPGQGVQSGKTSFGQCIDCASGTF 120
DB 61 YPGEECCSEWDCMCVPEFHCGDPCCCTTCRHHPCPPGQGVQSGKTSFGQCIDCASGTF 120
QY 121 SGGHEGHCXKPTWTDCTQFGTLTFPPGNKTHNAVCPGSPPAEPGLGWLTVLLAVAAVCVLL 180

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Db 121 sggheghckpwtcdctqfgltvfpngkthnavcvgpppaepglgwlvtvllavaacvlll 180
QY 181 TSAQLGLHIWQLR 193
Db 181 tsaqLgIhIwqlr 193

RESULT 5
AAW06605
ID AAY06605 standard; Protein: 241 AA.
XX
AC AAY06605;
XX
DT 26-OCT-1999 (first entry)
XX
DE Human TNF receptor homologue PRO364.
XX
KW PRO364; tumour necrosis factor receptor; human; apoptosis;
KW inflammation; antiinflammatory; NF-KB activation;
KW autoimmune disease; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..25
FT /note= "signal peptide"
FT Protein 26..241
FT /note= "mature protein"
FT Modified-site 146
FT /note= "N-glycosylated"
FT Domain 162..180
FT /note= "transmembrane domain"
XX
PN WO9940196-A1.
XX
PD 12-AUG-1999.
XX
PF 09-FEB-1999; 99WO-US026642.
XX
PR 09-FEB-1998; 98US-0024087.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;
PI Pitti RM, Wood WI;
XX
DR WPI: 1999-494296/41.
DR N-PSDB; AAX87670.
XX
PT Tumour necrosis factor receptor homologue - useful for, e.g.
PT modulating apoptosis and NF-KB activation and proinflammatory or
PT autoimmune responses
XX
PS Claim 17; Fig 2A; 104pp; English.
XX
CC The present sequence represents human PRO364, a novel member of the
CC tumour necrosis factor receptor family. The sequence was deduced
CC from a bone marrow cDNA clone (see AAX87670). Methods for the
CC recombinant production of PRO364 polypeptides, e.g. in CHO,
CC Escherichia coli or yeast host cells, are provided. Claimed
CC polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the
CC mature protein) and 26-X of the present sequence, where X is any
CC one of amino acid residues 157-167 of PRO364. PRO364 polypeptides
CC are useful for modulating apoptosis, NF-KB activation and
CC proinflammatory or autoimmune responses in mammalian cells
CC (claimed). Chimeric molecules comprising a PRO364 polypeptide
CC fused to a heterologous sequence such as epitope tag or
CC immunoglobulin Fc region are also claimed. PRO364 can be used in
CC assays to identify other proteins or molecules involved in binding
CC interactions. This is useful for identifying inhibitors or
CC agonists of receptor/ligand binding. The PRO364 polypeptides may
CC also be combined with an agent that is cytotoxic, chemotherapeutic

```



XX PR 21-OCT-1997; 97US-0063212.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PI N1 J, Ruben SM;  
XX DR WPI; 2000-061922/05.  
XX DR N-PSDB; AAZ37762.  
XX PT New tumour necrosis factor receptor-like polypeptides used to, e.g.  
XX PT treat Digeorge syndrome -  
XX PS Claim 14; Fig 1; 167pp; English.  
XX  
CC This is the amino acid sequence of the human tumour necrosis factor  
CC receptor-like protein (TRL1 receptor). The invention relates to TRL1 and  
CC two splice variants TRL1SV1 and TRL1SV2. The nucleotide sequences were  
CC determined by sequencing cloned cDNAs AAZ37765-237766. The TRL1 receptor  
CC and its splice variants show homology to the murine glucocorticoid  
CC induced tumour necrosis factor receptor family-related gene (GIFR).  
CC TRL1, TRL1SV1 and TRL1SV2 polypeptides may be involved in the regulation  
CC of cell-type specific receptor-mediated cell growth, differentiation,  
CC and ultimately, cell death. They can be used for screening for  
CC agonists/antagonists. The polypeptides, agonists or antagonists can be  
CC used for treating a disease state associated with aberrant cell  
CC survival. They can be used for treating immune deficiency disorders,  
CC Digeorge syndrome, HIV infection, severe combined immunodeficiency  
CC (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood  
CC platelet disorders or wounds resulting from trauma or surgery. They can  
CC also be used to treat heart attacks, strokes, Addison's disease,  
CC haemolytic anaemia, rheumatoid arthritis, Goodpasture's syndrome, Grave's  
CC disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome,  
CC systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent  
CC diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,  
CC hypersensitivity to an antigenic molecule, organ rejection or graft  
CC versus host disease, inflammatory conditions, ischaemia-reperfusion  
CC injury, complement-mediated hyperacute rejection, nephritis, cytokine or  
CC chemokine induced lung injury, inflammatory bowel disease, Crohn's  
CC disease, hyperproliferative disorders, or infections. They can also be  
CC used to repair, replace, or protect tissue damaged by congenital  
CC defects, trauma, age, disease, surgery, including cosmetic plastic  
CC surgery, fibrosis, reperfusion injury, peripheral nerve injuries,  
CC neuropathies, and central nervous system disease (e.g. Alzheimer's  
CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral  
CC sclerosis, and Shy-Drager syndrome). The products can also be used for  
CC detection, diagnosis and prognosis.  
XX  
SQ Sequence 234 AA;

Query Match 100.0%; Score 234; DB 21; Length 234;  
Best Local Similarity 100.0%; Pred. No. 5.8e-214;  
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAQHGAMGAFRALCGLALLCALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
DB 1 maqhgamgafralcglallcalslgrptggpgcgprlllgtgdarccrvhttrccrd 60  
QY 61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRRHPCPPGGQVSGQKFSFGFCIDCASGTF 120  
DB 61 ypgeeccsewdcmcvqpefhcgdpcccttrhhpcppggvgvsgqkfsfgfcidcasgtf 120  
QY 121 SGGHEGCHKPWTCTQFGFLTVFPGNKTHNAVCPGSPPAEPLGWLTVVLLAVACVLL 180  
DB 121 sgghegchkpwtctqfgfltvfpgnktthnavcvgpsppaepglwltvvllavaacvll 180  
QY 181 TSAQLGHIWOLRKLTOLLLEVPPTEDARSCQFPPEERGERSAEKGRIGDLW 234  
DB 181 tsaqighiwlrkltolllevpptstedsarcsqfppeergeresaekgrigdlw 234

RESULT 3

AAW37840  
ID AAW37840 standard; Protein; 228 AA.  
XX  
AC AAW37840;  
XX  
DT 28-JUL-1998 (first entry)  
XX  
DE Truncated human 312C2 protein from clone\_A8 amino acid sequence.  
XX  
KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
KW antigen-specific T cell proliferation; cytokine production by T-cell;  
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
KW autoimmune disorders.  
XX  
OS Homo sapiens.  
XX  
PN WO9806842-A1.  
XX  
PD 19-FEB-1998.  
XX  
PF 14-AUG-1997; 97WO-US13931.  
XX  
PR 07-OCT-1996; 96US-0027901.  
PR 16-AUG-1996; 96US-0689943.  
XX  
XX (SCHE ) SCHERING CORP.  
XX  
PI Gorman DM, Randall TD, Zlotnik A;  
XX  
DR WPI; 1998-159534/14.  
DR N-PSDB; AAV19154.  
XX  
PT Isolated 312C2 T cell gene - used to develop products for treating,  
PT e.g. cancers, auto-immune disorders, transplantation rejection and  
PT other T cell disorders  
XX  
PS Disclosure; Pages 61-62; 71pp; English.  
XX  
CC This is the amino acid sequence of the truncated human 312C2 T cell  
CC protein from clone\_A8. The 312C2 proteins are expressed in thymus  
CC cells and are induced on T cells and spleen cells following activation.  
CC Engagement of 312C2 stimulates proliferation of T cell clones,  
CC antigen-specific proliferation and cytokine production by T-cells, and  
CC potentiates T cell expansion or apoptosis. The products can be used  
CC in the treatment of conditions associated with abnormal physiology or  
CC development, including abnormal proliferation, e.g. cancerous  
CC conditions or degenerative conditions. They can be used in the  
CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
CC which affect immunological responses, e.g. autoimmune disorders.  
XX  
SQ Sequence 228 AA;  
Query Match 97.4%; Score 228; DB 19; Length 228;  
Best Local Similarity 100.0%; Pred. No. 2.8e-208;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 MGAFRALCGLALLCALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYDGE 66  
DB 1 mgafralcgllallcalslgrptggpgcgprlllgtgdarccrvhttrccrdydg 60  
QY 67 CSEWDCMCVQPEFHCGDPCCTTCRRHPCPPGGQVSGQKFSFGFCIDCASGTFSGHEG 126  
DB 61 csewdcmcvqpefhcgdpcccttrhhpcppggvgvsgqkfsfgfcidcasgtsfsgheg 120  
QY 127 HCKPWTCTQFGFLTVFPGNKTHNAVCPGSPPAEPLGWLTVVLLAVACVLLLTSAQLG 186  
DB 127 hckpwtctqfgfltvfpgnktthnavcvgpsppaepglwltvvllavaacvllltsaqlg 180  
QY 187 LHWOLRKLTOLLLEVPPTEDARSCQFPPEERGERSAEKGRIGDLW 234  
DB 187 lhwolrkltolllevpptstedsarcsqfppeergeresaekgrigdlw 228

PD 14-SEP-2000.

XX 02-MAR-2000; 2000WO-US05841.

XX 08-MAR-1999; 99WO-US05028.

XX 10-MAR-1999; 99US-0123618.

PR 12-MAR-1999; 99US-0123957.

PR 23-MAR-1999; 99US-0125775.

PR 12-APR-1999; 99US-0128849.

PR 20-APR-1999; 99WO-US08615.

PR 28-APR-1999; 99US-0131445.

PR 04-MAY-1999; 99US-0132371.

PR 14-MAY-1999; 99US-0134287.

PR 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 26-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 28-JUL-1999; 99US-0146222.

PR 01-SEP-1999; 99WO-US20111.

PR 08-SEP-1999; 99WO-US20594.

PR 13-SEP-1999; 99WO-US20944.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.

PR 05-OCT-1999; 99WO-US23089.

PR 29-OCT-1999; 99US-0162506.

PR 29-NOV-1999; 99WO-US28214.

PR 30-NOV-1999; 99WO-US28313.

PR 30-NOV-1999; 99WO-US28409.

PR 01-DEC-1999; 99WO-US28301.

PR 01-DEC-1999; 99WO-US28634.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.

PR 02-DEC-1999; 99WO-US28565.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30999.

PR 30-DEC-1999; 99WO-US31274.

PR 05-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00277.

PR 06-JAN-2000; 2000WO-US00376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;

PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;

PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

XX WPI: 2000-572271/53.

DR N-PSDB; AAC58596.

XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of

PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid

PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -

XX Claim 33: Fig 36; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can

CC be used in the treatment of immune related diseases. The human PRO

CC proteins, anti-PRO antibodies, agonists and antagonists are useful for

CC treating and diagnosing immune related disorders. The disorders are

CC selected from systemic lupus erythematosus, rheumatoid arthritis,

CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,

CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's

CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic

CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,

CC immune-mediated renal disease, demyelinating diseases of the central

CC and peripheral nervous systems, hepatobiliary diseases, inflammatory

CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,

CC autoimmune or immune-mediated skin diseases, allergic diseases,

CC immunological diseases of the lung, and transplantation associated

CC diseases including graft rejection and graft-versus-host-disease.

CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used

CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and

CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein

CC sequences given in the exemplification of the present invention.

XX Sequence 241 AA;

SQ

Query Match 82.5%; Score 193; DB 21; Length 241;

Best Local Similarity 100.0%; Pred. No. 4.4e-175; Indels 0; Gaps 0;

Matches 193; Conservative 0; Mismatches 0;

QY 1 MAQHGMGAFRALCGIALLCALSLGQRPTGGPGCGPGRLLLTGTDCRCRVHTRCCRD 60

|||||

Db 1 maqhgamgafralcgiallcalslgqrptggpgcgrlllgtgdarcrcrvhtrccrd 60

|||||

QY 61 YPGECCSEWDCMCVQPEFHCGDPCCCTCRHPCPPGQGVQSQKFSGFQCIDCASGTF 120

|||||

Db 61 ypgeccsewdcmcvqpefhcgdpccctcrhpcppgqgvsgqkfsfgqcidcasgtf 120

|||||

QY 121 SGGHEGHCKEWTDCTQFGFLTVPFGKTHNAVCPGSPPAEPLGWLTVLLAVACVLLL 180

|||||

Db 121 sggheghckpwtcdctqfgfltvfpngkthnavcvpgsppepigtvllavaacvlll 180

|||||

QY 181 TSAQLGLHIWQLR 193

|||||

Db 181 tsaqlglhiwqlr 193

|||||

RESULT 8

AA95895

ID AA95895 standard; Protein; 241 AA.

XX AC AA95895;

XX DT 20-NOV-2000 (first entry)

XX Human tumour necrosis factor receptor-like protein TR11 mutein.

DE

XX TR11; human; tumour necrosis factor receptor-like protein;

KW immunodeficiency; autoimmune disease; rheumatoid arthritis;

KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;

KW dermatological; antiinflammatory; therapy; diagnosis; mutein;

KW mutant.

XX OS Homo sapiens.

XX PN WO200050459-A1.

XX PD 31-AUG-2000.

XX PF 23-FEB-2000; 2000WO-US04572.

XX PR 24-FEB-1999; 99US-0121648.

PR 13-MAY-1999; 99US-0134172.

PR 16-JUL-1999; 99US-0144076.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Ni J;

XX WPI: 2000-572072/53.

XX Human tumor necrosis factor receptor-like proteins useful for

PT diagnosis, prevention and treatment of disease states associated with

PT aberrant cell survival such as autoimmune disease and rheumatoid

PT arthritis -

XX Disclosure; 294-295; 278pp; English.

XX The present sequence is that of human tumour necrosis factor

CC receptor-like protein TR11 (see also AA95895), a novel protein

CC or a growth inhibitor. PRO364 antibodies are useful in diagnostic  
CC methods, purification methods and also in therapy, e.g. as  
CC inhibitors.

XX  
SQ Sequence 241 AA;

Query Match 82.5%; Score 193; DB 20; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4.4e-175;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAMGAFRALCGALCALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
|||||  
DB 1 maqhgamafralcgalcalcsls19qrptggpgcgprlll1gtgdarccrvhttrccrd 60  
|||||

QY 61 YPGECCSEWDCMCVQPEFHCGDPCTTCRHHPCPPGQGVQSGQSFQFCIDCASGTF 120  
|||||  
DB 61 ypgeccsewdcmcvqpefhcgdpcttcrhhpcppgqgvsgqkfsfgfcidcasgtf 120  
|||||

QY 121 SGHEGCHKPWTDCQTQGFGLTVFPGKTHNAVCPGSPPAEPLGWLTVLLAAVACVLLL 180  
|||||  
DB 121 sghegchckpwtcdtqgfgltvfpgkthnavcvpgspppaep1gwlvtvllavaacvlll 180  
|||||

QY 181 TSAQLGLHIWQLR 193  
|||||  
DB 181 tsaqlglhiwqlr 193  
|||||

RESULT 6  
ID AAB27651 standard; Protein; 241 AA.  
XX  
AC AAB27651;  
XX  
DT 26-JAN-2001 (first entry)  
XX  
DE Human protein PRO364.  
XX  
KW Cardiovascular; endothelial; angiogenic disorder; PRO179;  
KW PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333;  
KW PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;  
KW gene therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..25  
FT /label= "Signal peptide"  
XX  
PN WO200053757-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 24-FEB-2000; 2000WO-US05004.  
XX  
PR 08-MAR-1999; 99WO-US050028.  
PR 12-MAR-1999; 99US-0123957.  
PR 02-JUN-1999; 99WO-US12252.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28565.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.

(GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
PI Goddard A, Gurney AL, Hillan KJ, Marsters SA, Paoni NF, Pitti RM;  
PI Watanabe CK, Williams PM, Wood WI;

XX  
DR N-PSDB; AAA99903.

PT Novel PRO polypeptides and agonists and antagonists of them, used to  
PT diagnose and treat cardiovascular, endothelial and angiogenic disorders  
PT -

XX Claim 71; Fig 6; 181pp; English.

XX The present invention relates to methods for stimulating or inhibiting  
PS angiogenesis and cardiovascularization. The methods involve the use of  
CC pharmaceutical compositions based on the following proteins, PRO179,  
CC PRO238, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333,  
CC PRO840, PRO877, PRO878, PRO879, PRO882, PRO885 or PRO887. These  
CC proteins were identified by isolating cDNA clones encoding secreted  
CC proteins. The proteins of the invention may be used to diagnose and  
CC treat cardiovascular, endothelial or angiogenic disorders. The present  
CC sequence is one of the proteins of the invention.

XX Sequence 241 AA;

Query Match 82.5%; Score 193; DB 21; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4.4e-175;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAMGAFRALCGALCALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
|||||  
DB 1 maqhgamafralcgalcalcsls19qrptggpgcgprlll1gtgdarccrvhttrccrd 60  
|||||

QY 61 YPGECCSEWDCMCVQPEFHCGDPCTTCRHHPCPPGQGVQSGQSFQFCIDCASGTF 120  
|||||  
DB 61 ypgeccsewdcmcvqpefhcgdpcttcrhhpcppgqgvsgqkfsfgfcidcasgtf 120  
|||||

QY 121 SGHEGCHKPWTDCQTQGFGLTVFPGKTHNAVCPGSPPAEPLGWLTVLLAAVACVLLL 180  
|||||  
DB 121 sghegchckpwtcdtqgfgltvfpgkthnavcvpgspppaep1gwlvtvllavaacvlll 180  
|||||

QY 181 TSAQLGLHIWQLR 193  
|||||  
DB 181 tsaqlglhiwqlr 193  
|||||

RESULT 7  
AAB33431  
ID AAB33431 standard; Protein; 241 AA.  
XX  
AC AAB33431;  
XX  
DT 29-JAN-2001 (first entry)  
XX  
DE Human PRO364 protein UNQ319 SEQ ID NO:92.

XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;  
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;  
KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;  
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;  
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
KW autoimmune thrombocytopaenia; immune-mediated renal disease;  
KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
KW inflammatory bowel disease; gluten-sensitive enteropathy;  
KW autoimmune disease; immune-mediated skin disease; allergic disease;  
KW immunological disease; transplantation associated disease;  
KW graft rejection; graft-versus-host-disease.

XX Homo sapiens.

XX WO200053758-A2.

XX

XX Human PRO364 protein.  
DE  
XX PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;  
KW neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;  
KW breast; prostate; colon; lung; renal; ovarian; central nervous system;  
KW CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue;  
KW tumour necrosis factor receptor; GTR protein homologue.  
XX  
OS Homo sapiens.  
XX  
XX Location/Qualifiers  
FH Key 1..25  
FT Peptide /label= Signal\_peptide  
FT Modified-site 5..11  
FT Modified-site /note= "N-myristoylation site"  
FT Modified-site 8..14  
FT Modified-site /note= "N-myristoylation site"  
FT Modified-site 25..31  
FT Modified-site /note= "N-myristoylation site"  
FT Protein 26..241  
FT /label= Mature\_PRO364\_protein  
FT Modified-site 30..36  
FT /note= "N-myristoylation site"  
FT Modified-site 33..39  
FT Modified-site /note= "N-myristoylation site"  
FT Modified-site 118..124  
FT Modified-site /note= "N-myristoylation site"  
FT Modified-site 122..128  
FT Modified-site /note= "N-myristoylation site"  
FT Modified-site 146..150  
FT Modified-site /note= "Asn is N-glycosylated"  
FT Modified-site 156..162  
FT Modified-site /note= "N-myristoylation site"  
FT Domain 163..183  
FT /label= Transmembrane\_domain  
FT Binding-site 166..177  
FT /note= "Prokaryotic membrane lipoprotein lipid attachment site"  
FT Region 171..193  
FT /note= "Leucine zipper pattern"  
XX  
XX WO200032778-A2.  
PN  
XX  
XX 08-JUN-2000.  
PD  
XX  
XX 30-NOV-1999; 99WO-US28409.  
XX  
XX 01-DEC-1998; 98WO-US25108.  
PR 16-DEC-1998; 98US-0112850.  
PR 22-DEC-1998; 98US-0113296.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
XX  
XX (GETH ) GENENTECH INC.  
PA  
XX  
XX Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;  
PI  
XX WPI: 2000-412325/35.  
DR  
XX N-PSDB; AAD01240.  
DR  
XX New composition useful for inhibiting neoplastic cell growth and for  
PT treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or  
PT their antagonists  
PT  
XX  
XX Claim 31; Fig 4; 108pp; English.  
PS  
XX  
XX The present sequence is the human PRO364 protein, encoded by the cDNA  
CC clone, designated as DNA47365-1206. It is isolated from human small  
CC intestine tissue cDNA library, identified using probes based on the  
CC consensus sequence DNA44825, relative to the Inocyte expressed sequence  
CC tag (EST) 3003460. This EST has homology to tumour necrosis factor  
CC receptor (TNFR) family of polypeptides. PRO364 sequence also shows

CC homology to members of the TNFR family and mouse GTR protein.  
CC This clone is assigned the ATCC deposit No: 209436. PRO364 functions as  
CC a neoplastic cell growth inhibitor and is used for treating tumours,  
CC using an effective amount of PRO655, PRO364 and PRO344. This composition  
CC is especially useful for treatment of human cancers such as breast,  
CC prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.  
XX  
XX Sequence 241 AA;  
SQ  
Query Match 82.5%; Score 193; DB 21; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4.4e-175;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAQHAGMAGFALCGLALCALSLGQRTGGPGCGPGRLLLTGCTDARCCRVHTTCCRD 60  
DB 1 maqhgamgafalcgiallcalalslgqrptgpgcgprllltgctdarccrvhttccrd 60  
QY 61 YPGECCSEWDCMCVQPEFHCGDPCCCTCRHHPCCPPGQGVQSGKFSFGQCIDCASGTF 120  
DB 61 ypgeccsewdcmcvqpefhcgdpccctcrhpcppgvgvsgkfsfgqcidcasgtf 120  
QY 121 SGGHEGHCKPWTCTQFGFLTVFPGNKTHNAVCPGSPPAEPGLWLTWVLLAVACVLL 180  
DB 121 sggheghckpwtctqfgfltvfpgnkthnavcvpgspapiepigtvltvllavaacvll 180  
QY 181 TSAQLGLHIWQLR 193  
DB 181 tsaqlglhiwqlr 193  
RESULT 11  
AAB20115  
ID AAB20115 standard; Protein; 241 AA.  
XX  
AC AAB20115;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Human immunostimulant PRO364.  
XX  
KW PRO364; UNQ319; human; immune disease; autoimmune disease;  
KW antirheumatic; antiarthritic; antiinflammatory; antianaemic;  
KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;  
KW hepatotropic; virucide; dermatological; antipsoriatic;  
KW antiasthmatic; antiallergic; immunostimulant.  
XX  
OS Homo sapiens.  
XX  
XX Location/Qualifiers  
FH Key 1..25  
FT Peptide /label= Signal\_peptide  
FT Protein 26..241  
FT Domain 163..183  
FT /note= "transmembrane domain"  
FT Modified-site 5..11  
FT /note= "N-myristoylation site"  
FT Modified-site 8..14  
FT /note= "N-myristoylation site"  
FT Modified-site 25..31  
FT /note= "N-myristoylation site"  
FT Modified-site 30..36  
FT /note= "N-myristoylation site"  
FT Modified-site 33..39  
FT /note= "N-myristoylation site"  
FT Modified-site 118..124  
FT /note= "N-myristoylation site"  
FT Modified-site 122..128  
FT /note= "N-myristoylation site"  
FT Modified-site 156..162  
FT /note= "N-myristoylation site"  
FT Modified-site 146..150

CC showing identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The invention provides  
 CC highly conserved Tril1, TrilSV1 and TrilSV2 proteins (see AAY95879-81),  
 CC as well as vectors, host cells and recombinant methods for their  
 CC production. Tril1, TrilSV1 and/or TrilSV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an  
 CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. Tril1, TrilSV1 and/or TrilSV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IGA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.  
 XX  
 SQ Sequence 241 AA;

Query Match 82.5%; Score 193; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-175;  
 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMAGAFRALCGLALCALSLGQRTGGPGCGPGRLLLTGTGTARCRVHTTRCCRD 60  
 |||||  
 Db 1 maqhgamafralcgallcalcslsgrptggpgcgprlllgtgtardarcrvhttrccrd 60  
 QY 61 YPGECCSEWDCMCVQPEFHCGDPCCCTTCRHHPCPPGGVQSQKFSGFCIDCASGTF 120  
 |||||  
 Db 61 ypgeccsewdcmcvqpefhcgdpcccttrhhpcppggvgvsgqkfsfgfcidcasgtf 120  
 QY 121 SGGHEGCHKPWTDCDTQFGFLTVFPGNKTHNAVCPGSPPAEPLGLWLTVVLLAVACVLLL 180  
 |||||  
 Db 121 sggheghckpwtcdctqfgfltvfpgnkthnavcvpgspppaeplglwltvllavaacvlll 180  
 QY 181 TSAQLGLHIWQLR 193  
 |||||  
 Db 181 tsaqglghlwqlr 193

RESULT 9  
 AAB24409  
 ID AAB24409 standard; Protein; 241 AA.  
 XX  
 AC AAB24409;  
 XX  
 DT 07-NOV-2000 (first entry)  
 XX  
 DE Human PRO364 protein sequence SEQ ID NO:117.  
 XX  
 KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
 KW cytostatic; gene therapy; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200032221-A2.  
 XX  
 PD 08-JUN-2000.  
 XX  
 PF 30-NOV-1999; 99WO-US28313.  
 XX  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 16-DEC-1998; 98US-0112850.  
 PR 12-JAN-1999; 99US-0115554.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 28-APR-1999; 99US-0131445.  
 PR 14-MAY-1999; 99US-0134287.

PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1998; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-OCT-1999; 99US-0162506.  
 XX (GETH ) GENENTECH INC.  
 PA Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;  
 XX Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;  
 PI Watanabe CK, Williams PM, Wood WI;  
 XX  
 DR WPI; 2000-412154/35.  
 DR N-PSDB; AAA77604.

XX Nucleic acids encoding PRO polypeptides useful for preventing,  
 PT diagnosing and treating diagnosing a cardiovascular, endothelial or  
 PT angiogenic disorders in mammals -  
 XX

PS Claim 72; Fig 44; 315pp; English.

XX The present invention describes nucleic acids encoding PRO polypeptides  
 CC useful for preventing, diagnosing and treating diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder in mammals by  
 CC modulating cell proliferation, angiogenesis and cardiovascularisation,  
 CC and for identifying agonists and antagonists of these processes. The  
 CC nucleic acids and the proteins they encode may be used in the  
 CC prevention, treatment and diagnosis of diseases associated with  
 CC inappropriate PRO expression such as cardiovascular, endothelial or  
 CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and  
 CC cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors  
 CC containing them and the PRO polypeptide may be used to treat disorders  
 CC associated with decreased PRO expression. AAA77510 to AAA77721 and  
 CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in  
 CC the exemplification of the present invention.  
 XX

SQ Sequence 241 AA;

Query Match 82.5%; Score 193; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-175;  
 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMAGAFRALCGLALCALSLGQRTGGPGCGPGRLLLTGTGTARCRVHTTRCCRD 60  
 |||||  
 Db 1 maqhgamafralcgallcalcslsgrptggpgcgprlllgtgtardarcrvhttrccrd 60  
 QY 61 YPGECCSEWDCMCVQPEFHCGDPCCCTTCRHHPCPPGGVQSQKFSGFCIDCASGTF 120  
 |||||  
 Db 61 ypgeccsewdcmcvqpefhcgdpcccttrhhpcppggvgvsgqkfsfgfcidcasgtf 120  
 QY 121 SGGHEGCHKPWTDCDTQFGFLTVFPGNKTHNAVCPGSPPAEPLGLWLTVVLLAVACVLLL 180  
 |||||  
 Db 121 sggheghckpwtcdctqfgfltvfpgnkthnavcvpgspppaeplglwltvllavaacvlll 180  
 QY 181 TSAQLGLHIWQLR 193  
 |||||  
 Db 181 tsaqglghlwqlr 193

RESULT 10  
 AAY71467  
 ID AAY71467 standard; Protein; 241 AA.  
 XX  
 AC AAY71467;  
 XX  
 DT 08-NOV-2000 (first entry)

CC cardiovascular, endothelial, angiogenic or angiostatic disorder. The  
CC PRO364 cDNA sequence was isolated from an expressed sequence tag (EST)  
CC database as having homology to members of the tumour necrosis factor  
CC receptor (TNFR) family of polypeptides. The PRO175 cDNA sequence was  
CC isolated from a library of cDNA fragments derived from human umbilical  
CC vein endothelial cells (HUVEC). Administering an effective amount of  
CC PRO364 or PRO175 or their antagonists is useful for treating cardiac  
CC hypertrophy (which is initiated by myocardial infarction and  
CC trauma, a cancer, or age-related macular degeneration in a human).  
CC Administering a therapeutically effective amount of an antibody that  
CC binds PRO364 or PRO175 is useful for inhibiting angiogenesis induced  
CC by PRO364 or PRO175 in a human suffering from a tumor or a retinal  
CC disorder. PRO364 or PRO175, or their antagonists, are useful for the  
CC vascular-related drug targeting or as therapeutic targets for the  
CC treatment or prevention of atherosclerosis, hypertension, inflammatory  
CC vasculitides, Reynaud's disease, aneurysms, arterial restenosis,  
CC thrombophlebitis, tumor angiogenesis, gut protection or regeneration  
CC and treatment of lung or liver fibrosis, periodontal diseases,  
CC attraction of bone-forming cells, central and peripheral nervous  
CC system disease and neuropathies and rheumatoid arthritis.  
XX  
SQ Sequence 241 AA;

Query Match 82.5%; Score 193; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4.4e-175;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMGAFRALCGLALCALSLGQRTGGPGCGGRLLLTGTGTCARCRVHTTCRCD 60  
DB 1 maqhgmgafraicglallcalslgrptggpgcgrlllgtgdarcrcvhttrcrrd 60  
QY 61 YPGECCSEWDCMVQPEFHCGDPCTTCRHHPCPGQGVQSGKSFQFCIDCASGTF 120  
DB 61 ypgeccsewdcmvqpefhcgdpcttcrrhhpcpgqgvsggkfsfqfcidcasgtf 120  
QY 121 SGHGHGCKPWTDCQFGFLTFPPGNKTHNVCVPGSPPAEPLGLWTLVLLAVAAACVLL 180  
DB 121 sghghgckpwtcdqfgfltfvpgnknthnvcvpgsppeaplgwltvllavaacvlll 180  
QY 181 TSAQGLLHWQLR 193  
DB 181 tsaqglhlwqlr 193

RESULT 13  
ID AAB50910 standard; Protein; 241 AA.  
XX  
AC AAB50910;  
XX  
DT 21-MAR-2001 (first entry)  
XX  
DE Human PRO364 protein.  
XX  
KW Human; PRO; antiinflammatory; dermatological; antiarthritic;  
KW antirheumatic; cardiant; antianaemic; immunosuppressive; anti  
KW antidiabetic; nontropic; neuroprotective; hepatotropic; virucide;  
KW antiallergic; antiasthmatic; immune related disorder;  
KW hepatobiliary disease; autoimmune disease; allergy.  
XX  
OS Homo sapiens.  
XX  
PN WO200073452-A2.  
XX  
PD 07-DEC-2000.  
XX  
PF 02-JUN-2000; 2000WO-US15264.  
XX  
PR 02-JUN-1999; 99WO-US12252.  
PR 20-JUL-1999; 99US-0144732.  
PR 20-JUL-1999; 99US-0144758.

PR 28-JUL-1999; 99US-0146222.  
PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 29-OCT-1999; 99US-0162506.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28634.  
PR 09-DEC-1999; 99US-0170262.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;  
PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tamas D, Watanabe CK;  
PI Wood WI;  
XX  
DR WPI; 2001-025253/03.  
XX N-PSDB; AAC91469.  
XX  
PT Thirty three nucleic acids encoding PRO polypeptides which are useful  
PT in the diagnosis and treatment of immune related disorders, e.g.  
PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
PT thyroiditis and diabetes mellitus -  
XX  
PS Claim 58; Fig 18; 218pp; English.  
XX  
CC The present sequence is one of thirty three novel PRO polypeptides.  
CC The PRO polypeptides, anti-PRO antibodies, agonists and  
CC antagonists are useful for treating and diagnosing immune related  
CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central  
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic  
CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases  
CC (such as infectious, autoimmune chronic active hepatitis, primary  
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
CC inflammatory bowel disease, gluten-sensitive enteropathy and whipple's  
CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
CC food hypersensitivity and urticaria), immunological diseases of the  
CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
CC and hypersensitivity pneumonitis), transplantation associated diseases  
CC including graft rejection and graft-versus-host diseases.  
XX  
SQ Sequence 241 AA;

Query Match 82.5%; Score 193; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4.4e-175;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMGAFRALCGLALCALSLGQRTGGPGCGGRLLLTGTGTCARCRVHTTCRCD 60  
DB 1 maqhgmgafraicglallcalslgrptggpgcgrlllgtgdarcrcvhttrcrrd 60

FT Peptide /note= "Asn is N-glycosylated"

FT 166..177 /note= "prokaryotic membrane lipoprotein lipid

FT attachment site"

FT Peptide 171..193

FT /note= "leucine zipper pattern"

PN W0200105972-A1.

XX

XX

XX 25-JAN-2001.

XX

XX 15-MAR-2000; 2000WO-US06884.

XX

XX 20-JUL-1999; 99US-0144758.

XX

XX (GETH ) GENENTECH INC.

XX

PI Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;

PI Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK;

PI Wood WI;

XX

XX WPI: 2001-103149/11.

XX

XX N-PSDB; AAF30057.

XX

XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for

PT diagnosing and treating immune-related disorders, such as multiple

PT sclerosis, rheumatoid arthritis and diabetes -

XX

XX Claim 20; Fig 16; 127pp; English.

XX

XX The present sequence is that of novel human immunomodulator PRO364

CC (UNQ319), as deduced from cDNA (see AAF30057) isolated from a

CC small intestine library. PRO364 (26 kDa, pI 6.34) shows sequence

CC homology to mouse GITR protein and may be its human counterpart.

CC The invention provides polynucleotides (see AAF30050-62) encoding

CC novel human PRO proteins (see AAF30050-62) including PRO364.

CC Claimed compositions comprising these proteins or their agonists

CC are useful for increasing infiltration of inflammatory cells into

CC a tissue of a mammal, stimulating or enhancing an immune

CC response, or increasing the proliferation of T-lymphocytes in a

CC mammal in response to an antigen. Claimed compositions comprising

CC a PRO polypeptide or its antagonist have the opposite effect. A

CC claimed method for treating an immune related disorder, such as a T

CC cell disorder, involves administering a PRO polypeptide, an agonist

CC antibody or an antagonist antibody. The disorder is selected from

CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,

CC juvenile chronic arthritis, spondyloarthritis, systemic sclerosis,

CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic

CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune

CC thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated

CC renal disease, demyelinated diseases (such as multiple sclerosis),

CC autoimmune chronic active hepatitis, primary biliary cirrhosis,

CC granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel

CC disease (ulcerative colitis and Crohn's disease), gluten-sensitive

CC enteropathy, Whipple's disease, (auto)immune-mediated skin diseases

CC (such as bullous skin disease, erythema multiforme and psoriasis),

CC allergic diseases (such as asthma, allergic rhinitis, atopic

CC dermatitis, food hypersensitivity and urticaria), immunologic

CC diseases of the lung and transplantation associated diseases (such

CC as graft rejection and graft-versus-host disease) (all claimed).

CC Claimed methods of diagnosing these disorders comprise detecting

CC the level of expression of the PRO gene. Also claimed are a method

CC of identifying a compound capable of inhibiting the expression or

CC activity of the PRO polypeptide, vectors, host cells, antibodies,

CC and a method of stimulating the proliferation of T lymphocytes

CC using PRO364.

XX

SQ Sequence 241 AA;

Query Match 82.5%; Score 193; DB 22; Length 241;

Best Local Similarity 100.0%; Pred. No. 4.4e-175;

Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMAGAFRALCGLLALCALSLGQRPTGGPGCGPGRLLLTGTDArcRVHTTCCRD 60

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

1 maqhgamgafRALCGllalcalSLgRptgpgcgpgRlllgtgtdarCrvhttrccrd 60

QY 61 YPGECCSSEWDCMCVQPEPHCGDPCCCTTCRRHHPCCPGQGVQSGQKFSFGQCIDCASGTF 120

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

61 ypgeccssewdcmcvqpefhcgdpcccttcrrhhppccpgqgvsgqkfsfgqcidasgtf 120

QY 121 SGGHEGCHKPWTDCQTFQGLTVFPNGKTHNAVCPGSPAPPLGWLTVVLLAVAAACVLLL 180

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

121 sgghgchkpwtDCtQfGltVfPngkthNAVcVpGSPaPPLgWltVvLLaVaAcVLLL 180

QY 181 TSAQLGLHIWQLR 193

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

181 tsaqlglhiwqlr 193

RESULT 12

AAAB47054

ID AAB47054 standard; Protein; 241 AA.

XX

AC AAB47054;

XX

DT 08-MAY-2001 (first entry)

XX

DE Human PRO364.

XX

KW PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;

KW hGfTR; ligand; hGfTR; PRO175; tumor necrosis factor receptor; TNFR;

KW human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;

KW myocardial infarction; PCF-2alpha; trauma; cancer; angiogenesis;

KW age-related macular degeneration; antibody; periodontal disease;

KW vascular-related drug targeting; atherosclerosis; hypertension;

KW inflammatory vasculitides; Reynaud's disease; aneurysm;

KW arterial restenosis; thrombophlebitis; tumor angiogenesis;

KW lung; liver; fibrosis; neuropathy; rheumatoid arthritis.

XX

OS Homo sapiens.

XX

Key Location/Qualifiers

FT Peptide 1..26 /note= "Potential signal peptide"

FT Modified-site 146

FT /note= "N-glycosylated"

FT Domain 162..180

FT /note= "Potential transmembrane domain"

XX

WO200103720-A2.

XX

XX 18-JAN-2001.

XX

PF 11-JUL-2000; 2000WO-US18867.

XX

XX 12-JUL-1999; 99US-0143304.

PR

XX (GETH ) GENENTECH INC.

PA

XX Williams PM, Gerritsen ME;

PI

XX WPI: 2001-138257/14.

DR

XX N-PSDB; AAC85433.

DR

XX Composition for diagnosing and treating cardiovascular, endothelial and

PT angiogenic disorders, comprises a PRO364 or PRO175 polypeptide -

PT

XX Claim 1; Fig 1; 76pp; English.

PS

XX This sequence represents PRO364 polypeptide, which is a human gluco-

CC corticoid-induced tumor necrosis factor receptor (hGfTR). The

CC corresponding ligand (hGfTRL), PRO175, is given in AAB47056.

CC PRO364 and PRO175 may be used in a mixture with a cardiovascular,

CC endothelial, angiogenic or angiostatic agent for the treatment of a

```
PR 05-OCT-1999; 99WO-US23089.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
XX (GETH ) GENENTECH INC.
PA
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI,
XX WPI; 2001-090793/10.
DR N-PSDB; AAC97479.
XX
XX New isolated nucleic acid for producing a PRO polypeptide, analyzing
PT genetic disorders and treating cardiovascular, endothelial or
PT anglogenetic disorders, such as atherosclerosis, wounds or cancer -
XX
XX Claim 69; Fig 54; 293pp; English.
XX
XX The invention relates to novel human angiogenesis-associated proteins
CC designated PRO proteins (AB53064-B53097), and to nucleic acids encoding
CC PRO proteins. The invention also relates to vectors and host cells
CC comprising a PRO nucleic acid, the recombinant production of a PRO
CC protein, PRO antibodies specific for a PRO protein, fusion proteins
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
CC compounds which inhibit the expression of a PRO gene. The invention
CC additionally encompasses methods of identifying modulators of PRO
CC expression or activity; diagnosing a cardiovascular, endothelial or
CC anglogenetic disorder, or a susceptibility to such a disorder by detecting
CC mutations in a PRO gene, or the expression level of a PRO gene within a
CC particular tissue; treating a cardiovascular, endothelial or anglogenetic
CC disorder via the administration of a PRO protein, PRO nucleic acid, or
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
CC administration of a PRO protein, or an agonist or antagonist thereof.
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
CC agonists and PRO antagonists may be used as therapeutic agents to treat
CC cardiovascular, endothelial or anglogenetic disorders, such as
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
CC disease, or stroke. PRO nucleic acids are additionally useful in the
CC recombinant production of PRO proteins, as hybridisation probes to
CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in
CC gene therapy. PRO nucleic acids can also be used to produce transgenic
CC animals useful for the development and screening of potential
CC therapeutic agents. The present sequence represents a PRO protein of the
XX invention.
XX
XX Sequence 241 AA;
SQ
Query Match 82.5%; Score 193; DB 22; Length 241;
Best Local Similarity 100.0%; Pred. No. 4.4e-175;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQHGMAGFALCGIALCALSLGQRPTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60
Db 1 maqhgmagfalcgialcalslgqrptgpgcgprllltgtgdarccrvhttrccrd 60
QY 61 YGEBECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPCGQVQSGKFSFGFCIDCASGTF 120
Db 61 ypgeeccewcdmcvqpefhcgdpcccttcrrhhpcppcgvgvqsgkfsfgfcidcasgtf 120
QY 121 SGGHGHGCHKPWTCTQFGFLTVPFGNKNTHAVCVPGSPPAEPLGWLTVLLVAACVLLL 180
Db 121 sggheghchkpwtctqfgfltvfpgnkthnavcvpgspppaeplgwlvtvllavaacvlll 180
QY 181 TSAQLGLHIWQLR 193
```

Db 181 tsaglglnhwqlr 193

Search completed: September 5, 2001, 09:47:03  
Job time: 49 sec



QY 61 YPGECCSEWDCMCVQPEFHGCGDPCCTTCRHHPCPPGGVQSGKFSFGFCIDCASGTF 120  
|||||  
Db 61 ypgeccsewdcmcvqpefhcgdpcttcrhhpcppggvgsgkfsgfqcidasgtf 120  
QY 121 SGHGEHCKPWTCTQFGELTVFPGNKTNAVCVPGSPPAEPLGLWLVVLLAVAAACVLL 180  
|||||  
Db 121 sghgegckpwtctqfgeltvfpgnktnavcvpgspppaepglwltvllavaacvll 180  
QY 181 TSAQLGLHIWQLR 193  
|||||  
Db 181 tsaqglhiwqlr 193

RESULT 14  
AAB50982  
ID AAB50982 standard; Protein; 241 AA.  
XX  
AC AAB50982;  
XX  
DT 21-MAR-2001 (first entry)  
XX  
DE Human PRO364 protein.  
XX  
KW Human; PRO; cardiac; antiangiogenic; antiarteriosclerotic; hypotensive;  
KW vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;  
KW vulnary; antianginal; gene therapy; cardiovascular disease;  
KW endothelial disorder; angiogenic disorder; cancer; periodontal disease;  
KW wound healing.  
XX  
OS Homo sapiens.  
XX  
PN WO200073445-A2.  
XX  
PD 07-DEC-2000.  
XX  
PF 17-MAY-2000; 2000WO-US13705.  
XX  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 28-JUL-1999; 99US-0146222.  
PR 01-SEP-1999; 99WO-US20111.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28565.  
PR 10-DEC-1999; 99WO-US30095.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gertschen ME;  
PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;  
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
XX  
DR WPI; 2001-025251/03.  
DR N-PSDB; AAC90566.  
XX  
PT Seventeen nucleic acids encoding PRO polypeptides which are useful in  
PT diagnosis and treatment of cardiovascular, endothelial or angiogenic  
PT disorders in a mammal -  
XX  
PS Claim 71; Fig 8; 182pp; English.  
XX  
CC The present sequence is one of seventeen novel PRO polypeptides. The PRO

CC nucleic acids, polypeptides, agonists and antagonists are useful for  
CC treating cardiovascular, endothelial or angiogenic disorders in a mammal.  
CC Examples of these disorders include cardiac hypertrophy, trauma, cancer,  
CC age-related macular degeneration, atherosclerosis, hypertension, arterial  
CC stenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial  
CC infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and  
CC antagonists are also used to prevent tumour angiogenesis and for treating  
CC periodontal diseases. They are also used to stimulate wound healing and  
CC tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO  
CC antibodies are useful for diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder.  
XX  
SQ Sequence 241 AA;

Query Match 82.5%; Score 193; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4.4e-175;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMGAFRALCGLALCALSLGQRPTGGPGCGPGRLLLTGTDAACRCRVHTRCCRD 60  
|||||  
Db 1 maqhgmgafralcgllalcalslgqrptggpgcpgprlllgtgtatccrvhtrccrd 60  
QY 61 YPGECCSEWDCMCVQPEFHGCGDPCCTTCRHHPCPPGGVQSGKFSFGFCIDCASGTF 120  
|||||  
Db 61 ypgeccsewdcmcvqpefhcgdpcttcrhhpcppggvgsgkfsgfqcidasgtf 120  
QY 121 SGHGEHCKPWTCTQFGELTVFPGNKTNAVCVPGSPPAEPLGLWLVVLLAVAAACVLL 180  
|||||  
Db 121 sghgegckpwtctqfgeltvfpgnktnavcvpgspppaepglwltvllavaacvll 180  
QY 181 TSAQLGLHIWQLR 193  
|||||  
Db 181 tsaqglhiwqlr 193

RESULT 15  
AAB53090  
ID AAB53090 standard; Protein; 241 AA.  
XX  
AC AAB53090;  
XX  
DT 28-FEB-2001 (first entry)  
XX  
DE Human angiogenesis-associated protein PRO364, SEQ ID NO:142.  
XX  
KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
KW gene therapy; transgenic animal.  
XX  
OS Homo sapiens.  
XX  
PN WO200053753-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 05-JAN-2000; 2000WO-US00219.  
XX  
PR 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.



---

CC mutations in a PRO gene, or the expression level of a PRO gene within a  
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
 CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
 CC administration of a PRO protein, or an agonist or antagonist thereof.  
 CC PRO nucleic acids, PRO proteins, or an agonist or antagonist thereof.  
 CC agonists and PRO antagonists may be used as therapeutic agents to treat  
 CC cardiovascular, endothelial or angiogenic disorders, such as  
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
 CC disease, or stroke. PRO nucleic acids are additionally useful in the  
 CC recombinant production of PRO proteins, as hybridisation probes to  
 CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
 CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
 CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
 CC animals useful for the development and screening of potential  
 CC therapeutic agents. The present sequence represents a PRO protein of the  
 CC invention.

XX  
 SQ Sequence 241 AA;

Query Match 98.7%; Score 1322.5; DB 22; Length 241;  
 Best Local Similarity 96.7%; Pred. No. 1e-99;  
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

QY 1 MAQHGAMGAFRALGALLCALSLGQRTGCGPGCGRLILGTGTARCCRVHTRCCRD 60  
 DB 1 maqhgamgafraicgallcalslgqrptgpgcgprillgtgtarccrvhtrccrd 60  
 QY 61 YPGEECCSEWDCMCVQPEFHCGDPCCCTTCRRHPPCPGQGVQSGKFSFGFCIDCASGTF 120  
 DB 61 ypgeecsewdcmcvqpefhcgdpccctcrhpcppggvgvsgkfsgfgcicagstf 120  
 QY 121 SGHGEHCKPWTCTQGFVTFPGNKTTHNAVCPGSPAPLGLWLTVLLAVACVLL 180  
 DB 121 sgghgchckpwtctqgfvtvpgnktthnavcvgpsppaeglglwltvllavaacvll 180  
 QY 181 TSAQLGLHIWQL-----BKTOLLLEVPPTEDARSCQPEEERGSAAEKGRLGLDW 233  
 DB 181 tsqqlglhiwqlsqmwpretqlillevppstedarscqfpeeeersaeeekgrlgdlw 240  
 QY 234 V 234  
 DB 241 V 241

RESULT 15  
 AAW37840  
 ID AAW37840 standard; Protein; 228 AA.

XX AAW37840;  
 XX  
 XX 28-JUL-1998 (first entry)  
 XX Truncated human 312C2 protein from clone\_A8 amino acid sequence.

XX Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 KW antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
 KW autoimmune disorders.

OS Homo sapiens.

XX W09806842-A1.

XX 19-FEB-1998.

XX 14-AUG-1997; 97WO-US13931.

XX

PR 07-OCT-1996; 96US-0027901.  
 PR 16-AUG-1996; 96US-0689943.  
 XX (SCHE ) SCHERING CORP.  
 XX Gorman DM, Randall TD, Zlotnik A;  
 XX WPI; 1998-159534/14.  
 DR N-PSDB; AAV19154.  
 XX Isolated 312C2 T cell gene - used to develop products for treating,  
 PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 PT other T cell disorders  
 XX Disclosure; Pages 61-62; 71pp; English.  
 XX This is the amino acid sequence of the truncated human 312C2 T cell  
 CC protein from clone\_A8. The 312C2 proteins are expressed in thymus  
 CC cells and are induced on T cells and spleen cells following activation.  
 CC Engagement of 312C2 stimulates proliferation of T cell clones,  
 CC antigen-specific proliferation and cytokine production by T-cells, and  
 CC potentiates T cell expansion or apoptosis. The products can be used  
 CC in the treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.

XX SQ Sequence 228 AA;

Query Match 97.6%; Score 1308; DB 19; Length 228;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-98;  
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGAFRALGGLALLCALSLGQRTGCGPGCGRLILGTGTARCCRVHTRCCRDYPGEEC 66  
 DB 1 mgafralcgllalcalcslgqrptgpgcgprillgtgtarccrvhtrccrdypgeec 60  
 QY 67 CSEWDCMCVQPEFHCGDPCCCTTCRRHPPCPGQGVQSGKFSFGFCIDCASGTFSGGHEG 126  
 DB 61 csewdcmcvqpefhcgdpccctcrhpcppggvgvsgkfsgfgcicagstfsggheg 120  
 QY 127 HCKPWTCTQGFVTFPGNKTTHNAVCPGSPAPLGLWLTVLLAVACVLLLSAQIG 186  
 DB 121 hckpwtctqgfvtvpgnktthnavcvgpsppaeglglwltvllavaacvllltsaig 180  
 QY 187 LHIWQLRKTOLLLEVPPTEDARSCQPEEERGSAAEKGRLGLDW 234  
 DB 181 lhiwqlrktqlllevppstedarscqfpeeeersaeeekgrlgdlw 228

Search completed: September 4, 2001, 15:56:21  
 Job time: 338 sec

PF 17-MAY-2000; 2000WO-US13705.  
 XX 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
 PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;  
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
 XX  
 DR WPI: 2001-025251/03.  
 DR N-PSDB; AAC90566.  
 XX  
 XX Seventeen nucleic acids encoding PRO polypeptides which are useful in  
 PT diagnosis and treatment of cardiovascular, endothelial or angiogenic  
 PT disorders in a mammal -  
 XX  
 XX Claim 71; Fig 8; 182pp; English.  
 XX  
 CC The present sequence is one of seventeen novel PRO polypeptides. The PRO  
 CC nucleic acids, polypeptides, agonists and antagonists are useful for  
 CC treating cardiovascular, endothelial or angiogenic disorders in a mammal.  
 CC Examples of these disorders include cardiac hypertrophy, trauma, cancer,  
 CC age-related macular degeneration, atherosclerosis, hypertension, arterial  
 CC restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial  
 CC infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and  
 CC antagonists are also used to prevent tumour angiogenesis and for treating  
 CC periodontal diseases. They are also used to stimulate wound healing and  
 CC tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO  
 CC antibodies are useful for diagnosing a cardiovascular, endothelial or  
 CC angiogenic disorder.  
 XX  
 SQ Sequence 241 AA:  
 Query Match 98.7%; Score 1322.5; DB 22; Length 241;  
 Best Local Similarity 96.7%; Pred. No. 1e-99;  
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;  
 QY 1 MAQHGAMGAFRALCGALLCALSLGQRTGGCGGGRLLLTGTGDARCCRVHTTRCCRD 60  
 Db 1 maqhgamafralcgallcalslgrptggpgcggrlllgtgdarccrvhttrccrd 60  
 QY 61 YPGECCEWCMQVQPFHCGDPCCTTCRHHPCPGQGVQSGKFSFGQCIDCASGTF 120  
 Db 61 ypgecccewcmqvqpfhcgdpcccttrhhpcppggvgvsggkfsfgqcidcasgtf 120  
 QY 121 SGGHEGHCKPTDCQFGLTVFPGKNTNNAVCPGSPAPLGMLTVVLLAAVACVLLL 180  
 Db 121 sggheghckpwtcdctqfgltvfpngkntnavcvp9spapelpglvtvllavaacvlll 180  
 QY 181 TSAQLGLHIWLQ-----RKTQLLEVPPTSDARSQCFPEEGERGSAEKGRLGDLW 233  
 Db 181 tsaqglghlwlrsqcmwpretdqllevpptstedarscfpeegergsaeekgrlgdlw 240

QY 234 V 234  
 Db 241 V 241  
 RESULT 14  
 AAB53090  
 ID AAB53090 standard; Protein; 241 AA.  
 XX  
 AC AAB53090;  
 XX  
 DT 28-FEB-2001 (first entry)  
 XX  
 XX Human angiogenesis-associated protein PRO364, SEQ ID NO:142.  
 XX  
 KW Human: angiogenesis-associated protein; PRO: endothelial cell growth;  
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
 KW gene therapy; transgenic animal.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200053753-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 05-JAN-2000; 2000WO-US00219.  
 XX  
 XX 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
 XX  
 DR WPI: 2001-090793/10.  
 DR N-PSDB; AAC97479.  
 XX  
 PT New isolated nucleic acid for producing a PRO polypeptide, analyzing  
 PT genetic disorders and treating cardiovascular, endothelial or  
 PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
 XX  
 PS Claim 69; Fig 54; 293pp; English.  
 XX  
 CC The invention relates to novel human angiogenesis-associated proteins  
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
 CC PRO proteins. The invention also relates to vectors and host cells  
 CC comprising a PRO nucleic acid, the recombinant production of a PRO  
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
 CC compounds which inhibit the expression of a PRO gene. The invention  
 CC additionally encompasses methods of identifying modulators of PRO  
 CC expression or activity; diagnosing a cardiovascular, endothelial or  
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting

CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 CC rheumatoid arthritis, thyroiditis, diabetes mellitus, immune-mediated  
 CC renal disease, demyelinated diseases (such as multiple sclerosis),  
 CC autoimmune chronic active hepatitis, primary biliary cirrhosis,  
 CC granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel  
 CC disease (ulcerative colitis and Crohn's disease), gluten-sensitive  
 CC enteropathy, Whipple's disease, (auto)immune-mediated skin diseases  
 CC (such as bullous skin disease, erythema multiforme and psoriasis),  
 CC allergic diseases (such as asthma, allergic rhinitis, atopic  
 CC dermatitis, food hypersensitivity and urticaria), immunologic  
 CC diseases of the lung and transplantation associated diseases (such  
 CC as graft rejection and graft-versus-host disease) (all claimed).  
 CC Claimed methods of diagnosing these disorders comprise detecting  
 CC the level of expression of the PRO gene. Also claimed are a method  
 CC of identifying a compound capable of inhibiting the expression or  
 CC activity of the PRO polypeptide, vectors, host cells, antibodies,  
 CC and a method of stimulating the proliferation of T lymphocytes  
 CC using PRO364.

XX SQ Sequence 241 AA;

Query Match 98.7%; Score 1322.5; DB 22; Length 241;  
 Best Local Similarity 96.7%; Pred. NO. 1e-99;  
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

QY 1 MAQHGMCAFALCALCALSLGORTGPGCGPGRLLLTGTDAACRVRHTRCCRD 60  
 Db 1 maqhgamafralcgialcalcalslgrptgpgcgprlllgtgdarcrrvhttrccrd 60  
 QY 61 YPGEECCSEWDCMCVQPFHCGDPCTTCRRHPCPPGCGVQSGKFSFGQICDASGTF 120  
 Db 61 ypgeeccewcdmcvqpfhcgdpcttcrrhpcppgcvqsgkfsfgqicdasgtf 120  
 QY 121 SGGHEGCHKPWTCTQFGFLTVFPGNKTHNAVVCVPSPPAELGLWTLVLLAVAAACVLL 180  
 Db 121 sgghegchckpwtctqfgfltvfpgnkthnavcvpsppaelglwltvllavaacvll 180  
 QY 181 TSAQLGLHIWOL-----RKTLLEVPSTEDARSCQFPEEGERSAEKGRLGDLW 233  
 Db 181 tsqqlglhlwlsqcmwpretklllevpstedsqfpeegerseaeekgrlgdlw 240  
 QY 234 V 234  
 Db 241 V 241

RESULT 11

AAB47054

ID AAB47054 standard; Protein; 241 AA.

XX AC AAB47054;

XX DT 08-MAY-2001 (first entry)

XX DE Human PRO364.

XX KW PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;  
 KW hGTR; ligand; hGTR; PRO175; tumor necrosis factor receptor; TNFR;  
 KW human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;  
 KW myocardial infarction; PGF<sub>2</sub>alpha; trauma; cancer; angiogenesis;  
 KW age-related macular degeneration; antibody; periodontal disease;  
 KW vascular-related drug targeting; atherosclerosis; hypertension;  
 KW inflammatory vasculitides; Reynaud's disease; aneurysm;  
 KW arterial restenosis; thrombophlebitis; tumor angiogenesis;  
 KW lung; liver; fibrosis; neuropathy; rheumatoid arthritis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..26

FT /note= "Potential signal peptide"

FT Modified-site 146 /note= "N-glycosylated"  
 FT Domain 162..180  
 XX /note= "Potential transmembrane domain"

PN WO200103720-A2.

PD 18-JAN-2001.

XX 11-JUL-2000; 2000WO-US18867.

XX 12-JUL-1999; 99US-0143304.

PA (GETH ) GENENTECH INC.

XX Williams PM, Gerritsen ME;

XX WPI; 2001-138257/14.

DR N-PSDB; AAC85433.

XX Composition for diagnosing and treating cardiovascular, endothelial and  
 PT angiogenic disorders, comprises a PRO364 or PRO175 polypeptide -

PS Claim 1; Fig 1; 76pp; English.

CC This sequence represents PRO364 polypeptide, which is a human gluco-  
 CC corticoid-induced tumor necrosis factor receptor (hGTR). The  
 CC corresponding ligand (hGTRL), PRO175, is given in AAB47056.

CC PRO364 and PRO175 may be used in a mixture with a cardiovascular,  
 CC endothelial, angiogenic or angiotensin agent for the treatment of a  
 CC cardiovascular, endothelial, angiogenic or angiotensin disorder. The  
 CC PRO364 cDNA sequence was isolated from an expressed sequence tag (EST)  
 CC database as having homology to members of the tumor necrosis factor  
 CC receptor (TNFR) family of polypeptides. The PRO175 cDNA sequence was  
 CC isolated from a library of cDNA fragments derived from human umbilical  
 CC vein endothelial cells (HUVEC). Administering an effective amount of  
 CC PRO364 or PRO175 or their antagonists is useful for treating cardiac  
 CC hypertrophy (which is initiated by myocardial infarction and  
 CC characterized by the presence of an elevated level of PGF<sub>2</sub>alpha),  
 CC trauma, a cancer, or age-related macular degeneration in a human.

CC Administering a therapeutically effective amount of an antibody that  
 CC binds PRO364 or PRO175 is useful for inhibiting angiogenesis induced  
 CC by PRO364 or PRO175 in a human suffering from a tumor or a retinal  
 CC disorder. PRO364 or PRO175, or their antagonists, are useful for  
 CC vascular-related drug targeting or as therapeutic targets for the  
 CC treatment or prevention of atherosclerosis, hypertension, inflammatory  
 CC vasculitides, Reynaud's disease, aneurysms, arterial restenosis,  
 CC thrombophlebitis, tumor angiogenesis, gut protection or regeneration  
 CC and treatment of lung or liver fibrosis, periodontal diseases,  
 CC attraction of bone-forming cells, central and peripheral nervous  
 CC system disease and neuropathies and rheumatoid arthritis.

XX SQ Sequence 241 AA;

Query Match 98.7%; Score 1322.5; DB 22; Length 241;  
 Best Local Similarity 96.7%; Pred. NO. 1e-99;  
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

QY 1 MAQHGMCAFALCALCALSLGORTGPGCGPGRLLLTGTDAACRVRHTRCCRD 60  
 Db 1 maqhgamafralcgialcalcalslgrptgpgcgprlllgtgdarcrrvhttrccrd 60  
 QY 61 YPGEECCSEWDCMCVQPFHCGDPCTTCRRHPCPPGCGVQSGKFSFGQICDASGTF 120  
 Db 61 ypgeeccewcdmcvqpfhcgdpcttcrrhpcppgcvqsgkfsfgqicdasgtf 120  
 QY 121 SGGHEGCHKPWTCTQFGFLTVFPGNKTHNAVVCVPSPPAELGLWTLVLLAVAAACVLL 180  
 Db 121 sgghegchckpwtctqfgfltvfpgnkthnavcvpsppaelglwltvllavaacvll 180  
 QY 181 TSAQLGLHIWOL-----RKTLLEVPSTEDARSCQFPEEGERSAEKGRLGDLW 233  
 Db 181 tsqqlglhlwlsqcmwpretklllevpstedsqfpeegerseaeekgrlgdlw 240

Db 181 tsaglgihwqlrsqcmwpretdqllvppstedsqfpeergersaeekgrlgdlw 240  
 QY 234 V 234  
 Db 241 V 241

RESULT 12  
 AAB50910  
 ID AAB50910 standard; Protein; 241 AA.  
 AC AAB50910;  
 XX  
 DT 21-MAR-2001 (first entry)  
 DE Human PRO364 protein.  
 XX  
 KW Human; PRO; antiinflammatory; dermatological; antiarthritic;  
 KW antirheumatic; cardiant; antianemic; immunosuppressive; antithyroid;  
 KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;  
 KW antiallergic; antialsthmatic; immune related disorder;  
 KW hepatobiliary disease; autoimmune disease; allergy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200073452-A2.  
 XX  
 PD 07-DEC-2000.  
 XX  
 XX 02-JUN-2000; 2000WO-US15264.  
 PF  
 XX 02-JUN-1999; 99WO-US12252.  
 PR 20-JUL-1999; 99US-0144732.  
 PR 20-JUL-1999; 99US-0144732.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;  
 PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;  
 PI Wood WI;  
 XX  
 DR WPI: 2001-025253/03.  
 DR N-PSDB; AAC91469.  
 XX  
 XX Thirty three nucleic acids encoding PRO polypeptides which are useful  
 PT in the diagnosis and treatment of immune related disorders, e.g.  
 PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 PT thyroiditis and diabetes mellitus -  
 XX  
 XX Claim 58; Fig 18; 218pp; English.

CC The present sequence is one of thirty three novel PRO polypeptides.  
 CC The PRO polypeptides, anti-PRO antibodies, agonists and  
 CC antagonists are useful for treating and diagnosing immune related  
 CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
 CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic  
 CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases  
 CC (such as infectious, autoimmune chronic active hepatitis, primary  
 CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
 CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
 CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
 CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
 CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
 CC food hypersensitivity and urticaria), immunological diseases of the  
 CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
 CC and hypersensitivity pneumonitis), transplantation associated diseases  
 CC including graft rejection and graft-versus-host diseases.  
 XX  
 XX Sequence 241 AA;  
 SQ

Query Match 98.7%; Score 1322.5; DB 22; Length 241;  
 Best Local Similarity 96.7%; Pred. No. 1e-99;  
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

QY 1 MAQHGMCAFRALCGLALLCALSLGCRPTGGPGCGPRLILGTGTDAACCRVHTTRCCRD 60  
 Db 1 maqhgmcafralcgllallcalslgrptggpgcgprllilgtgtddarccrvhttrccrd 60  
 QY 61 YPGECCSEWDCMCVQPEFHGCDPCCTTCRHPCPPGGVQSGQKFSFGFCIDCASGTF 120  
 Db 61 ypgeccsewdcmcvqpefhgdcpccttcrrhpcppggvgvsgqkfsfgfcidcasgtf 120  
 QY 121 SGGHEGHCKPWTCTQFGFLTVFPGNKTNAVCVPGSPAPPLGWLTVVLLAVAAACVLL 180  
 Db 121 sggheghckpwtctqfgfltvfpgnktcnavcvpgspapelpglwtvllavaacvlll 180  
 QY 181 TSAQLGLHIWOL-----RKTQLLEVPPTEDARSCQFPEEERGERSAEKGRLGDLW 233  
 Db 181 tsaglgihwqlrsqcmwpretdqllvppstedsqfpeergersaeekgrlgdlw 240  
 QY 234 V 234  
 Db 241 V 241

RESULT 13  
 AAB50982  
 ID AAB50982 standard; Protein; 241 AA.  
 XX  
 AC AAB50982;  
 XX  
 DT 21-MAR-2001 (first entry)  
 DE Human PRO364 protein.  
 XX  
 KW Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive;  
 KW vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;  
 KW vulneryary; antiangular; gene therapy; cardiovascular disease;  
 KW endothelial disorder; angiogenic disorder; cancer; periodontal disease;  
 KW wound healing.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200073445-A2.  
 XX  
 PD 07-DEC-2000.  
 XX





```

PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PA (GETH ) GENENTECH INC.
XX
XX Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;
XX WPI; 2000-412325/35.
XX N-PSDB; AAD01240.
XX
XX New composition useful for inhibiting neoplastic cell growth and for
XX treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or
XX their antagonists
XX
XX Claim 31; Fig 4; 108pp; English.
XX
XX The present sequence is the human PRO364 protein, encoded by the cDNA
XX clone, designated as DNA7365-1206. It is isolated from human small
XX intestine tissue cDNA library, identified using probes based on the
XX consensus sequence DNA44825, relative to the incyte expressed sequence
XX tag (EST) 3003460. This EST has homology to tumour necrosis factor
XX receptor (TNFR) family of polypeptides. PRO364 sequence also shows
XX homology to members of the TNFR family and mouse G1R protein.
XX This clone is assigned the ATCC deposit No: 209436. PRO364 functions as
XX a neoplastic cell growth inhibitor and is used for treating tumours,
XX using an effective amount of PRO655, PRO364 and PRO344. This composition
XX is especially useful for treatment of human cancers such as breast,
XX prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.
XX
XX Sequence 241 AA;
SQ

```

Query Match 98.7%; Score 1322.5; DB 21; Length 241;  
 Best Local Similarity 96.7%; Pred. No. 1e-99;  
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

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QY 1 MAQHGANGAFRALCGLALLCALSLGQRTGGPGCGPGRLLILGTGDARCCRVHTRCCRD 60
Db 1 maqhgangafralcgallcalslgqrtggpgcgprllilgtgdarccrvhtrccrd 60
QY 61 YPGEECCSEWDCMCVQPEFHGDCCTTCRHHPCPPGGVGSGKFSFGFCIDCASGTF 120
Db 61 ypgeecsewdcmcvqpefhgdccttcrrhhpcppggvgsgkfsfgfcidcasgtf 120
QY 121 SGGHEGHCKPWTDCTQCFGLTVFPGNKNTHNAVCPGSPAPPLGWLTVVLLAVACVLL 180
Db 121 sgghgchckpwtcdtqcfglftvfgnknthnavcvgpsppaepglwltvllavaacvll 180
QY 181 TSAQLGHIWQL-----RKTQLLLEVPPTEDARSCQFPPEERGERSAEKGRLGLW 233
Db 181 tsaqlgihlwlrscmqwprctqillevpstedarscfpeeeergersaeekgrlgdlw 240
QY 234 V 234
Db 241 V 241

```

RESULT 10  
 AAB20115  
 ID AAB20115 standard; Protein; 241 AA.  
 XX  
 AC AAB20115;  
 XX  
 DT 30-APR-2001 (first entry)  
 XX  
 DE Human immunostimulant PRO364.  
 XX  
 KW PRO364; UNQ319; human; immune disease; autoimmune disease;  
 KW antirheumatic; antiarthritic; antiinflammatory; antianaemic;  
 KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;  
 KW hepatotropic; virucide; dermatological; antipsoriatic;  
 KW antiasthmatic; antiallergic; immunostimulant.  
 XX

```

OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 1..25
FT /label= Signal_peptide
FT 26..241
FT /label= Mature_protein
FT 163..183
FT /note= "transmembrane domain"
FT 5..11
FT /note= "N-myristoylation site"
FT 8..14
FT /note= "N-myristoylation site"
FT 25..31
FT /note= "N-myristoylation site"
FT 30..36
FT /note= "N-myristoylation site"
FT 33..39
FT /note= "N-myristoylation site"
FT 118..124
FT /note= "N-myristoylation site"
FT 122..128
FT /note= "N-myristoylation site"
FT 156..162
FT /note= "N-myristoylation site"
FT 146..150
FT /note= "Asn is N-glycosylated"
FT 166..177
FT /note= "prokaryotic membrane lipoprotein lipid attachment site"
FT 171..193
FT /note= "leucine zipper pattern"
XX
XX WO200105972-A1.
XX
XX 25-JAN-2001.
XX
XX 15-MAR-2000; 2000WO-US06884.
XX
XX 20-JUL-1999; 99US-0144758.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;
XX Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK;
XX Wood WI;
XX
XX WPI; 2001-103149/11.
XX N-PSDB; AAF30057.
XX
XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for
XX diagnosing and treating immune-related disorders, such as multiple
XX sclerosis, rheumatoid arthritis and diabetes -
XX
XX Claim 20; Fig 16; 127pp; English.
XX
XX The present sequence is that of novel human immunomodulator PRO364
XX (UNQ319), as deduced from cDNA (see AAF30057) isolated from a
XX small intestine library. PRO364 (26 kDa, pI 6.34) shows sequence
XX homology to mouse G1R protein and may be its human counterpart.
XX The invention provides polynucleotides (see AAF30050-62) encoding
XX novel human PRO proteins (see AAB20108-20) including PRO364.
XX Claimed compositions comprising these proteins or their agonists
XX are useful for increasing infiltration of inflammatory cells into
XX a tissue of a mammal, stimulating or enhancing an immune
XX response, or increasing the proliferation of T-lymphocytes in a
XX mammal in response to an antigen. Claimed compositions comprising
XX a PRO polypeptide or its antagonist have the opposite effect. A
XX claimed method for treating an immune related disorder, such as a T
XX cell disorder, involves administering a PRO polypeptide, an agonist
XX antibody or an antagonist antibody. The disorder is selected from
XX systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
XX juvenile chronic arthritis, spondyloarthritis, systemic sclerosis,
XX

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XX (GETH ) GENENTECH INC.  
 XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
 PI Goddard A, Gurney AL, Hillan KJ, Marsters SA, Paoni NF, Pitti RM;  
 PI Watanabe CK, Williams PM, Wood WI;  
 XX WPI: 2000-611444/58.  
 DR N-PSDB; AAA99903.  
 XX Novel PRO polypeptides and agonists and antagonists of them, used to  
 PT diagnose and treat cardiovascular, endothelial and angiogenic disorders  
 PT .  
 XX Claim 71; Fig 6; 181pp; English.  
 PS The present invention relates to methods for stimulating or inhibiting  
 XX angiogenesis and cardiovascularization. The methods involve the use of  
 CC pharmaceutical compositions based on the following proteins, PRO179,  
 CC PRO238, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333,  
 CC PRO840, PRO877, PRO878, PRO879, PRO882, PRO885 or PRO887. These  
 CC proteins were identified by isolating cDNA clones encoding secreted  
 CC proteins. The proteins of the invention may be used to diagnose and  
 CC treat cardiovascular, endothelial or angiogenic disorders. The present  
 CC sequence is one of the proteins of the invention.  
 XX Sequence 241 AA;  
 SQ

Query Match 98.7%; Score 1322.5; DB 21; Length 241;  
 Best Local Similarity 96.7%; Pred. No. le-99;  
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

Oy 1 MAQHGMAGAFRALGIALCALSLGPRPGCGPGRLLLGNGTDARCRVHTTRCCRD 60  
 |||||||  
 Db 1 maqhgmagafRALGIALCALSLGPRPGCGPGRLLLGNGTDARCRVHTTRCCRD 60  
 |||||||  
 Oy 61 YGEECCSWDCMCVQPEFHCGDPDCTTCRHHPCPPGQGVQSGKFSFGQCIDCASGTF 120  
 |||||||  
 Db 61 YGEECCSWDCMCVQPEFHCGDPDCTTCRHHPCPPGQGVQSGKFSFGQCIDCASGTF 120  
 |||||||  
 Oy 121 SGHGHGCHKPWTCTQFGFLTFVFPNGKTNVAVCPGSPPAEPGLWTLVLLAVAAVLLL 180  
 |||||||  
 Db 121 sghghgchkpwtctqfgfltfvfpngktnavcpvpgspppaepglwtlvllavaacvlll 180  
 |||||||  
 Oy 181 TSAQLGLHTWQL-----RKQTLLLEVPSTEDARSCQFPEERGERSAEKGRGLDLW 233  
 |||||||  
 Db 181 tsaqlglhwiqrsgcmwprctqlillevpstedarscdfpeergersaeekgrigdlw 240  
 |||||||  
 Oy 234 V 234  
 |  
 Db 241 V 241

RESULT 6  
 AAB33431  
 ID AAB33431 standard; Protein; 241 AA.  
 AC AAB33431;  
 XX  
 XX 29-JAN-2001 (first entry)  
 DT  
 XX Human PRO364 protein UNQ319 SEQ ID NO:92.  
 DE  
 XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
 KW dermatological; antirheumatic; antirheumatic; immunosuppressive;  
 KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;  
 KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;  
 KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
 KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;  
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
 KW autoimmune thrombocytopaenia; immune-mediated renal disease;

KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
 KW inflammatory bowel disease; gluten-sensitive enteropathy;  
 KW autoimmune disease; immune-mediated skin disease; allergic disease;  
 KW immunological disease; transplantation associated disease;  
 KW graft rejection; graft-versus-host-disease.  
 XX  
 OS Homo sapiens.  
 XX WO200053758-A2.  
 PN  
 XX 14-SEP-2000.  
 PD  
 XX 02-MAR-2000; 2000WO-US05841.  
 PF  
 XX 08-MAR-1999; 99WO-US05028.  
 PR 10-MAR-1999; 99US-0123618.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 23-MAR-1999; 99US-0125775.  
 PR 12-APR-1999; 99US-0128849.  
 PR 20-APR-1999; 99WO-US08615.  
 PR 28-APR-1999; 99US-0131445.  
 PR 04-MAY-1999; 99US-0132371.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 26-JUL-1999; 99US-0144758.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 16-DEC-1999; 99WO-US28565.  
 PR 20-DEC-1999; 99WO-US30095.  
 PR 30-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 03-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;  
 XX  
 DR WPI: 2000-572271/53.  
 DR N-PSDB; AAC58596.  
 XX  
 PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
 XX  
 XX Claim 33; Fig 36; 309pp; English.  
 PS The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are

CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC anemias, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems, demyelinating diseases, inflammatory  
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
 CC autoimmune or immune-mediated skin diseases, allergic diseases,  
 CC immunological diseases of the lung, and transplantation associated  
 CC diseases including graft rejection and graft-versus-host-disease.  
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.  
 XX  
 SQ Sequence 241 AA;

Query Match 98.7%; Score 1322.5; DB 21; Length 241;  
 Best Local Similarity 96.7%; Pred. No. 1e-99;  
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

QY 1 MAQHGMAGAFRALCGLALCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
 DB 1 maqhgmagafralcglalcalslgrptgpgcgprlllgtgdarccrvhttrccrd 60  
 QY 61 YPGECCSEWDCMCVQPEFHGCDPCTTCRHHPCPPGQVQSGKFSFGQICDASGTF 120  
 DB 61 ypgeccsewdcmcvqpefhcgdpcttcrhhpcppgqvgvsgkfsfgqicdasgtf 120  
 QY 121 SGGHEGCHKPWTCTQFGFLVFPGNKTHNAVCPGSPAPPLGLWLTVLLAVAACVLL 180  
 DB 121 sgghegchkpwtctqfgflvfpgnkthnavcpgspapplglwltvllavaacvll 180  
 QY 181 TSAQLGLHIWQL-----RKTQLLEVPSTEDARSCQFPPEERGERSAEEKGRIGDLW 233  
 DB 181 tsaqglghlwiqlsqcmwpreqlqllvppstedsarcsqfpeeeergersaeeekgrigdlw 240  
 QY 234 V 234  
 DB 241 v 241

RESULT 7  
 AAY95895  
 ID AAY95895 standard; Protein; 241 AA.

XX AAY95895;  
 AC AAY95895;  
 DT 20-NOV-2000 (first entry)  
 XX Human tumour necrosis factor receptor-like protein TR11 mutein.  
 DE  
 XX TR11; human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antiarthritis; haemostatic;  
 KW dermatological; antiinflammatory; therapy; diagnosis; mutein;  
 KW mutant.

XX Homo sapiens.

XX WO200050459-A1.

XX 31-AUG-2000.

XX 23-FEB-2000; 2000WO-US04572.

XX 24-FEB-1999; 99US-0121648.

XX 13-MAY-1999; 99US-0134172.

XX 16-JUL-1999; 99US-0144076.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Ni J;  
 XX WPI; 2000-572072/53.  
 XX Human tumor necrosis factor receptor-like proteins useful for  
 PT diagnosis, prevention and treatment of disease states associated with  
 PT aberrant cell survival such as autoimmune disease and rheumatoid  
 PT arthritis -  
 XX  
 PS Disclosure; 294-295; 278pp; English.

XX The present sequence is that of human tumour necrosis factor  
 CC receptor-like protein TR11 (see also AAY95879), a novel protein  
 CC showing identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The invention provides  
 CC highly conserved TR11, TR11SV1 and TR11SV2 proteins (see AAY95879-81),  
 CC as well as vectors, host cells and recombinant methods for their  
 CC production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an  
 CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency,  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.

XX Sequence 241 AA;

Query Match 98.7%; Score 1322.5; DB 21; Length 241;  
 Best Local Similarity 96.7%; Pred. No. 1e-99;  
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

QY 1 MAQHGMAGAFRALCGLALCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
 DB 1 maqhgmagafralcglalcalslgrptgpgcgprlllgtgdarccrvhttrccrd 60  
 QY 61 YPGECCSEWDCMCVQPEFHGCDPCTTCRHHPCPPGQVQSGKFSFGQICDASGTF 120  
 DB 61 ypgeccsewdcmcvqpefhcgdpcttcrhhpcppgqvgvsgkfsfgqicdasgtf 120  
 QY 121 SGGHEGCHKPWTCTQFGFLVFPGNKTHNAVCPGSPAPPLGLWLTVLLAVAACVLL 180  
 DB 121 sgghegchkpwtctqfgflvfpgnkthnavcpgspapplglwltvllavaacvll 180  
 QY 181 TSAQLGLHIWQL-----RKTQLLEVPSTEDARSCQFPPEERGERSAEEKGRIGDLW 233  
 DB 181 tsaqglghlwiqlsqcmwpreqlqllvppstedsarcsqfpeeeergersaeeekgrigdlw 240  
 QY 234 V 234  
 DB 241 v 241

RESULT 8  
 AAB24409  
 ID AAB24409 standard; Protein; 241 AA.

XX AAB24409;

XX 07-NOV-2000 (first entry)

XX Human PRO364 protein sequence SEQ ID NO:117.

XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;

Result 3

XX 21-OCT-1997; 97US-0063212.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX N1 J, Ruben SM;  
 PI WPI; 2000-061922/05.  
 DR N-PSDB; AA237762.

XX New tumour necrosis factor receptor-like polypeptides used to, e.g.  
 PT treat Digeorge syndrome -  
 XX

PS Claim 14; Fig 1; 167pp; English.

XX This is the amino acid sequence of the human tumour necrosis factor  
 CC receptor-like protein (TR11 receptor). The invention relates to TR11 and  
 CC two splice variants TR11SV1 and TR11SV2. The nucleotide sequences were  
 CC determined by sequencing cloned cDNAs AA37765-237766. The TR11 receptor  
 CC and its splice variants show homology to the murine glucocorticoid  
 CC induced tumour necrosis factor receptor family-related gene (GIR).  
 CC TR11, TR11SV1 and TR11SV2 polypeptides may be involved in the regulation  
 CC of cell-type specific receptor-mediated cell growth, differentiation,  
 CC and ultimately, cell death. They can be used for screening for  
 CC agonists/antagonists. The polypeptides, agonists or antagonists can be  
 CC used for treating a disease state associated with aberrant cell  
 CC survival. They can be used for treating immune deficiency disorders,  
 CC Digeorge syndrome, HIV infection, severe combined immunodeficiency,  
 CC (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood  
 CC platelet disorders or wounds resulting from trauma or surgery. They can  
 CC also be used to treat heart attacks, strokes, Addison's disease,  
 CC haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's  
 CC disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome,  
 CC systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent  
 CC diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,  
 CC hypersensitivity to an antigenic molecule, organ rejection or graft  
 CC versus host disease, inflammatory conditions, ischaemia-reperfusion  
 CC injury, complement-mediated hyperacute rejection, nephritis, cytokine or  
 CC chemokine induced lung injury, inflammatory bowel disease, Crohn's  
 CC disease, hyperproliferative disorders, or infections. They can also be  
 CC used to repair, replace, or protect tissue damaged by congenital  
 CC defects, trauma, age, disease, surgery, including cosmetic plastic  
 CC surgery, fibrosis, reperfusion injury, peripheral nerve injuries,  
 CC neuropathies, and central nervous system disease (e.g. Alzheimer's  
 CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral  
 CC sclerosis, and Shy-Drager syndrome). The products can also be used for  
 CC detection, diagnosis and prognosis.

XX Sequence 234 AA;

Query Match 100.0%; Score 1340; DB 21; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-101;  
 Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAAGAFALCGALLCALSLGQRTGGPGCGPGRLLLGTTGTDARCRVHTTRCCRD 60  
 DB 1 maqhgaagafalcgallcalslgqrtpgpgcgprlllgtgtardcrvrhttrccrd 60  
 QY 61 YPGECCSEWDCMCVQPEFHCGDPCTTCRRHPCPPGQGVQSGKFSFGQCIDCASGTF 120  
 DB 61 ypgeccsewdcmcvqpefhcgdpcttcrhpcppgqgvqsgkfsgfqcidasgtf 120  
 QY 121 SGGHEGCHKPWTDCQFGFLTVFPNGKTNHNCVCPGSPPAELGWLTVLLAVAACVLL 180  
 DB 121 sgghegchkpwtcdctqfgfltvfpngktnhncvcpgpsppaelgwlvtvllavaacvll 180  
 QY 181 TSAQLGLHQLWRKTLQLLEVPSTEDARSCOPPEERGERSAEERKGLDLWV 234  
 DB 181 tsaq19lhlwlrkqlqllevpstedarscqfpeeergerseaeerkglldlwv 234

RESULT 3

AAW37839  
 XX ID AAW37839 standard; Protein; 241 AA.  
 XX AC AAW37839;  
 XX 28-JUL-1998 (first entry)  
 XX Amino acid sequence of the human 312C2 T cell protein.  
 XX Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 KW antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
 KW autoimmune disorders.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FT CDS 1..726  
 FT /\*tag= a  
 FT /product= "human 312C2 protein"  
 XX WO9806842-A1.  
 XX 19-FEB-1998.  
 XX 14-AUG-1997; 97WO-US13931.  
 XX 07-OCT-1996; 96US-0027901.  
 XX 16-AUG-1996; 96US-0689943.  
 XX (SCHE ) SCHERING CORP.  
 XX Gorman DM, Randall TD, Zlotnik A;  
 WPI; 1998-159534/14.  
 N-PSDB; AAV19153.  
 XX Isolated 312C2 T cell gene - used to develop products for treating,  
 PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 PT other T cell disorders  
 XX Claim 2; Pages 59-60; 71pp; English.  
 XX This is the amino acid sequence encoding the human 312C2 T cell  
 CC protein. The 312C2 proteins are expressed in thymus cells and are  
 CC induced on T cells and spleen cells following activation. Engagement  
 CC of 312C2 stimulates proliferation of T cell clones, antigen-specific  
 CC proliferation and cytokine production by T-cells, and potentiates T  
 CC cell expansion or apoptosis. The products can be used in the  
 CC treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX Sequence 241 AA;

Query Match 98.7%; Score 1322.5; DB 19; Length 241;  
 Best Local Similarity 96.7%; Pred. No. 1e-99;  
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

QY 1 MAQHGAAGAFALCGALLCALSLGQRTGGPGCGPGRLLLGTTGTDARCRVHTTRCCRD 60  
 DB 1 maqhgaagafalcgallcalslgqrtpgpgcgprlllgtgtardcrvrhttrccrd 60  
 QY 61 YPGECCSEWDCMCVQPEFHCGDPCTTCRRHPCPPGQGVQSGKFSFGQCIDCASGTF 120  
 DB 61 ypgeccsewdcmcvqpefhcgdpcttcrhpcppgqgvqsgkfsgfqcidasgtf 120  
 QY 121 SGGHEGCHKPWTDCQFGFLTVFPNGKTNHNCVCPGSPPAELGWLTVLLAVAACVLL 180  
 DB 121 sgghegchkpwtcdctqfgfltvfpngktnhncvcpgpsppaelgwlvtvllavaacvll 180



GenCore version 4.5

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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:50:43 ; Search time 126.12 Seconds  
(without alignments)  
112.480 Million cell updates/sec

Title: US-09-512-363-2

Perfect score: 1340

Sequence: 1 MAQHGAMGAPRALCGLALLC.....EEERGSRAEKGRLGLW 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
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21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1340	100.0	234	21 AAY95879	Human tumour necro
2	1340	100.0	234	21 AAY52158	Tumour necrosis fa
3	1322.5	98.7	241	19 AAW37839	Amino acid sequenc
4	1322.5	98.7	241	20 AAY06605	Human TNF receptor
5	1322.5	98.7	241	21 AAB27651	Human protein PRO3
6	1322.5	98.7	241	21 AAB33431	Human PRO364 prote
7	1322.5	98.7	241	21 AAY95895	Human tumour necro
8	1322.5	98.7	241	21 AAB24409	Human PRO364 prote
9	1322.5	98.7	241	21 AAY71467	Human PRO364 prote
10	1322.5	98.7	241	22 AAB20115	Human immunostimul
11	1322.5	98.7	241	22 AAB47054	Human PRO364. Hom

12	1322.5	98.7	241	22 AAB50910	Human PRO364 prote
13	1322.5	98.7	241	22 AAB50982	Human PRO364 prote
14	1322.5	98.7	241	22 AAB53090	Human angiogenesis
15	1308	97.6	228	19 AAW37840	Truncated human 31
16	1292	96.4	240	21 AAY95881	Human tumour necro
17	1292	96.4	240	21 AAY52160	TRILSV2 amino acid
18	1283.5	95.8	235	21 AAY44825	Human molecule ass
19	1093	81.6	311	19 AAW37842	Human 312C2 protei
20	992.5	74.1	241	21 AAY95880	Human tumour necro
21	992.5	74.1	241	21 AAY52159	TRILSV1 amino acid
22	905	67.5	317	20 AAY06645	PRO364-related EST
23	900	67.2	316	22 AAB47055	Polypeptide encode
24	703	52.5	228	19 AAW49016	Mouse glucocortic
25	703	52.5	228	19 AAW37838	Amino acid sequenc
26	625.5	46.7	294	19 AAW49017	Mouse glucocortic
27	618	46.1	222	19 AAW49018	Mouse glucocortic
28	605	45.1	232	19 AAW37841	Human 312C2 protei
29	255	19.0	89	21 AAY76013	Murine TNF-alpha f
30	255	19.0	89	22 AAB55952	Skin cell protein,
31	201.5	15.0	256	16 AAR70978	4-1BB receptor pro
32	201.5	15.0	256	16 AAR64199	Murine 4-1BB polyp
33	201.5	15.0	256	17 AAW04173	Mouse receptor 4-1
34	201.5	15.0	256	18 AAW26659	Mouse 4-1BB recept
35	201.5	15.0	256	20 AAY33215	Murine CD137 prote
36	201.5	15.0	256	20 AAY28687	Mouse Receptor 4-1
37	197	14.7	255	16 AAR70977	H4-1BB receptor pr
38	197	14.7	255	16 AAR64197	Human 4-1BB polype
39	197	14.7	255	18 AAW26658	Human 4-1BB recept
40	197	14.7	255	20 AAY33214	Human receptor pro
41	197	14.7	255	20 AAY28688	Human tumour necro
42	197	14.7	255	22 AAB50521	Human tumour necro
43	194	14.5	219	18 AAW31759	A novel human h4-1
44	194	14.5	219	20 AAW92523	Human h4-1BBSV rec
45	191	14.3	219	20 AAW92524	Human h4-1BBSV rec

## ALIGNMENTS

RESULT 1

AAY95879 1  
ID AAY95879 standard; Protein; 234 AA.

XX AC AAY95879;

XX DT 20-NOV-2000 (first entry)

XX DE Human tumour necrosis factor receptor-like protein TR11.  
XX KW TR11: human; tumour necrosis factor receptor-like protein;  
XX KW Immunodeficiency; autoimmune disease; rheumatoid arthritis;  
XX KW Immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
XX KW dermatological; antiinflammatory; therapy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..25

FT Protein /label= Signal\_peptide

FT Domain /label= Mature\_protein

FT Domain /label= Extracellular\_domain

FT Domain /label= Transmembrane\_domain

FT Domain /label= Intracellular\_domain

FT Modified-site /note= "N-glycosylated"

FT Domain /note= "conserved domain CD-II"

FT Domain /note= "conserved domain CD-III"

FT Domain 107..113 /note= "conserved domain CD-IV"  
 FT Domain 128..134 /note= "conserved domain CD-V"  
 FT Domain 153..160 /note= "conserved domain CD-VI"  
 FT Domain 176..186 /note= "conserved domain CD-VII"  
 FT Domain 204..209 /note= "conserved domain CD-IX"  
 FT Domain 224..233 /note= "conserved domain CD-X"  
 FT Region 27..36 /note= "epitope-bearing region"  
 FT Region 43..51 /note= "epitope-bearing region"  
 FT Region 59..67 /note= "epitope-bearing region"  
 FT Region 56..64 /note= "epitope-bearing region"  
 FT Region 66..71 /note= "epitope-bearing region"  
 FT Region 99..107 /note= "epitope-bearing region"  
 FT Region 125..133 /note= "epitope-bearing region"  
 FT Region 143..151 /note= "epitope-bearing region"  
 FT Region 156..164 /note= "epitope-bearing region"  
 FT Region 203..211 /note= "epitope-bearing region"  
 FT Region 222..230 /note= "epitope-bearing region"  
 FT Region 222..230 /note= "epitope-bearing region"  
 XX WO200050459-A1.

XX 31-AUG-2000.

XX 23-FEB-2000; 2000WO-US04572.

XX 24-FEB-1999; 99US-0121648.

XX 13-MAY-1999; 99US-0134172.

XX 16-JUL-1999; 99US-0144076.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Ni J;

XX WPI; 2000-572072/53.

XX N-PSDB; AAA50304.

XX Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid arthritis -

XX Claim 14(c); Fig 1A-B; 278pp; English.

XX The present sequence is that of human tumor necrosis factor receptor-like protein TR11, a novel 25 kDa protein which shows 58.6% identity to murine glucocorticoid induced tumour necrosis factor receptor family-related gene. The sequence was deduced from a cDNA clone (see AAA50304) discovered in a T-helper cell library. TR11 activated NF-kappaB through a TRAF2-mediated mechanism. Expression is activation-inducible. The TR11 ligand is constitutively expressed in an endothelial cell line. This suggests that TR11 and its ligand may be involved in activated T-cell trafficking. The invention provides TR11, TR11SV1 and TR11SV2 nucleic acids (see AAA50304-06) and highly conserved encoded proteins (see AAA5879-81), as well as vectors, host cells and recombinant methods for their production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful for treating, preventing, prognosis and/or diagnosis of an

CC immunodeficiency, especially common variable immunodeficiency, X-linked agammaglobulinemia, severe combined immunodeficiency (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2 antagonists (e.g. antibodies) are used to treat, prevent, prognosis and/or diagnose an autoimmune disease, especially rheumatoid arthritis, systemic lupus erythematosus, thrombocytopenia purpura or IgA nephropathy. The polypeptides, polynucleotides and/or antibodies can be administered to cells in vitro, ex vivo or in vivo or to a multicellular organism. Soluble forms of the polypeptides may also be used. Methods for screening for agonist/antagonist compounds are also provided.

XX Sequence 234 AA;

Query Match 100.0%; Score 1340; DB 21; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-101;  
 Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAQHGMGAFRALCGLALCALSLGQRTGGPGCGRLLLTGTDAKCRVHTTRCCRD 60  
 DB 1 maqhgmgaftalcglaallcalslgprtgpgcgprlllgtgdarcrrvhttrccrd 60  
 QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQIDCASGTF 120  
 DB 61 ypgeccsewdcmcvqpefhcgdpctctcrhhpcppgqgvqsgkfsfgqidcasgtf 120  
 QY 121 SGGHEGHCKPMTDCTQFGFLTVFPGNKTHNAVCPGSPAEPLGWLTVVLLAAACVLLL 180  
 DB 121 sggheghckpwtcdtqfgfltvfpgnkthnavcvpgspaeplgwlvtvllaaacvlll 180  
 QY 181 TSAQLGLHIWLRKTLQLLEVPPTSDARSCQFPEERGERSAEEKGRIGDLWV 234  
 DB 181 tsaqlglhlwlrktqllevpptsdarscqfpeeergerseaeekgrlgdlwv 234

RESULT 2

AA52158

ID AA52158 standard; Protein; 234 AA.

XX AC AA52158;

XX DT 01-FEB-2000 (first entry)

XX DE Tumour necrosis factor receptor-like protein (TR11) amino acid sequence.

XX KW Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2; GRTR; growth; differentiation; cell death; immune deficiency disorder; Digesorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia; Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes; Alzheimer's disease; Parkinson's disease; Huntington's disease; inflammatory condition.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..25

FT Protein /label= Signal\_peptide

FT Domain /label= TR11

FT Domain /note= "Extracellular domain"

FT Domain /note= "Transmembrane domain"

FT Domain /note= "Intracellular domain"

XX WO9920758-A1.

XX PD 29-APR-1999.

XX 21-OCT-1998; 98WO-US22085.





Search completed: September 4, 2001, 15:57:34  
Job time: 376 sec

Db 111 PRQDSGKGLGVDCVPCPPGPHFSPGNNAQKPTWNTCTLSGKQTRHPASDSLDAVC----- 164  
QY 160 AEPGLWTFVVLAVACVLLTSAQLGLHIW----QLRKQTOLLLEVPSP-----TEDARSCQ 212  
Db 165 -EDRSLATLLWETQRTFRFTTVO-STTVWPRTSSELPSTPTLVE-PRSCDKTHTCPCPCP 221  
QY 213 FPTEE 217  
Db 222 APEAE 226

## RESULT 15

US-08-097-827-7

; Sequence 7, Application US/08097827

; Patent No. 5457035

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter

; APPLICANT: Goodwin, Ray

; APPLICANT: Fanslow, William

; APPLICANT: Gayle, Richard

; TITLE OF INVENTION: No. 5457035el Cytokine which is a Ligand for

; TITLE OF INVENTION: OX40

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/097,827

; FILING DATE:

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia A.

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2806

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-587-0730

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 206 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-097-827-7

## Query Match

12.4%; Score 166.5; DB 1; Length 206;

Best Local Similarity 28.7%; Pred. No. 5e-08;

Matches 50; Conservative 12; Mismatches 51; Indels 61; Gaps 9;

QY 26 QRTGCGCGGPRLLLG--TGTDR--CCRVHT----TRCRD-YPG-----EECCSEWDC 72

Db 6 QOPT-----ALLLGLTLGVTARRLNCVKRHTYPSGHKCCRECQPGHGMVNRCDHTRDT 58

QY 73 MCVPFHCQDPC-----CCTCRHHP-----CPCGQG 99

Db 59 LC-----HPCTGYNEAVNTDCTQCTQCNHRSGSELKQNCPTQDTVCRCPGTQ 110

QY 100 VQSGKSFQFCIDCASGTFSGGHEGCKPWTDCQTFGFLTVPFGNKTNAVC 153

Db 111 PRQDSGKGLGVDCVPCPPGPHFSPGNNAQKPTWNTCTLSGKQTRHPASDSLDAVC 164

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Qy 100 VQSGKFSFGFQCIDCASGTFSGGHEGCHKPWTDCQTFGLTVFPGNKTHNAVCPGSP 159
      :      :      :      :      :      :      :      :      :      :
Db 111 PRQDSGYKLGDCVPCPPGCFHSPGNQACKPWNTCTLSGKQTRHPASDLDAVC----- 164

Qy 160 AEPLGLWTVVLLAVANAACVLLLTSAQLGLHW---QLRKQTQLLEVPSP--TEDARSCO 212
      :      :      :      :      :      :      :      :      :      :
Db 165 -EDRSLLATLWETQRPFRFTVQ-SITVMPRTSELPSTPLVE-PRSCDKTHTCPCP 221

Qy 213 FPEE 217
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Db 222 APEE 226

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RESULT 14
US-08-494-574-11
; Sequence 11, Application US/08494574
; Patent No. 5783665
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5783665el Cytokine which is a Ligand for
; NAME OF INVENTOR: OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,574
; FILING DATE: 22-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE: 23-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-494-574-11

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Query Match	13.1%	Score 175.5	DB 1	Length 438
Best Local Similarity	27.3%	Pred. No. 1.7e-08		
Matches	67	Conservative 17	Mismatches 84	Indels 77
Gaps	14			
QY	26	QRPRTGGGCGGRLLG--TGTDA--CCRVHT-----TRCCRD-YPG-----ECCSEWDC	72	
		: :	: :	: :
Db	6	QOQT-----ALLLGLTGTARRLCNVKHTYPSGHKKRCQCPQHGVMNRCDHTRDT	58	
QY	73	MCVQPEFHCGDPC-----CITCRHP-----CPCGG	99	
		:	:	:
Db	59	LC-----HPCETGYNEAVNYDTCKQCQCNRHRSSELKQNCPTPQDVTVCRCRPTQ	110	
QY	100	VOSQKTSFGFOCIDCASGTESGGHEGCHKPWTCTQGFETVTPGNKTNHAVCVPGSP	159	

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/922,996  
; FILING DATE: 30-JUL-1992  
PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/267,577  
; FILING DATE: 07-NOV-1988  
ATTORNEY/AGENT INFORMATION:  
; NAME: Michaels, Christopher A  
; REGISTRATION NUMBER: 34,390  
; REFERENCE/DOCKET NUMBER: KW05  
TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 607-273-1711  
; TELEFAX: 607-273-2609  
INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 256 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US96-03965-2

Query Match 15.0%; Score 201.5; DB 5; Length 256;  
Best Local Similarity 28.7%; Pred. No. 4.2e-11;  
Matches 62; Conservative 26; Mismatches 85; Indels 43; Gaps 10;  
QY 34 CGPGRLL-LTGTDARCCRVHTTRCCRDYPGEGECSEW---DCMCVQPEPHCGDPCCTTC 89  
Db 47 CPSTFSSIGGPGNCRV---CAGYFRKFKCSTHNAECECIE-GPHCLGPGQTRC 101  
QY 90 RHHPCCPGGVQSGVQSGKFSFGFCIDCASGTFSGGH-EGHCKPWTDCQTFQGLTVFPNGKT 148  
Db 102 -EKDCRPGQELTKG-----CKTCSLGTFTNDONGTGVCRPWTNCSLDGRSVLKTGTTE 153  
QY 149 HNAVCV-----GSPAPPLGLWTVVLLAVACVLLTSAQLGLHI--W 190  
Db 154 KDVCGPPVVSFSPSTTISVTPGEGGHSQVLTFLTALTSALLALIFITLLFSVLKW 213  
QY 191 QLQKTKLLEVP-----PSTEDARSCQFPPEERG 219  
Db 214 TRKKPHIFKQPKTKTGAQAEDACSCRCQPEERG 249

RESULT 9  
US-08-236-918A-8  
; Sequence 8, Application US/08236918A  
; Patent No. 5674704  
; GENERAL INFORMATION:  
; APPLICANT: Alderson, Mark R.  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple 7.5.3  
; SOFTWARE: Microsoft Word, Version #6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/236,918A  
; FILING DATE: 06-May-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/060,843  
; FILING DATE: 07-May-1993  
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
; NAME: Anderson, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2801-B  
TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 255 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-236-918A-8  
Query Match 14.7%; Score 197; DB 1; Length 255;  
Best Local Similarity 30.2%; Pred. No. 1.1e-10;  
Matches 67; Conservative 20; Mismatches 81; Indels 54; Gaps 12;  
QY 34 CGPGRLLLTGTDARCCRVHTTRCCRDYPG-----EECCS-----EWDCCMCVQPEPHCGDP 84  
Db 48 CPPNSFSAGG--QRTCDI-----CRCKGVFRTRKCSSTSNACDC---TPGFHCLGA 97  
QY 85 CCTCRHHPCCPGGVQSGVQSGKFSFGFCIDCASGTFSGHGHGCKPWTDCQTFQGLTVFP 144  
Db 98 GCSMC-EQDCKQGOELTKG-----CKDCGFTGNDOKRGICRPWTNCSLDGKSVLVN 149  
QY 145 GNKTHNAVCPG-----SPPA---EPLGLWTVV---LLAVACVLLTSAQLGLH 188  
Db 150 GTKERDVVCGSPADLSPGASSVTPAPAREPGHSPQIISFFLALTSTALLFLFLFLTLR 209  
QY 189 ---IWLRKTKLLEVP-----STEDARSCQFPPEERG 219  
Db 210 FSVYKRGKKLLYIFKQFMRPVQTTQEDGCSRCRFPPEERG 251  
RESULT 10  
US-08-816-605-9  
; Sequence 9, Application US/08816605  
; Patent No. 5874240  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Gentz, Reiner  
; TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/816,605  
; FILING DATE: 13-MAR-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF254  
TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8512  
INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 255 amino acids

Query Match	14.5%;	Score 194;	DB 2;	Length 219;
Best Local Similarity	31.2%;	Pred. No. 1.7e-10;		

[illegible]

RESULT 5  
US-08-911-423-7  
: Sequence 7, Application US/08911423  
: Patent No. 6111090  
: GENERAL INFORMATION:  
: APPLICANT: Gorman, Daniel M.  
: APPLICANT: Randall, Troy D.  
: APPLICANT: Zlotnik, Albert  
: TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
: TYPE OF INVENTION: REAGENTS

Query Match	52.5%	Score 703;	DB 3;	Length 228;	Query Match	45.1%;	Score 605;	DB 3;	Length 232;
Best Local Similarity	54.9%;	Pred. No. 9.4e-57;			Best Local Similarity	78.1%;	Pred. No. 7.7e-48;		
Matches 129; Conservative	32;	Mismatches 58;	Indels 16;	Gaps 4;	Matches 107; Conservative	5;	Mismatches 17;	Indels	
					Qy	7	MGAFTALCGLLALLCALSLGQRTPTGGCGGPGRLLLGTGTDAFCCRCRVHTTTCRCDT		

Db 1 MGAFRALCGLALLCALSILGORTGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 60  
QY 67 CSEWDCMCVQPEFHCGDPCCCTTCHRHHCPCPGQGVQSGKFSFGQCI-----DCASGTFSG 122  
Db 61 CSEWDCMCVQPEFHCGDPCCCTTCHRHHCPCPGQGVQSGK----SWRCLWESTQARGSTRAR 117  
QY 123 GH-EGHCKPWTDCQTFG 138  
Db 118 GRAGRHCPARTCCGVWG 134

RESULT 6  
US-09-188-930-191  
; Sequence 191, Application US/09188930A  
; Patent No. 6150502  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene  
; APPLICANT: Murison, James Greg  
; TITLE OF INVENTION: Compositions Isolated From Skin Cells  
; FILE REFERENCE: 11000.1011c1  
; CURRENT FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 348  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 191  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-188-930-191

Query Match 19.0%; Score 255; DB 4; Length 89;  
Best Local Similarity 46.3%; Pred. No. 1.8e-15;  
Matches 44; Conservative 17; Mismatches 26; Indels 8; Gaps 2;  
QY 8 GAFRALCGLALLCALSILGQ-RPTGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 66  
Db 1 GAWAMLYGVSMCLVDLGLQGSVVEEPGCGKGVQNGSGNTRCCSLYA-----PGKED 53

QY 67 CSEWDCMCVQPEFHCGDPCCCTTCHRHHCPCPGQGVQ 101  
Db 54 CPERCICVTPEYHCGDPQCKICKHYPCQPGQORVE 88

RESULT 7  
US-08-236-918A-6  
; Sequence 6, Application US/08236918A  
; Patent No. 5674704  
; GENERAL INFORMATION:  
; APPLICANT: Alderson, Mark R.  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple 7.5.3  
; SOFTWARE: Microsoft Word, Version #6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/236,918A  
; FILING DATE: 06-May-1994

; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/060,843  
; FILING DATE: 07-May-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Anderson, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2801-B  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 256 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-236-918A-6

Query Match 15.0%; Score 201.5; DB 1; Length 256;  
Best Local Similarity 28.7%; Pred. No. 4.2e-11;  
Matches 62; Conservative 26; Mismatches 85; Indels 43; Gaps 10;  
QY 34 CGPGRLL-LTGTGDARCCRVHTTRCCRDYPGEECCSEW----DCMCVQPEFHCGDPCCCTTC 89  
Db 47 CPPSTFSSIGGQPCNICRV-----CAGYFRFKKFCSSHNACECIE-GFHCLGSPQCTRC 101  
QY 90 RHHPCCPGQGVQSGKFSFGQCIDCASGTFSGGH-EGHCKPWTDCQTFGLTVFPGNKT 148  
Db 102 -EKCRPCQELTKQG-----CKTCSLGTFNQNGTGVCRPWTNCSLDGRSVLKTGTE 153  
QY 149 HNAVCP-----GSPPAEPLGWLTVLLVAACVLLTSAQLGHI--W 190  
Db 154 KDVCVGPVVSFSPSTTISVTPEGGPGGSHLQLVTLFLALTSALLLALIFITLLFSVLKW 213  
QY 191 QLRKTQLLEVP-----PSTEDARSCQFPPEERG 219  
Db 214 IRKKPHFPKPPFKTKTGAAGQEDACSCRCPOEERG 249

RESULT 8  
PCT-US96-03965-2  
; Sequence 2, Application PC/TUS9603965  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung Se  
; APPLICANT: Kang, Chang-Yuul  
; TITLE OF INVENTION: Monoclonal antibody against human  
; TITLE OF INVENTION: receptor 4-1BB  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Barnard, Brown & Michaels  
; STREET: 306 East State Street, Suite 220  
; CITY: Ithaca  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 14850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/03965  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/122,796  
; FILING DATE: 16-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/012,269  
; FILING DATE: 01-FEB-1993

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:51:18 ; Search time 65.86 Seconds  
(without alignments)  
73.157 Million cell updates/sec

Title: US-09-512-363-2  
Perfect score: 1340  
Sequence: 1 MAQHGMAGFALCGLALIC.....EEERGSABEKGRLGLDW 234

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

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- 2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1322.5	98.7	241	3	US-08-911-423-4
2	1308	97.6	228	3	US-08-911-423-6
3	1093	81.6	311	3	US-08-911-423-8
4	703	52.5	228	3	US-08-911-423-2
5	605	45.1	232	3	US-08-911-423-7
6	255	19.0	89	4	US-09-188-930-191
7	201.5	15.0	256	1	US-08-236-918A-6
8	201.5	15.0	256	5	PCT-US96-03965-2
9	197	14.7	255	1	US-08-236-918A-8
10	197	14.7	255	2	US-08-816-605-9
11	197	14.7	255	5	PCT-US96-03965-8
12	194	14.5	219	2	US-08-816-605-2
13	175.5	13.1	438	1	US-08-097-827-11
14	175.5	13.1	438	1	US-08-494-574-11
15	166.5	12.4	206	1	US-08-097-827-7
16	166.5	12.4	206	1	US-08-494-574-7
17	165	12.3	277	2	US-08-147-784-2
18	165	12.3	277	4	US-08-195-967-2
19	160.5	12.0	205	3	US-08-974-022-51
20	157	11.7	191	3	US-08-974-022-52
21	153	11.4	300	2	US-08-794-796-2
22	150	11.2	451	3	US-08-996-139-4
23	150	11.2	451	4	US-08-995-659-4
24	150	11.2	616	3	US-08-996-139-6
25	150	11.2	616	4	US-08-995-659-6
26	149	11.1	140	4	US-08-477-347-17
27	142.5	10.6	591	3	US-08-996-139-2

Query Match 98.7%; Score 1322.5; DB 3; Length 241;

28	142.5	10.6	591	4	US-08-995-659-2	Sequence 2, Appl
29	141.5	10.6	401	3	US-08-974-022-2	Sequence 2, Appl
30	141.5	10.6	461	4	US-09-042-785A-7	Sequence 7, Appl
31	139.5	10.4	139	2	US-08-219-237B-8	Sequence 8, Appl
32	139.5	10.4	401	3	US-08-974-022-4	Sequence 4, Appl
33	139.5	10.4	401	4	US-09-042-785A-13	Sequence 13, Appl
34	139.5	10.4	461	1	US-08-385-229-2	Sequence 2, Appl
35	139.5	10.4	461	2	US-08-650-000-2	Sequence 2, Appl
36	139.5	10.4	461	4	US-08-477-347-3	Sequence 3, Appl
37	139.5	10.4	461	6	5395760-2	Patent No. 5395760
38	139	10.4	289	4	US-09-042-785A-11	Sequence 11, Appl
39	138	10.3	401	3	US-08-974-022-6	Sequence 6, Appl
40	138	10.3	401	4	US-09-042-785A-12	Sequence 12, Appl
41	135.5	10.1	197	3	US-08-974-022-49	Sequence 49, Appl
42	134.5	10.0	625	3	US-08-996-139-15	Sequence 15, Appl
43	134.5	10.0	625	4	US-08-995-659-15	Sequence 15, Appl
44	131.5	9.8	253	4	US-09-042-785A-4	Sequence 4, Appl
45	129.5	9.7	605	4	US-09-042-785A-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1  
US-08-911-423-4  
; Sequence 4, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-911-423-4

Best Local Similarity 96.7%; Pred. No. 4.8e-113;  
Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;  
QY 1 MAQHGAFAFRALCGLALLCALSIGQRTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
DB 1 MAQHGAFAFRALCGLALLCALSIGQRTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
QY 61 YPEECSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGVQSOGKFSFGQICDASGTF 120  
DB 61 YPEECSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGVQSOGKFSFGQICDASGTF 120  
QY 121 SGHEGCKPWTCTQGFGLTVFPGKTHNAVCPGSPAPBLGWLTVVLLAVAAACVLL 180  
DB 121 SGHEGCKPWTCTQGFGLTVFPGKTHNAVCPGSPAPBLGWLTVVLLAVAAACVLL 180  
QY 181 TSAQLGLHIWL-----RKTQLLLEVPSTEDARSCOFFPEERGERSAEKGRGLDW 233  
DB 181 TSAQLGLHIWLRSQCMWPRETQLLLEVPSTEDARSCOFFPEERGERSAEKGRGLDW 240  
QY 234 V 234  
DB 241 V 241

RESULT 2  
US-08-911-423-6  
; Sequence 6, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-6

Query Match 97.6%; Score 1308; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 9.3e-112;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 MGAFRALCGLALLCALSIGQRTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 66  
DB 1 MGAFRALCGLALLCALSIGQRTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 60  
QY 67 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGVQSOGKFSFGQICDASGTFSGGHEG 126  
DB 61 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGVQSOGKFSFGQICDASGTFSGGHEG 120  
QY 127 HCKPWTCTQGFGLTVFPGKTHNAVCPGSPAPBLGWLTVVLLAVAAACVLLLTSAQLG 186  
DB 121 HCKPWTCTQGFGLTVFPGKTHNAVCPGSPAPBLGWLTVVLLAVAAACVLLLTSAQLG 180  
QY 187 LHIWOLRKTQLLLEVPSTEDARSCOFFPEERGERSAEKGRGLDW 234  
DB 181 LHIWOLRKTQLLLEVPSTEDARSCOFFPEERGERSAEKGRGLDW 228  
RESULT 3  
US-08-911-423-8  
; Sequence 8, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 311 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-8

Query Match 81.6%; Score 1093; DB 3; Length 311;



PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 XX other T cell disorders  
 PS Disclosure; Pages 61-62; 71pp; English.  
 XX  
 CC This is the amino acid sequence of the truncated human 312C2 T cell  
 CC protein from clone A8. The 312C2 proteins are expressed in thymus  
 CC cells and are induced on T cells and spleen cells following activation.  
 CC Engagement of 312C2 stimulates proliferation of T cell clones,  
 CC antigen-specific proliferation and cytokine production by T-cells, and  
 CC potentiates T cell expansion or apoptosis. The products can be used  
 CC in the treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX  
 SQ Sequence 228 AA;

Query Match 100.0%; Score 246; DB 19; Length 228;  
 Best Local Similarity 100.0%; Pred. NO. 2.5e-24;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DCASGTFSGCGHGCKPWTCTQPGFLTVPPGKNTKTHNAVCV 41  
 DB 108 dcasgtfsgghgckpwtctqpgfltvppgkntkthnavcv 148  
 |||||

RESULT 2  
 AAY95879  
 ID AAY95879 standard; Protein; 234 AA.  
 XX  
 AC AAY95879;  
 XX  
 DT 20-NOV-2000 (first entry)  
 XX  
 DE Human tumour necrosis factor receptor-like protein TR11.  
 XX  
 KW TR11; human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
 KW dermatological; antiinflammatory; therapy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT /label= Signal\_peptide  
 FT Protein 26..234  
 FT /label= Mature\_protein  
 FT Domain 26..162  
 FT /label= Extracellular\_domain  
 FT Domain 163..179  
 FT /label= Transmembrane\_domain  
 FT Domain 180..234  
 FT /label= Intracellular\_domain  
 FT Modified-site 146  
 FT /note= "N-glycosylated"  
 FT Domain 72..81  
 FT /note= "conserved domain CD-II"  
 FT Domain 84..93  
 FT /note= "conserved domain CD-III"  
 FT Domain 107..113  
 FT /note= "conserved domain CD-IV"  
 FT Domain 128..134  
 FT /note= "conserved domain CD-V"  
 FT Domain 153..160  
 FT /note= "conserved domain CD-VI"  
 FT Domain 176..186  
 FT /note= "conserved domain CD-VII"  
 FT Domain 204..209  
 FT /note= "conserved domain CD-IX"

FT Domain 224..233  
 FT /note= "conserved domain CD-X"  
 FT Region 27..36  
 FT /note= "epitope-bearing region"  
 FT Region 43..51  
 FT /note= "epitope-bearing region"  
 FT Region 59..67  
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 FT Region 56..64  
 FT /note= "epitope-bearing region"  
 FT Region 66..71  
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 FT Region 203..211  
 FT /note= "epitope-bearing region"  
 FT Region 222..230  
 FT /note= "epitope-bearing region"  
 XX WO200050459-A1.  
 PN 31-AUG-2000.  
 XX  
 PD 23-FEB-2000; 2000WO-US04572.  
 XX  
 PF 24-FEB-1999; 99US-0121648.  
 PR 13-MAY-1999; 99US-0134172.  
 PR 16-JUL-1999; 99US-0144076.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Ruben SM, NI J;  
 PI  
 XX WPI; 2000-572072/53.  
 DR N-PSDB; AAA50304.  
 XX  
 PT Human tumor necrosis factor receptor-like proteins useful for  
 PT diagnosis, prevention and treatment of disease states associated with  
 PT aberrant cell survival such as autoimmune disease and rheumatoid  
 PT arthritis  
 XX  
 PS Claim 14(c); Fig 1A-B; 278pp; English.  
 XX  
 CC The present sequence is that of human tumour necrosis factor  
 CC receptor-like protein TR11, a novel 25 kDa protein which shows  
 CC 58.6% identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The sequence was deduced from  
 CC a cDNA clone (see AAA50304) discovered in a T-helper cell library.  
 CC TR11 activated NF-kappaB through a TRAF2-mediated mechanism.  
 CC Expression is activation-inducible. The TR11 ligand is constitutively  
 CC expressed in an endothelial cell line. This suggests that TR11 and  
 CC its ligand may be involved in activated T-cell trafficking.  
 CC The invention provides TR11, TR11SV1 and TR11SV2 nucleic acids  
 CC (see AAA50304-06) and highly conserved encoded proteins (see  
 CC AAY95879-81), as well as vectors, host cells and recombinant methods for  
 CC their production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an  
 CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency,  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:56:24 ; Search time 126.12 Seconds  
(without alignments)  
19.708 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_114\_154

Perfect score: 246

Sequence: 1 DCASGTGSGHGCKPWT.....TQFGFLTVFPGKTHNAVCV 41

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
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4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
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16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	246	100.0	228	19 AAW37840	Truncated human 31
2	246	100.0	234	21 AAY95879	Human tumour necro
3	246	100.0	234	21 AAY52158	Tumour necrosis fa
4	246	100.0	235	21 AAY44825	Human molecule ass
5	246	100.0	240	21 AAY95881	Human tumour necro
6	246	100.0	240	21 AAY52160	TR11SV2 amino acid
7	246	100.0	241	19 AAW37839	Amino acid sequenc
8	246	100.0	241	20 AAY08605	Human TNF receptor
9	246	100.0	241	20 AAB27651	Human protein PRO3
10	246	100.0	241	21 AAB33431	Human PRO364 prote
11	246	100.0	241	21 AAY95880	Human tumour necro

12	246	100.0	241	21 AAY95895	Human tumour necro
13	246	100.0	241	21 AAB24409	Human PRO364 prote
14	246	100.0	241	21 AAY71467	Human PRO364 prote
15	246	100.0	241	21 AAY52159	TR11SV1 amino acid
16	246	100.0	241	21 AAB20115	Human immunostimul
17	246	100.0	241	22 AAB47054	Human PRO364. Hom
18	246	100.0	241	22 AAB50910	Human PRO364 prote
19	246	100.0	241	22 AAB50982	Human PRO364 prote
20	246	100.0	241	22 AAB53090	Human angiogenesis
21	246	100.0	311	19 AAW37842	Human 312C2 protei
22	196	79.7	316	22 AAB47055	Polypeptide encode
23	196	79.7	317	20 AAY06645	PRO364-related EST
24	192	78.0	222	19 AAW49018	Mouse glucocortico
25	192	78.0	228	19 AAW49016	Mouse glucocortico
26	192	78.0	228	19 AAW37838	Amino acid sequenc
27	192	78.0	294	19 AAW49017	Mouse glucocortico
28	96	39.0	277	16 AAR74737	ACT-4 cell surface
29	96	39.0	277	16 AAR79904	ACT-4-h-1 receptor
30	96	39.0	277	22 AAB35329	Human OX40 protein
31	96	39.0	277	22 AAB50522	Human tumour necro
32	95	38.6	206	16 AAR81881	Mouse type-II memb
33	95	38.6	206	19 AAW48977	Mouse OX40 extrace
34	95	38.6	277	16 AAR76936	Deduced sequence e
35	95	38.6	438	16 AAR81882	Plasmid pDC406/OX4
36	95	38.6	438	19 AAW48976	OX40/Fc mutein. C
37	93	37.8	219	18 AAW31759	A novel human h4-1
38	93	37.8	219	20 AAW92523	Human h4-1BBSV rec
39	93	37.8	219	20 AAW92524	Human h4-1BBSV rec
40	93	37.8	255	16 AAR74087	Human receptor ind
41	93	37.8	255	16 AAR70977	H4-1BB receptor pr
42	93	37.8	255	16 AAR64197	Human 4-1BB polype
43	93	37.8	255	18 AAW26658	Human 4-1BB recept
44	93	37.8	255	20 AAY33214	Human CD137 protei
45	93	37.8	255	20 AAY28688	Human receptor pro

#### ALIGNMENTS

RESULT 1  
AAW37840  
ID AAW37840 standard; Protein; 228 AA.  
XX  
AC AAW37840;  
XX  
DT 28-JUL-1998 (first entry)  
XX  
DE Truncated human 312C2 protein from clone\_A8 amino acid sequence.  
XX  
KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
KW antigen-specific T cell proliferation; cytokine production by T-cell;  
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
KW autoimmune disorders.  
OS Homo sapiens.  
XX  
XX W0906842-A1.  
XX  
PD 19-FEB-1998.  
XX  
XX 14-AUG-1997; 97WO-US13931.  
XX  
PR 07-OCT-1996; 96US-0027901.  
PR 16-AUG-1996; 96US-0689943.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Gorman DM, Randall TD, Zlotnik A;  
XX  
DR WPI; 1998-159534/14.  
DR N-PSDB; AAV19154.  
XX  
PT Isolated 312C2 T cell gene - used to develop products for treating,

FT Modified-site /note= "Potential phosphorylation site"  
 FT 48  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 62  
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 FT 82  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 205  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 223  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 140  
 FT Modified-site /note= "N-glycosylated"  
 XX  
 PN W0200005374-A2.  
 XX  
 XX 03-FEB-2000.  
 XX  
 PF 21-JUL-1999; 99WO-US16537.  
 XX  
 XX 22-JUL-1998; 98US-0093827.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 PI Tang YT, Lal P, Hillman JL, Corley NC, Patterson C, Baughn MR;  
 XX  
 DR WPI; 2000-182699/16.  
 DR N-PSDB; AA249948.  
 XX  
 DR Polypeptides and polynucleotides useful for treating and detecting cell  
 PT proliferation disorders e.g. actinic keratosis, and immune disorders  
 PT e.g. Crohn's disease  
 PT  
 PS Claim 1; Pages 64-65; 67pp; English.  
 XX  
 XX The present sequence is a molecule associated with cell  
 CC proliferation, MACP-5 from Incyte clone 2809903 isolated from TLYMN0706  
 CC cDNA library. This sequence is expressed in cardiovascular and  
 CC haematopoietic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV,  
 CC hepatotropic, antiinflammatory, antipsoriatic, cytostatic, antiasthmatic,  
 CC dermatologic, antidiabetic, nephrotropic, antithyroid, thyromimetic,  
 CC immunosuppressive, osteopathic, antiarthritic, uropathic, antiulcer,  
 CC and ophthalmological activities. The present sequence is useful in the  
 CC diagnosis, treatment and prevention of cell proliferative disorders e.g.  
 CC actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and  
 CC hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and  
 CC anaemia.  
 XX  
 SQ Sequence 235 AA;

Query Match 100.0%; Score 246; DB 21; Length 235;  
 Best Local Similarity 100.0%; Pred No. 2.6e-24;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCASGTFSGGHEGCKPWTCTQFGFLTFPGNKTNAVCV 41  
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 Db 108 dcasgtfsgghegckpwtctqfgfltfpgnktnavcv 148  
 |||||||

RESULT 5  
 AAY95881  
 ID AAY95881 standard; Protein; 240 AA.  
 XX  
 AC AAY95881;  
 XX  
 DT 20-NOV-2000 (first entry)  
 XX  
 XX Human tumour necrosis factor receptor-like protein TR11SV2.  
 DE  
 XX TR11SV2; human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;

dermatological; antiinflammatory; therapy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /label= Signal\_peptide  
 FT 20..240  
 FT /label= Mature\_protein  
 FT 20..168  
 FT Domain  
 FT /label= Extracellular\_domain  
 FT 169..185  
 FT /label= Transmembrane\_domain  
 FT 186..240  
 FT Domain  
 FT /label= Intracellular\_domain  
 FT 152  
 FT Modified-site  
 FT /note= "N-glycosylated"  
 FT 57..68  
 FT Domain  
 FT /note= "conserved domain CD-I"  
 FT 78..87  
 FT Domain  
 FT /note= "conserved domain CD-II"  
 FT 91..100  
 FT Domain  
 FT /note= "conserved domain CD-III"  
 FT 114..121  
 FT Domain  
 FT /note= "conserved domain CD-IV"  
 FT 134..140  
 FT Domain  
 FT /note= "conserved domain CD-V"  
 FT 159..166  
 FT Domain  
 FT /note= "conserved domain CD-VI"  
 FT 182..192  
 FT Domain  
 FT /note= "conserved domain CD-VII"  
 FT 210..215  
 FT Domain  
 FT /note= "conserved domain CD-IX"  
 FT 230..239  
 FT Domain  
 FT /note= "conserved domain CD-X"  
 FT 20..28  
 FT Region  
 FT /note= "epitope-bearing region"  
 FT 24..32  
 FT Region  
 FT /note= "epitope-bearing region"  
 FT 37..45  
 FT Region  
 FT /note= "epitope-bearing region"  
 FT 48..56  
 FT Region  
 FT /note= "epitope-bearing region"  
 FT 67..75  
 FT Region  
 FT /note= "epitope-bearing region"  
 FT 106..114  
 FT Region  
 FT /note= "epitope-bearing region"  
 FT 130..139  
 FT Region  
 FT /note= "epitope-bearing region"  
 FT 149..157  
 FT Region  
 FT /note= "epitope-bearing region"  
 FT 162..170  
 FT Region  
 FT /note= "epitope-bearing region"  
 FT 209..217  
 FT Region  
 FT /note= "epitope-bearing region"  
 FT 228..236  
 FT Region  
 FT /note= "epitope-bearing region"  
 XX  
 XX W02000050459-A1.  
 PN  
 XX  
 XX 31-AUG-2000.  
 PD  
 XX  
 XX 23-FEB-2000; 2000WO-US04572.  
 PF  
 XX  
 XX 24-FEB-1999; 99US-0121648.  
 PR 13-MAY-1999; 99US-0134172.  
 PR 16-JUL-1999; 99US-0144076.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX Ruben SM, Ni J;  
 XX WPI; 2000-572072/53.  
 DR

CC polypeptides may also be used. Methods for screening for  
 XX agonist/antagonist compounds are also provided.

SQ Sequence 234 AA;

Query Match 100.0%; Score 246; DB 21; Length 234;

Best Local Similarity 100.0%; Pred. No. 2.6e-24;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DCASGTFSGGHEGCKPWTCTQFGFLTVFPGNKTHNAVCV 41

Db 114 dcasgtfsgghegchckpwtcdctqfgfltvfpgnkthnavcv 154

RESULT 3

AAAY52158  
 ID AA52158 standard; Protein; 234 AA.

XX  
 AC AA52158;

XX  
 DT 01-FEB-2000 (first entry)

XX  
 DE Tumour necrosis factor receptor-like protein (TR11) amino acid sequence.

XX  
 KW Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2;

XX  
 KW G1TR; growth; differentiation; cell death; immune deficiency disorder;

XX  
 KW Digeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia;

XX  
 KW Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes;

XX  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;

XX  
 KW inflammatory condition.

XX  
 OS Homo sapiens.

XX  
 FH Key Location/Qualifiers

FT Peptide 1..23

FT Protein /label= Signal\_peptide

FT FT 26..234

FT FT /label= TR11

FT FT 26..162

FT FT /note= "Extracellular domain"

FT FT 163..179

FT FT /note= "Transmembrane domain"

FT FT 180..234

FT FT /note= "Intracellular domain"

XX  
 PN W0920758-A1.

XX  
 PD 29-APR-1999.

XX  
 XX 21-OCT-1998; 98WO-US22085.

XX  
 PF 21-OCT-1997; 97US-0063212.

XX  
 PR (HUMA-) HUMAN GENOME SCI INC.

XX  
 PA N1 J, Ruben SM;

XX  
 PI WPI; 2000-061922/05.

XX  
 DR N-PSDB; AA237762.

XX  
 XX New tumour necrosis factor receptor-like polypeptides used to, e.g.

XX  
 PT treat Digeorge syndrome -

XX  
 XX Claim 14; Fig 1; 167pp; English.

XX  
 PS This is the amino acid sequence of the human tumour necrosis factor

XX  
 XX receptor-like protein (TR11 receptor). The invention relates to TR11 and

XX  
 CC two splice variants TR11SV1 and TR11SV2. The nucleotide sequences were

XX  
 CC determined by sequencing cloned cDNAs AA237765-237766. The TR11 receptor

XX  
 CC and its splice variants show homology to the murine glucocorticoid

XX  
 CC induced tumour necrosis factor receptor family-related gene (G1TR).

XX  
 CC TR11, TR11SV1 and TR11SV2 polypeptides may be involved in the regulation

CC of cell-type specific receptor-mediated cell growth, differentiation,  
 CC and ultimately, cell death. They can be used for screening for  
 CC agonists/antagonists. The polypeptides, agonists or antagonists can be  
 CC used for treating a disease state associated with aberrant cell  
 CC survival. They can be used for treating immune deficiency disorders,  
 CC Digeorge syndrome, HIV infection, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood  
 CC platelet disorders or wounds resulting from trauma or surgery. They can  
 CC also be used to treat heart attacks, strokes, Addison's disease,  
 CC haemolytic anaemia, rheumatoid arthritis, Goodpasture's syndrome, Grave's  
 CC disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome,  
 CC systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent  
 CC diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,  
 CC hypersensitivity to an antigenic molecule, organ rejection or graft  
 CC versus host disease, inflammatory conditions, ischaemia-reperfusion  
 CC injury, complement-mediated hyperacute rejection, nephritis, cytokine or  
 CC chemokine induced lung injury, inflammatory bowel disease, Crohn's  
 CC disease, hyperproliferative disorders, or infections. They can also be  
 CC used to repair, replace, or protect tissue damaged by congenital  
 CC defects, trauma, age, disease, surgery, including cosmetic plastic  
 CC surgery, fibrosis, reperfusion injury, peripheral nerve injuries,  
 CC neuropathies, and central nervous system disease (e.g. Alzheimer's  
 CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral  
 CC sclerosis, and Shy-Drager syndrome). The products can also be used for  
 CC detection, diagnosis and prognosis.

XX  
 SQ Sequence 234 AA;

Query Match 100.0%; Score 246; DB 21; Length 234;

Best Local Similarity 100.0%; Pred. No. 2.6e-24;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DCASGTFSGGHEGCKPWTCTQFGFLTVFPGNKTHNAVCV 41

Db 114 dcasgtfsgghegchckpwtcdctqfgfltvfpgnkthnavcv 154

RESULT 4

AAAY44825

ID AAY44825 standard; Protein; 235 AA.

XX  
 AC AA444825;

XX  
 DT 18-MAY-2000 (first entry)

XX  
 DE Human molecule associated with cell proliferation, MACP-5.

XX  
 KW Human; molecule associated with cell proliferation; MACP-5;

XX  
 KW Incyte clone 2809903; antiarteriosclerotic; hepatotropic; cytostatic;

XX  
 KW anti-inflammatory; antipsoriatic; anti-HIV; antidiabetic; anaemia;

XX  
 KW dermatological; antidiabetic; nephrotropic; antichyroid; thyromimetic;

XX  
 KW immunosuppressive; osteopathic; antiarthritic; uropathic; antitumor;

XX  
 KW ophthalmological; diagnosis; treatment; prevention; immune disorder;

XX  
 KW cell proliferative disorder; actinic keratosis; arteriosclerosis;

XX  
 KW atherosclerosis; bursitis; hepatitis; Crohn's disease; amyloidosis.

XX  
 OS Homo sapiens.

XX  
 FH Key Location/Qualifiers

FT Region 1..19

FT FT /label= Signature\_sequence

FT FT 68..96

FT FT /label= Signature\_sequence

FT FT 109..147

FT FT /label= Signature\_sequence

FT FT 122..129

FT FT /label= Signature\_sequence

FT FT 157..175

FT FT /label= Signature\_sequence

FT FT 165..186

FT FT /label= Signature\_sequence

FT  
 FT Modified-site 37

DT 28-JUL-1998 (first entry)  
 DE Amino acid sequence of the human 312C2 T cell protein.  
 XX  
 KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 KW antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
 KW autoimmune disorders.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..726  
 FT /tag= a  
 FT /product= "human 312C2 protein"  
 XX  
 PN WO9806842-A1.  
 XX  
 PD 19-FEB-1998.  
 XX  
 PF 14-AUG-1997; 97WO-US13931.  
 XX  
 PR 07-OCT-1996; 96US-0027901.  
 PR 16-AUG-1996; 96US-0689943.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 XX  
 PI Gorman DM, Randall TD, Zlotnik A;  
 XX  
 DR WPI: 1998-159534/14.  
 DR N-PSDB; AAV19153.  
 XX  
 XX Isolated 312C2 T cell gene - used to develop products for treating,  
 PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 PT other T cell disorders  
 PT  
 PS Claim 2; Pages 59-60; 71pp; English.  
 XX  
 CC This is the amino acid sequence encoding the human 312C2 T cell  
 CC protein. The 312C2 proteins are expressed in thymus cells and are  
 CC induced on T cells and spleen cells following activation. Engagement  
 CC of 312C2 stimulates proliferation of T cell clones, antigen-specific  
 CC proliferation and cytokine production by T-cells, and potentiates T  
 CC cell expansion or apoptosis. The products can be used in the  
 CC treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX  
 SQ Sequence 241 AA;  
 Query Match 100.0%; Score 246; DB 19; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-24;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DCASGTFSGGHEGCKPWTDTCTQFGFLTVFPGNKTHNAVCV 41  
 DB 114 dcasgtfsgghegckpwtctctqfgfltvfpgnkthnavcv 154  
 RESULT 8  
 ID AAY06605 standard; Protein; 241 AA.  
 XX  
 AC AAY06605;  
 XX  
 XX 26-OCT-1999 (first entry)  
 DT Human TNF receptor homologue PRO364.  
 DE  
 DE PRO364; tumour necrosis factor receptor; human; apoptosis;  
 KW

KW inflammation; antiinflammatory; NF-KB activation;  
 KW autoimmune disease; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..25 "signal peptide"  
 FT Protein 26..241  
 FT /note= "mature protein"  
 FT Modified-site 146  
 FT /note= "N-glycosylated"  
 FT Domain 162..180  
 FT /note= "transmembrane domain"  
 XX  
 PN WO9940196-A1.  
 XX  
 PD 12-AUG-1999.  
 XX  
 PF 09-FEB-1999; 99WO-US02642.  
 XX  
 PR 09-FEB-1998; 98US-0024087.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;  
 PI Pitti RM, Wood WI;  
 XX  
 DR WPI: 1999-494296/41.  
 DR N-PSDB; AAX87670.  
 XX  
 XX Tumour necrosis factor receptor homologue - useful for, e.g.  
 PT modulating apoptosis and NF-KB activation and proinflammatory or  
 PT autoimmune responses  
 PT  
 PS Claim 17; Fig 2A; 104pp; English.  
 XX  
 CC The present sequence represents human PRO364, a novel member of the  
 CC tumour necrosis factor receptor family. The sequence was deduced  
 CC from a bone marrow cDNA clone (see AAX87670). Methods for the  
 CC recombinant production of PRO364 polypeptides, e.g. in CHO,  
 CC Escherichia coli or yeast host cells, are provided. Claimed  
 CC polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the  
 CC mature protein) and 26-X of the present sequence, where X is any  
 CC one of amino acid residues 157-167 of PRO364. PRO364 polypeptides  
 CC are useful for modulating apoptosis, NF-KB activation and  
 CC proinflammatory or autoimmune responses in mammalian cells  
 CC (claimed). Chimeric molecules comprising a PRO364 polypeptide  
 CC fused to a heterologous sequence such as epitope tag or  
 CC immunoglobulin Fc region are also claimed. PRO364 can be used in  
 CC assays to identify other proteins or molecules involved in binding  
 CC interactions. This is useful for identifying inhibitors or  
 CC agonists of receptor/ligand binding. The PRO364 polypeptides may  
 CC also be combined with an agent that is cytotoxic, chemotherapeutic  
 CC or a growth inhibitor. PRO364 antibodies are useful in diagnostic  
 CC methods, purification methods and also in therapy, e.g. as  
 CC inhibitors.  
 XX  
 SQ Sequence 241 AA;  
 Query Match 100.0%; Score 246; DB 20; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-24;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DCASGTFSGGHEGCKPWTDTCTQFGFLTVFPGNKTHNAVCV 41  
 DB 114 dcasgtfsgghegckpwtctctqfgfltvfpgnkthnavcv 154  
 RESULT 9  
 ID AAB27651 standard; Protein; 241 AA.



```

XX PA (GETH ) GENENTECH INC.
XX PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
XX PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
XX PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX XX WPI: 2000-572271/53.
XX DR N-PSDB; AAC58596.
XX XX
XX XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of
XX PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
XX PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
XX XX
XX PS Claim 33; Fig 36; 309pp; English.
XX XX
XX CC The present invention describes sixty four human PRO proteins which can
XX CC be used in the treatment of immune related diseases. The human PRO
XX CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
XX CC treating and diagnosing immune related disorders. The disorders are
XX CC selected from systemic lupus erythematosus, rheumatoid arthritis,
XX CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
XX CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
XX CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
XX CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
XX CC immune-mediated renal disease, demyelinating diseases of the central
XX CC and peripheral nervous systems, hepatobiliary diseases, inflammatory
XX CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,
XX CC autoimmune or immune-mediated skin diseases, allergic diseases,
XX CC immunological diseases of the lung, and transplantation associated
XX CC diseases including graft rejection and graft-versus-host-disease.
XX CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
XX CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and
XX CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein
XX CC sequences given in the exemplification of the present invention.
XX XX
XX SQ Sequence 241 AA;

Query Match 100.0%; Score 246; DB 21; Length 241;
Best Local Similarity 100.0%; Pred. No. 2,7e-24;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCASGTFSGGHEGCKPWTCTQFGFLTVFPGNKTHNAVCV 41
Db 114 dcasgtfsgghegckpwtctqfgfltvfpgnkthnavcv 154
|||||
|||||

RESULT 11
AA95880
ID AAY95880 standard; Protein: 241 AA.
XX AC AAY95880;
XX DT 20-NOV-2000 (first entry)
XX DE Human tumour necrosis factor receptor-like protein TRLLSV1.
XX KW TRLLSV1; human; tumour necrosis factor receptor-like protein;
XX KW immunodeficiency; autoimmune disease; rheumatoid arthritis;
XX KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;
XX KW dermatological; antiinflammatory; therapy; diagnosis.
XX OS Homo sapiens.
XX XX
XX PH Location/Qualifiers
XX FT 1..162
XX FT /label= Extracellular_domain
XX FT 163..179
XX FT /label= Transmembrane_domain
XX FT 180..241
XX FT /label= Intracellular_domain
XX FT Modified-site 146

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FT Domain /note= "N-glycosylated"
FT 51..61 /note= "conserved domain CD-I"
FT 72..81 /note= "conserved domain CD-II"
FT 85..94 /note= "conserved domain CD-III"
FT 108..115 /note= "conserved domain CD-IV"
FT 128..134 /note= "conserved domain CD-V"
FT 153..160 /note= "conserved domain CD-VI"
FT 176..186 /note= "conserved domain CD-VII"
FT 195..201 /note= "conserved domain CD-VIII"
FT 211..216 /note= "conserved domain CD-IX"
FT 231..240 /note= "conserved domain CD-X"
FT 2..10 /note= "epitope-bearing region"
FT 11..19 /note= "epitope-bearing region"
FT 27..35 /note= "epitope-bearing region"
FT 38..46 /note= "epitope-bearing region"
FT 42..50 /note= "epitope-bearing region"
FT 31..46 /note= "epitope-bearing region"
FT 61..69 /note= "epitope-bearing region"
FT 99..107 /note= "epitope-bearing region"
FT 125..133 /note= "epitope-bearing region"
FT 143..151 /note= "epitope-bearing region"
FT 156..164 /note= "epitope-bearing region"
FT 196..204 /note= "epitope-bearing region"
FT 209..217 /note= "epitope-bearing region"
FT 229..237 /note= "epitope-bearing region"
FT 241..241 /note= "epitope-bearing region"
XX WO200050459-A1.
XX PN 31-AUG-2000.
XX PD 23-FEB-2000; 2000WO-US04572.
XX PF 24-FEB-1999; 99US-0121648.
XX PR 13-MAY-1999; 99US-0134172.
XX PR 16-JUL-1999; 99US-0144076.
XX XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX XX Ruben SM, NI J;
XX PI WPI: 2000-572072/53.
XX DR N-PSDB; AAA50305.
XX XX
XX PT Human tumor necrosis factor receptor-like proteins useful for
XX PT diagnosis, prevention and treatment of disease states associated with
XX PT aberrant cell survival such as autoimmune disease and rheumatoid
XX PT arthritis -
XX XX
XX PS Claim 14(1); Fig 2A-B; 278pp; English.

```

XX AAB27651;  
 XX AC  
 XX DT 26-JAN-2001 (first entry)  
 XX DE  
 XX DE Human protein PRO364.  
 XX KW Cardiovascular; endothelial; angiogenic disorder; PRO179;  
 KW PRO238; PRO364; PRO844; PRO1760; PRO205; PRO321; PRO333;  
 KW PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;  
 KW gene therapy.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT /label= "Signal peptide"  
 XX PN WO200053757-A2.  
 XX PD 14-SEP-2000.  
 XX PF 24-FEB-2000; 2000WO-US05004.  
 XX PR 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 XX (GETH ) GENENTECH INC.  
 XX AShenkazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
 PI Goddard A, Gurney AL, Hillan KJ, Marsters SA, Paoni NF, Pitti RM;  
 PI Watanabe CK, Williams PM, Wood WI;  
 XX WPI; 2000-611444/58.  
 DR N-PSDB; AAA99903.  
 XX Novel PRO polypeptides and agonists and antagonists of them, used to  
 PT diagnose and treat cardiovascular, endothelial and angiogenic disorders  
 PT .  
 XX Claim 71; Fig 6; 181pp; English.  
 XX The present invention relates to methods for stimulating or inhibiting  
 CC angiogenesis and cardiovascularization. The methods involve the use of  
 CC pharmaceutical compositions based on the following proteins, PRO179,  
 CC PRO238, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333,  
 CC PRO840, PRO877, PRO878, PRO879, PRO882, PRO885 or PRO887. These  
 CC proteins were identified by isolating cDNA clones encoding secreted  
 CC proteins. The proteins of the invention may be used to diagnose and  
 CC treat cardiovascular, endothelial or angiogenic disorders. The present  
 CC sequence is one of the proteins of the invention.  
 XX Sequence 241 AA;

Query Match 100.0%; Score 246; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-24;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DCASGTFSGGHEGCKPWTDCQFGLTVPNGKTNVAVCV 41  
 Db 114 dcasgtfsgghegckpwtcdctqfgltvpngktnvavcv 154

RESULT 10  
 AAB33431  
 ID AAB33431 standard; Protein; 241 AA.  
 XX AC  
 XX AC AAB33431;  
 XX DT 29-JAN-2001 (first entry)  
 XX DE  
 DE Human PRO364 protein UNQ319 SEQ ID NO:92.  
 XX KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
 KW dermatological; antiarthritic; antirheumatic; immunosuppressive;  
 KW haemostatic; antithyroid; antidiabetic; antipsoriatic; antiallergic;  
 KW antianaemic; hepatotropic; virucide; antiparasitic; rheumatoid arthritis;  
 KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
 KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;  
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
 KW autoimmune thrombocytopaenia; immune-mediated renal disease;  
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
 KW inflammatory bowel disease; gluten-sensitive enteropathy;  
 KW autoimmune disease; immune-mediated skin disease; allergic disease;  
 KW immunological disease; transplant-associated disease;  
 KW graft rejection; graft-versus-host-disease.  
 XX OS Homo sapiens.  
 XX PN WO200053757-A2.  
 XX PD 14-SEP-2000.  
 XX PF 02-MAR-2000; 2000WO-US05841.  
 XX PR 08-MAR-1999; 99WO-US05028.  
 PR 10-MAR-1999; 99US-0123618.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 23-MAR-1999; 99US-0125775.  
 PR 12-APR-1999; 99US-0128849.  
 PR 20-APR-1999; 99WO-US08615.  
 PR 28-APR-1999; 99US-0131445.  
 PR 04-MAY-1999; 99US-0132371.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0147058.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.



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PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21347.
PR 05-OCT-1999; 99WO-US23089.
PR 29-OCT-1999; 99US-0162506.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;
PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;
PI Watanabe CK, Williams PM, Wood WI;
XX
XX WPI: 2000-412154/35.
DR N-PSDB; AAA77604.
XX
XX Nucleic acids encoding PRO polypeptides useful for preventing,
PT diagnosing and treating a cardiovascular, endothelial or
PT angiogenic disorders in mammals.
XX
XX Claim 72; Fig 44; 315pp; English.
XX
XX The present invention describes nucleic acids encoding PRO polypeptides
CC useful for preventing, diagnosing and treating a
CC cardiovascular, endothelial or angiogenic disorder in mammals by
CC modulating cell proliferation, angiogenesis and cardiovascularisation,
CC and for identifying agonists and antagonists of these processes. The
CC nucleic acids and the proteins they encode may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PRO expression such as cardiovascular, endothelial or
CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
CC cardiac hypertrophy). For example, the nucleic acids (Ncs) and vectors
CC containing them and the PRO polypeptide may be used to treat disorders
CC associated with decreased PRO expression. AAA77510 to AAA77721 and
CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in
CC the exemplification of the present invention.
XX
XX Sequence 241 AA;
SQ
Query Match 100.0%; Score 246; DB 21; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.7e-24;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DCASGTFSGGHEGCKPWTDCQFGFLTVFPGNKTNAVCV 41
Db 114 dcasgtfsgghegckpwtcdctqfgfltvfpngkthnavcv 154
RESULT 14
AA771467
ID AA771467 standard; Protein; 241 AA.
XX
XX AA771467;
XX
XX 08-NOV-2000 (first entry)
XX
XX Human PRO364 protein.
XX
XX PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;
KW neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;
KW breast; prostate; colon; lung; renal; ovarian; central nervous system;
KW CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue;
KW tumour necrosis factor receptor; GTR protein homologue.
XX
XX Homo sapiens.
XX
XX Query Match 100.0%; Score 246; DB 21; Length 241;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-24;
XX Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Key Location/Qualifiers
XX Peptide 1..25
XX /label= Signal_peptide
XX Modified-site 5..11
XX /note= "N-myristoylation site"
XX Modified-site 8..14
XX /note= "N-myristoylation site"

```

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FT Modified-site 25..31
FT /note= "N-myristoylation site"
FT Protein 26..241
FT /label= Mature_PRO364_protein
FT Modified-site 30..36
FT /note= "N-myristoylation site"
FT Modified-site 33..39
FT /note= "N-myristoylation site"
FT Modified-site 118..124
FT /note= "N-myristoylation site"
FT Modified-site 122..128
FT /note= "N-myristoylation site"
FT Modified-site 146..150
FT /note= "Asn is N-glycosylated"
FT Modified-site 156..162
FT /note= "N-myristoylation site"
FT Domain 163..183
FT /label= Transmembrane_domain
FT Binding-site 166..177
FT /note= "Prokaryotic membrane lipoprotein lipid
FT attachment site"
FT Region 171..193
FT /note= "Leucine zipper pattern"
XX
XX WO2000032778-A2.
XX
XX 08-JUN-2000.
XX
XX 30-NOV-1999; 99WO-US28409.
XX
XX 01-DEC-1998; 98WO-US25108.
XX 16-DEC-1998; 98US-0112850.
XX 22-DEC-1998; 98US-0113296.
XX 20-JUL-1999; 99US-0144758.
XX 26-JUL-1999; 99US-0145698.
XX
XX (GETH ) GENENTECH INC.
XX
XX Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;
XX
XX WPI: 2000-412325/35.
XX N-PSDB; AAD01240.
XX
XX New composition useful for inhibiting neoplastic cell growth and for
XX treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or
XX their antagonists.
XX
XX Claim 31; Fig 4; 108pp; English.
XX
XX The present sequence is the human PRO364 protein, encoded by the cDNA
XX clone, designated as DNA47365-1206. It is isolated from human small
XX intestine tissue cDNA library, identified using probes based on the
XX consensus sequence DNA4825, relative to the Incyte expressed sequence
XX tag (EST) 3003460. This EST has homology to tumour necrosis factor
XX receptor (TNFR) family of polypeptides. PRO364 sequence also shows
XX homology to members of the TNFR family and mouse GTR protein.
XX This clone is assigned the ATCC deposit No: 209436. PRO364 functions as
XX a neoplastic cell growth inhibitor and is used for treating tumours,
XX using an effective amount of PRO655, PRO364 and PRO344. This composition
XX is especially useful for treatment of human cancers such as breast,
XX prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.
XX
XX Sequence 241 AA;
SQ
Query Match 100.0%; Score 246; DB 21; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.7e-24;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DCASGTFSGGHEGCKPWTDCQFGFLTVFPGNKTNAVCV 41
Db 114 dcasgtfsgghegckpwtcdctqfgfltvfpngkthnavcv 154

```

XX The present sequence is that of human tumour necrosis factor  
 CC receptor-like protein TR1SV1, a novel 26 kDa protein which shows  
 CC 58.6% identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The sequence was deduced from  
 CC cDNA (see AA50305) discovered in a PHA-stimulated T-cell library.  
 CC The invention provides TR1L, TR1SV1 and TR1SV2 nucleic acids  
 CC (see AA50304-06) and highly conserved encoded proteins (see  
 CC AA95879-81), as well as vectors, host cells and recombinant methods for  
 CC their production. TR1L, TR1SV1 and/or TR1SV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an  
 CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. TR1L, TR1SV1 and/or TR1SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.  
 XX  
 SQ Sequence 241 AA;

Query Match 100.0%; Score 246; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-24;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCASGTFSGGHEGCHKPWTDCQFGFLTVPFGNKTHNAVCV 41  
 |||||  
 DB 114 dcasgtsfgghegchckpwtcdctqfgltvfpgnkthnavcv 154

## RESULT 12

AA955895  
 ID AA955895 standard; Protein; 241 AA.  
 XX  
 AC AA955895;  
 XX  
 DT 20-NOV-2000 (first entry)  
 XX  
 DE Human tumour necrosis factor receptor-like protein TR11 mutein.  
 XX  
 KW TR1L; human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
 KW dermatological; antiinflammatory; therapy; diagnosis; mutein;  
 KW mutant.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200050459-A1.  
 XX  
 PD 31-AUG-2000.  
 XX  
 PF 23-FEB-2000; 2000WO-US04572.  
 XX  
 PR 24-FEB-1999; 99US-0121648.  
 PR 13-MAY-1999; 99US-0134172.  
 PR 16-JUL-1999; 99US-0144076.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, N1 J;  
 XX  
 DR WPI; 2000-572072/53.  
 XX  
 PT Human tumor necrosis factor receptor-like proteins useful for  
 PT diagnosis, prevention and treatment of disease states associated with  
 PT aberrant cell survival such as autoimmune disease and rheumatoid

PT arthritis  
 XX  
 PS Disclosure; 294-295; 278pp; English.  
 XX  
 CC The present sequence is that of human tumour necrosis factor  
 CC receptor-like protein TR1L (see also AA95879), a novel protein  
 CC showing identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The invention provides  
 CC highly conserved TR1L, TR1SV1 and TR1SV2 proteins (see AA95879-81),  
 CC as well as vectors, host cells and recombinant methods for their  
 CC production. TR1L, TR1SV1 and/or TR1SV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an  
 CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. TR1L, TR1SV1 and/or TR1SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.  
 XX  
 SQ Sequence 241 AA;

Query Match 100.0%; Score 246; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-24;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCASGTFSGGHEGCHKPWTDCQFGFLTVPFGNKTHNAVCV 41  
 |||||  
 DB 114 dcasgtsfgghegchckpwtcdctqfgltvfpgnkthnavcv 154

## RESULT 13

AA955895  
 ID AAB24409 standard; Protein; 241 AA.  
 XX  
 AC AAB24409;  
 XX  
 DT 07-NOV-2000 (first entry)  
 XX  
 DE Human PRO364 protein sequence SEQ ID NO:117.  
 XX  
 KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
 KW cytostatic; gene therapy; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200032221-A2.  
 XX  
 PD 08-JUN-2000.  
 XX  
 PF 30-NOV-1999; 99WO-US28313.  
 XX  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 16-DEC-1998; 98US-0112850.  
 PR 12-JAN-1999; 99US-0115554.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 28-APR-1999; 99US-0131445.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.

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Claim 14; Fig 2; 167pp; English.

This is the amino acid sequence of the human tumour necrosis factor receptor-like protein splice variant 1 (TRLISV1 receptor). The invention relates to Tril and two splice variants TRLISV1 and TRLISV2. The nucleotide sequences were determined by sequencing cloned cDNAs AZ37765-237766. The Tril receptor and its splice variants show homology to the murine glucocorticoid induced tumour necrosis factor receptor family related gene (GTR). Tril1, TRLISV1 and TRLISV2 polypeptides may be involved in the regulation of cell-type specific receptor-mediated cell growth, differentiation, and ultimately, cell death. They can be used for screening for agonists/antagonists. The polypeptides, agonists or antagonists can be used for treating a disease state associated with aberrant cell survival. They can be used for treating immune deficiency disorders, pigeon syndrome, HIV infection, severe combined immunodeficiency (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood platelet disorders or wounds resulting from trauma or surgery. They can also be used to treat heart attacks, strokes, Addison's disease, haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome, systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis, hypersensitivity to an antigenic molecule, organ rejection or graft versus host disease, inflammatory conditions, ischaemia reperfusion injury, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, hyperproliferative disorders, or infections.

PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 XX other T cell disorders  
 PS Disclosure; Pages 61-62; 71pp; English.  
 XX This is the amino acid sequence of the truncated human 312C2 T cell  
 CC protein from clone A8. The 312C2 proteins are expressed in thymus  
 CC cells and are induced on T cells and spleen cells following activation.  
 CC Engagement of 312C2 stimulates proliferation of T cell clones,  
 CC antigen-specific proliferation and cytokine production by T-cells, and  
 CC potentiates T cell expansion or apoptosis. The products can be used  
 CC in the treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX  
 SQ Sequence 228 AA;

Query Match 100.0%; Score 252; DB 19; Length 228;  
 Best Local Similarity 100.0%; Pred. NO. 4e-20;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGPCTTCRHHCPCPGQGVQSQGKFSFGQCI 40  
 |||||||  
 Db 68 cvqpefhcgdpctctrhpcpggvggkfsfgfqi 107

RESULT 2  
 AAY95879  
 ID AAY95879 standard; Protein; 234 AA.  
 XX  
 AC AAY95879;  
 XX  
 DT 20-NOV-2000 (first entry)  
 XX  
 DE Human tumour necrosis factor receptor-like protein Trl1.  
 XX  
 KW Trl1; human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
 KW dermatological; antiinflammatory; therapy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT /label= Signal\_peptide  
 FT Protein 26..234  
 FT /label= Mature\_protein  
 FT Domain 26..162  
 FT /label= Extracellular\_domain  
 FT Domain 163..179  
 FT /label= Transmembrane\_domain  
 FT Domain 180..234  
 FT /label= Intracellular\_domain  
 FT Modified-site 146  
 FT /note= "N-glycosylated"  
 FT Domain 72..81  
 FT /note= "conserved domain CD-II"  
 FT Domain 84..93  
 FT /note= "conserved domain CD-III"  
 FT Domain 107..113  
 FT /note= "conserved domain CD-IV"  
 FT Domain 128..134  
 FT /note= "conserved domain CD-V"  
 FT Domain 153..160  
 FT /note= "conserved domain CD-VI"  
 FT Domain 176..186  
 FT /note= "conserved domain CD-VII"  
 FT Domain 204..209  
 FT /note= "conserved domain CD-IX"

FT Domain 224..233  
 FT /note= "conserved domain CD-X"  
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 FT Region 43..51  
 FT /note= "epitope-bearing region"  
 FT Region 59..67  
 FT /note= "epitope-bearing region"  
 FT Region 56..64  
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 FT Region 66..71  
 FT /note= "epitope-bearing region"  
 FT Region 99..107  
 FT /note= "epitope-bearing region"  
 FT Region 125..133  
 FT /note= "epitope-bearing region"  
 FT Region 143..151  
 FT /note= "epitope-bearing region"  
 FT Region 156..164  
 FT /note= "epitope-bearing region"  
 FT Region 203..211  
 FT /note= "epitope-bearing region"  
 FT Region 222..230  
 FT /note= "epitope-bearing region"  
 XX WO200050459-A1.  
 PN  
 XX 31-AUG-2000.  
 PD  
 XX 23-FEB-2000; 2000WO-US04572.  
 PF  
 XX 24-FEB-1999; 99US-0121648.  
 PR 13-MAY-1999; 99US-0134172.  
 PR 16-JUL-1999; 99US-0144076.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, NI J;  
 XX  
 XX WPI; 2000-572072/53.  
 DR N-PSDB; AAA50304.  
 DR  
 XX Human tumor necrosis factor receptor-like proteins useful for  
 PT diagnosis, prevention and treatment of disease states associated with  
 PT aberrant cell survival such as autoimmune disease and rheumatoid  
 PT arthritis -  
 PT  
 PS Claim 14(c); Fig 1A-B; 278pp; English.  
 XX  
 XX The present sequence is that of human tumour necrosis factor  
 CC receptor-like protein Trl1, a novel 25 kDa protein which shows  
 CC 58.6% identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The sequence was deduced from  
 CC a cDNA clone (see AAA50304) discovered in a T-helper cell library.  
 CC Trl1 activated NF-kappaB through a TRAF2-mediated mechanism.  
 CC Expression is activation-inducible. The Trl1 ligand is constitutively  
 CC expressed in an endothelial cell line. This suggests that Trl1 and  
 CC its ligand may be involved in activated T-cell trafficking.  
 CC The invention provides Trl1, Trl1SV1 and Trl1SV2 nucleic acids  
 CC (see AAA50304-06) and highly conserved encoded proteins (see  
 CC AAY95879-81), as well as vectors, host cells and recombinant methods for  
 CC their production. Trl1, Trl1SV1 and/or Trl1SV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an  
 CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency,  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. Trl1, Trl1SV1 and/or Trl1SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the

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OM protein - protein search, using sw model

Run on: - September 4, 2001, 15:56:24 ; Search time 126.12 Seconds  
(without alignments)  
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Total number of hits satisfying chosen parameters: 412676

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	252	100.0	228	19 AAW37840	Truncated human 31
2	252	100.0	234	21 AAY95879	Human tumour necro
3	252	100.0	234	21 AAY52158	Tumour necrosis fa
4	252	100.0	235	21 AAY44825	Human molecule ass
5	252	100.0	240	21 AAY95881	Human tumour necro
6	252	100.0	240	21 AAY52160	TRILSV2 amino acid
7	252	100.0	241	19 AAW37839	Amino acid sequenc
8	252	100.0	241	20 AAY06605	Human TNF receptor
9	252	100.0	241	21 AAB27651	Human protein PRO3
10	252	100.0	241	21 AAB32431	Human PRO364 prote
11	252	100.0	241	21 AAY95880	Human tumour necro

12	252	100.0	241	21 AAY95895	Human tumour necro
13	252	100.0	241	21 AAB24409	Human PRO364 prote
14	252	100.0	241	21 AAY71467	Human PRO364 prote
15	252	100.0	241	21 AAY52159	TRILSV1 amino acid
16	252	100.0	241	21 AAB20115	Human immunostimul
17	252	100.0	241	22 AAB47054	Human PRO364. Hom
18	252	100.0	241	22 AAB50910	Human PRO364 prote
19	252	100.0	241	22 AAB50982	Human PRO364 prote
20	252	100.0	241	22 AAB53090	Human angiogenesis
21	252	100.0	311	19 AAW37842	Human 312C2 protei
22	252	100.0	316	22 AAB47055	Polyptide encode
23	252	100.0	317	20 AAY06645	PRO364-related EST
24	207.5	82.3	232	19 AAW37841	Human 312C2 protei
25	168	66.7	222	19 AAW49018	Mouse glucocortico
26	168	66.7	228	19 AAW49016	Mouse glucocortico
27	168	66.7	228	19 AAW37838	Amino acid sequenc
28	168	66.7	224	19 AAW49017	Mouse glucocortico
29	125	49.6	89	21 AAY76013	Murine TNF-alpha f
30	125	49.6	89	22 AAB55952	Skin cell protein, 41bb
31	67	26.6	191	22 AAB66986	protein. Uni
32	67	26.6	256	16 AAR70978	4-1BB receptor pro
33	67	26.6	256	16 AAR64199	Murine 4-1BB polyp
34	67	26.6	256	17 AAW04173	Mouse receptor 4-1
35	67	26.6	256	18 AAW26659	Mouse 4-1BB recept
36	67	26.6	256	20 AAY33215	Murine CD137 prote
37	67	26.6	256	20 AAY28687	Mouse Receptor 4-1
38	64.5	25.6	255	21 AAY58213	Canine mature CD40
39	64.5	25.6	274	21 AAY58212	Canine CD40. Cani
40	64	25.4	478	22 AAB48033	EGF receptor relat
41	63	25.0	185	19 AAW60046	Human TNF receptor
42	63	25.0	185	21 AAY94716	Human TR2-receptor
43	63	25.0	186	21 AAY94716	Soluble herpesviru
44	63	25.0	193	21 AAY79204	Soluble herpesviru
45	63	25.0	197	21 AAY79205	Soluble herpesviru

#### ALIGNMENTS

RESULT 1

AAW37840

ID AAW37840 standard; Protein; 228 AA.

XX

AC AAW37840;

XX

DT 28-JUL-1998 (first entry)

XX

DE Truncated human 312C2 protein from clone\_A8 amino acid sequence.

XX

KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;

KW antigen-specific T cell proliferation; cytokine production by T-cell;

KW apoptosis; cancer; haematopoietic cells; lymphoid cell;

KW autoimmune disorders.

XX

OS Homo sapiens.

XX

PN WO9806842-A1.

XX

PD 19-FEB-1998.

XX

PF 14-AUG-1997; 97WO-US13931.

XX

PR 07-OCT-1996; 96US-0027901.

PR 16-AUG-1996; 96US-0689943.

XX

PA (SCHE ) SCHERING CORP.

XX

PI Gorman DM, Randall TD, Zlotnik A;

XX

WPI; 1998-159534/14.

DR N-PSDB; AAV19154.

XX

PT Isolated 312C2 T cell gene - used to develop products for treating,

FT Modified-site /note= "Potential phosphorylation site"  
 FT 48  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 62  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 82  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 205  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 223  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 140  
 FT Modified-site /note= "N-glycosylated"  
 FT 20200005374-A2.  
 PN XX  
 PD 03-FEB-2000.  
 XX XX  
 PF 21-JUL-1999; 99WO-US16637.  
 XX XX  
 PR 22-JUL-1998; 98US-0093827.  
 XX XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX XX  
 PI Tang YT, Lal P, Hillman JL, Corley NC, Patterson C, Baughn MR;  
 XX XX  
 DR WPI; 2000-182699/16.  
 XX XX  
 DR N-PSDB; AA249948.  
 XX XX  
 XX Polypeptides and polynucleotides useful for treating and detecting cell  
 PT proliferation disorders e.g. actinic keratosis, and immune disorders  
 PT e.g. Crohn's disease -  
 XX XX  
 PS Claim 1; Pages 64-65; 67pp; English.  
 XX XX  
 CC The present sequence is a molecule associated with cell  
 CC proliferation, MACP-5 from incyte clone 2809903 isolated from TLYMN0706  
 CC cDNA library. This sequence is expressed in cardiovascular and  
 CC haematopoietic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV,  
 CC hepatotrophic, antiinflammatory, antipsoriatic, cytostatic, antilashmatic,  
 CC dermatological, antidiabetic, nephrotropic, antithyroid, thyromimetic,  
 CC immunosuppressive, osteopathic, antiarthritic, uropathic, antiulcer,  
 CC and ophthalmological activities. The present sequence is useful in the  
 CC diagnosis, treatment and prevention of cell proliferative disorders e.g.  
 CC actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and  
 CC hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and  
 CC anaemia.  
 XX XX  
 SQ Sequence 235 AA;  
 Query Match 100.0%; Score 252; DB 21; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-20;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CVQPEHCGPCCTCTRHPPGQGVQSGKFSFGQCI 40  
 |||||  
 Db 68 cvqpehcgpcctctrhppgqgvsgqkfsfgqci 107  
 RESULT 5  
 ID AAY95881  
 XX AAY95881 standard; Protein; 240 AA.  
 AC AAY95881;  
 XX XX  
 XX 20-NOV-2000 (first entry)  
 DT XX  
 XX Human tumour necrosis factor receptor-like protein TR11SV2.  
 DE XX  
 XX TR11SV2: human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
 DR

KW dermatological; antiinflammatory; therapy; diagnosis.  
 XX Homo sapiens.  
 OS Key Location/Qualifiers  
 XX Peptide 1..19  
 FT /label= Signal\_peptide  
 FT 20..240  
 FT /label= Mature\_protein  
 FT 20..168  
 FT Domain /label= Extracellular\_domain  
 FT 169..185  
 FT /label= Transmembrane\_domain  
 FT 186..240  
 FT /label= Intracellular\_domain  
 FT 152  
 FT /note= "N-glycosylated"  
 FT 57..68  
 FT /note= "conserved domain CD-I"  
 FT 78..87  
 FT /note= "conserved domain CD-II"  
 FT 91..100  
 FT /note= "conserved domain CD-III"  
 FT 114..121  
 FT /note= "conserved domain CD-IV"  
 FT 134..140  
 FT /note= "conserved domain CD-V"  
 FT 159..166  
 FT /note= "conserved domain CD-VI"  
 FT 182..192  
 FT /note= "conserved domain CD-VII"  
 FT 210..215  
 FT /note= "conserved domain CD-IX"  
 FT 230..239  
 FT /note= "conserved domain CD-X"  
 FT 20..28  
 FT /note= "epitope-bearing region"  
 FT 24..32  
 FT /note= "epitope-bearing region"  
 FT 37..45  
 FT /note= "epitope-bearing region"  
 FT 48..56  
 FT /note= "epitope-bearing region"  
 FT 67..75  
 FT /note= "epitope-bearing region"  
 FT 106..114  
 FT /note= "epitope-bearing region"  
 FT 130..139  
 FT /note= "epitope-bearing region"  
 FT 149..157  
 FT /note= "epitope-bearing region"  
 FT 162..170  
 FT /note= "epitope-bearing region"  
 FT 209..217  
 FT /note= "epitope-bearing region"  
 FT 228..236  
 FT /note= "epitope-bearing region"  
 XX WO200050459-A1.  
 PN 31-AUG-2000.  
 XX 23-FEB-2000; 2000WO-US04572.  
 XX 24-FEB-1999; 99US-0121648.  
 PR 13-MAY-1999; 99US-0134172.  
 PR 16-JUL-1999; 99US-0144076.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA Ruben SM, Ni J;  
 XX WPI; 2000-572072/53.  
 DR

CC polypeptides may also be used. Methods for screening for  
 XX agonist/antagonist compounds are also provided.

SQ Sequence 234 AA;

Query Match 100.0%; Score 252; DB 21; Length 234;

Best Local Similarity 100.0%; Pred. No. 4.1e-20;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCTTCRHHPCCPGQGVQSGKFSFGFCI 40

Db 74 cvqpefhcgdpctctcrhhpcppgqgvsgkfsfgfc1 113

RESULT 3

AAV52158

ID AAV52158 standard; Protein; 234 AA.

XX AC AAV52158;

XX DT 01-FEB-2000 (first entry)

XX DE Tumour necrosis factor receptor-like protein (TR11) amino acid sequence.

XX KW Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2;

XX KW G1TR; growth; differentiation; cell death; Immune deficiency disorder;

XX KW Digeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia;

XX KW Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes;

XX KW Alzheimer's disease; Parkinson's disease; Huntington's disease;

XX KW inflammatory condition.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..25

XX FT Protein /label= Signal\_peptide

XX FT FT 26..234

XX FT FT /label= TR11

XX FT Domain 26..162

XX FT /note= "Extracellular domain"

XX FT Domain 163..179

XX FT /note= "Transmembrane domain"

XX FT Domain 180..234

XX FT /note= "Intracellular domain"

XX PN W09202758-A1.

XX PD 29-APR-1999.

XX PF 21-OCT-1998; 98WO-US22085.

XX PR 21-OCT-1997; 97US-0063212.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ni J, Ruben SM;

XX DR WPI; 2000-061922/05.

XX DR N-PSDB; AAZ37762.

XX FT New tumour necrosis factor receptor-like polypeptides used to, e.g.

XX FT treat Digeorge syndrome -

XX PS Claim 14; Fig 1; 167pp; English.

XX CC This is the amino acid sequence of the human tumour necrosis factor

XX CC receptor-like protein (TR11 receptor). The invention relates to TR11 and

XX CC two splice variants TR11SV1 and TR11SV2. The nucleotide sequences were

XX CC determined by sequencing cloned cDNAs AAZ37765-z37766. The TR11 receptor

XX CC and its splice variants show homology to the murine glucocorticoid

XX CC induced tumour necrosis factor receptor family-related gene (G1TR).

XX CC TR11, TR11SV1 and TR11SV2 polypeptides may be involved in the regulation

CC of cell-type specific receptor-mediated cell growth, differentiation,  
 CC and ultimately, cell death. They can be used for screening for  
 CC agonists/antagonists. The polypeptides, agonists or antagonists can be  
 CC used for treating a disease state associated with aberrant cell  
 CC survival. They can be used for treating immune deficiency disorders,  
 CC Digeorge syndrome, HIV infection, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood  
 CC platelet disorders or wounds resulting from trauma or surgery. They can  
 CC also be used to treat heart attacks, strokes, Addison's disease,  
 CC hemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's  
 CC disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome,  
 CC systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent  
 CC diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,  
 CC hypersensitivity to an antigenic molecule, organ rejection or graft  
 CC versus host disease, inflammatory conditions, ischaemia-reperfusion  
 CC injury, complement-mediated hyperacute rejection, nephritis, cytokine or  
 CC chemokine induced lung injury, inflammatory bowel disease, Crohn's  
 CC disease, hyperproliferative disorders, or infections. They can also be  
 CC used to repair, replace, or protect tissue damaged by congenital  
 CC defects, trauma, age, disease, surgery, including cosmetic plastic  
 CC surgery, fibrosis, reperfusion injury, peripheral nerve injuries,  
 CC neuropathies, and central nervous system disease (e.g. Alzheimer's  
 CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral  
 CC sclerosis, and Shy-Drager syndrome). The products can also be used for  
 CC detection, diagnosis and prognosis.

XX SQ Sequence 234 AA;

Query Match 100.0%; Score 252; DB 21; Length 234;

Best Local Similarity 100.0%; Pred. No. 4.1e-20;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCTTCRHHPCCPGQGVQSGKFSFGFCI 40

Db 74 cvqpefhcgdpctctcrhhpcppgqgvsgkfsfgfc1 113

RESULT 4

AAV44825

ID AAV44825 standard; Protein; 235 AA.

XX AC AAV44825;

XX DT 18-MAY-2000 (first entry)

XX DE Human molecule associated with cell proliferation, MACP-5.

XX KW Human; molecule associated with cell proliferation; MACP-5;

XX KW Incyte clone 2809903; antiarteriosclerotic; hepatotropic; cytostatic;

XX KW anti-inflammatory; antipapillary; anti-HIV; antithymic; anaemia;

XX KW dermatological; antidiabetic; nephrotropic; antithyroid; thyromimetic;

XX KW immunosuppressive; osteopathic; antiarthritic; uropathic; antitumor;

XX KW ophthalmological; diagnosis; treatment; prevention; immune disorder;

XX KW cell proliferative disorder; actinic keratosis; arteriosclerosis;

XX KW atherosclerosis; bursitis; hepatitis; Crohn's disease; amyloidosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Region 1..19

XX FT /label= Signature\_sequence

XX FT Region 68..96

XX FT /label= Signature\_sequence

XX FT Region 109..147

XX FT /label= Signature\_sequence

XX FT Region 122..129

XX FT /label= Signature\_sequence

XX FT Region 157..175

XX FT /label= Signature\_sequence

XX FT Region 165..186

XX FT /label= Signature\_sequence

XX FT Modified-site 37



DT 28-JUL-1998 (first entry)  
 DE Amino acid sequence of the human 312C2 T cell protein.  
 KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 KW antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
 KW autoimmune disorders.  
 OS Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..726  
 FT /tag= a  
 FT /product= "human 312C2 protein"  
 PN WO9806842-A1.  
 XX  
 XX  
 PD 19-FEB-1998.  
 XX  
 XX  
 PF 14-AUG-1997; 97WO-US13931.  
 PR 07-OCT-1996; 96US-0027901.  
 PR 16-AUG-1996; 96US-0689943.  
 XX  
 XX (SCHE ) SCHERING CORP.  
 XX Gorman DM, Randall TD, Zlotnik A;  
 XX WPI; 1998-159534/14.  
 DR N-PSDB; AAV19153.  
 XX  
 XX Isolated 312C2 T cell gene - used to develop products for treating,  
 PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 PT other T cell disorders  
 XX  
 PS Claim 2; Pages 59-60; 71pp; English.  
 CC This is the amino acid sequence encoding the human 312C2 T cell  
 CC protein. The 312C2 proteins are expressed in thymus cells and are  
 CC induced on T cells and spleen cells following activation. Engagement  
 CC of 312C2 stimulates proliferation of T cell clones, antigen-specific  
 CC proliferation and cytokine production by T-cells, and potentiates T  
 CC cell expansion or apoptosis. The products can be used in the  
 CC treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX  
 SQ Sequence 241 AA;  
 Query Match 100.0%; Score 252; DB 19; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-20;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CVQPEFHGDCPCTTCRHHPCPPGGVQSGKFSFGFCI 40  
 Db |||||||||||||||||||||||||||||||||||||||  
 74 cvqpefhgdcpccttcrrhhpcppggvgqsgkfsfgfcil 113  
 RESULT 8  
 ID AAY06605 standard; Protein; 241 AA.  
 XX  
 AC AAY06605;  
 XX  
 XX 26-OCT-1999 (first entry)  
 DT Human TNF receptor homologue PRO364.  
 DE  
 XX PRO364; tumour necrosis factor receptor; human; apoptosis;

KW inflammation; antiinflammatory; NF-KB activation;  
 KW autoimmune disease; therapy.  
 OS Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..25 /note= "signal peptide"  
 FT Protein 26..241 /note= "mature protein"  
 FT Modified-site 146 /note= "N-glycosylated"  
 FT Domain 162..180 /note= "transmembrane domain"  
 FT  
 FT  
 XX WO9940196-A1.  
 XX  
 XX 12-AUG-1999.  
 XX  
 PF 09-FEB-1999; 99WO-US02642.  
 PR 09-FEB-1998; 98US-0024087.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;  
 PI Pitti RM, Wood WI;  
 XX WPI; 1999-494296/41.  
 DR N-PSDB; AAX87670.  
 XX  
 XX Tumour necrosis factor receptor homologue - useful for, e.g.  
 PT modulating apoptosis and NF-KB activation and proinflammatory or  
 PT autoimmune responses  
 XX  
 PS Claim 17; Fig 2A; 104pp; English.  
 CC The present sequence represents human PRO364, a novel member of the  
 CC tumour necrosis factor receptor family. The sequence was deduced  
 CC from a bone marrow cDNA clone (see AAX87670). Methods for the  
 CC recombinant production of PRO364 polypeptides, e.g. in CHO,  
 CC Escherichia coli or yeast host cells, are provided. Claimed  
 CC polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the  
 CC mature protein) and 26-X of the present sequence, where X is any  
 CC one of amino acid residues 157-167 of PRO364. PRO364 polypeptides  
 CC are useful for modulating apoptosis, NF-KB activation and  
 CC proinflammatory or autoimmune responses in mammalian cells  
 CC (claimed). Chimeric molecules comprising a PRO364 polypeptide  
 CC fused to a heterologous sequence such as epitope tag or  
 CC immunoglobulin Fc region are also claimed. PRO364 can be used in  
 CC assays to identify other proteins or molecules involved in binding  
 CC interactions. This is useful for identifying inhibitors or  
 CC agonists of receptor/ligand binding. The PRO364 polypeptides may  
 CC also be combined with an agent that is cytotoxic, chemotherapeutic  
 CC or a growth inhibitor. PRO364 antibodies are useful in diagnostic  
 CC methods, purification methods and also in therapy, e.g. as  
 CC inhibitors.  
 XX  
 SQ Sequence 241 AA;  
 Query Match 100.0%; Score 252; DB 20; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-20;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CVQPEFHGDCPCTTCRHHPCPPGGVQSGKFSFGFCI 40  
 Db |||||||||||||||||||||||||||||||||||||||  
 74 cvqpefhgdcpccttcrrhhpcppggvgqsgkfsfgfcil 113  
 RESULT 9  
 ID AAB27651 standard; Protein; 241 AA.

DR N-PSDB; AAA50306.

XX Human tumor necrosis factor receptor-like proteins useful for

PT diagnosis, prevention and treatment of disease states associated with

PT aberrant cell survival such as autoimmune disease and rheumatoid

PT arthritis

XX

XX Claim 14(n); Fig 3A-B; 278pp; English.

PS

PS The present sequence is that of human tumour necrosis factor

CC receptor-like protein TR11SV2, a novel 26 kDa protein which shows

CC 58.6% identity to murine glucocorticoid induced tumour necrosis

CC factor receptor family-related gene. The sequence was deduced from

CC a cDNA clone (see AAA50306) discovered in an activated T-cell library.

CC The invention provides TR11, TR11SV1 and TR11SV2 nucleic acids

CC (see AAA50304-06) and highly conserved encoded proteins (see

CC AA95879-81), as well as vectors, host cells and recombinant methods for

CC their production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful

CC for treating, preventing, prognosis and/or diagnosis of an

CC immunodeficiency, especially common variable immunodeficiency,

CC X-linked agammaglobulinemia, severe combined immunodeficiency

CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin

CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2

CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis

CC and/or diagnose an autoimmune disease, especially rheumatoid

CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura

CC or IgA nephropathy. The polypeptides, polynucleotides and/or

CC antibodies can be administered to cells in vitro, ex vivo or in

CC vivo or to a multicellular organism. Soluble forms of the

CC polypeptides may also be used. Methods for screening for the

CC agonist/antagonist compounds are also provided.

XX

SQ Sequence 240 AA;

Query Match 100.0%; Score 252; DB 21; Length 240;

Best Local Similarity 100.0%; Pred. No. 4.2e-20;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCCTCRHHPCPPGQGVQSGKFSFGFCI 40

DB 80 cvqpfhcgdpccctcrhhpcppgqgvsgkfsfgfqi 119

RESULT 6

AAV52160

ID AAV52160 standard; Protein; 240 AA.

XX

XX AAV52160;

XX

DT 01-FEB-2000 (first entry)

XX

DE TR11SV2 amino acid sequence.

XX

KW Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2;

KW G1R; growth; differentiation; cell death; immune deficiency disorder;

KW Disgeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia;

KW Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes;

KW Alzheimer's disease; Parkinson's disease; Huntington's disease;

KW inflammatory condition.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..19

FT /label= Signal\_peptide

FT Protein 20..240

FT /label= TR11SV2

FT Domain 20..168

FT /note= "Extracellular domain"

FT Domain 169..185

FT /note= "Transmembrane domain"

FT Domain 186..240

FT

XX

PN WO9920758-A1.

PD 29-APR-1999.

XX

PF 21-OCT-1998; 98WO-US22085.

XX

PR 21-OCT-1997; 97US-0063212.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Ni J, Ruben SM;

XX

XX WPI; 2000-061922/05.

DR N-PSDB; AAZ37764.

XX

XX New tumour necrosis factor receptor-like polypeptides used to, e.g.

PT treat Disgeorge syndrome

XX

PS Claim 14; Fig 3; 167pp; English.

XX

CC This is the amino acid sequence of the human tumour necrosis factor

CC receptor-like protein splice variant 2 (TR11SV2 receptor). The invention

CC relates to TR11 and two splice variants TR11SV1 and TR11SV2. The

CC nucleotide sequences were determined by sequencing cloned cDNAs

CC AAZ37765-237766. The TR11 receptor and its splice variants show homology

CC to the murine glucocorticoid induced tumour necrosis factor receptor

CC family related gene (G1R). TR11, TR11SV1 and TR11SV2 polypeptides may

CC be involved in the regulation of cell-type specific receptor-mediated

CC cell growth, differentiation, and ultimately, cell death. They can be

CC used for screening for agonists/antagonists. The polypeptides, agonists

CC or antagonists can be used for treating a disease state associated with

CC aberrant cell survival. They can be used for treating immune deficiency

CC disorders, Disgeorge syndrome, HIV infection, severe combined

CC immunodeficiency (SCID), Wiskott-Aldrich disorder, blood coagulation

CC disorders, blood platelet disorders or wounds resulting from trauma or

CC surgery. They can also be used to treat heart attacks, strokes,

CC Addison's disease, haemolytic anaemia, rheumatoid arthritis, Goodpastures

CC syndrome, Grave's disease, multiple sclerosis, myasthenia gravis,

CC Stiff-Man syndrome, systemic lupus erythematosus, Guillain-Barre

CC syndrome, insulin dependent diabetes mellitus or autoimmune inflammatory

CC eye disease, anaphylaxis, hypersensitivity to an antigenic molecule,

CC organ rejection or graft versus host disease, inflammatory conditions,

CC ischaemia-reperfusion injury, complement-mediated hyperacute rejection,

CC nephritis, cytokine or chemokine induced lung injury, inflammatory bowel

CC disease, Crohn's disease, hyperproliferative disorders, or infections.

CC They can also be used to repair, replace, or protect tissue damaged by

CC congenital defects, trauma, age, disease, surgery, including cosmetic

CC plastic surgery, fibrosis, reperfusion injury, peripheral nerve

CC injuries, neuropathies, and central nervous system disease (e.g.

CC Alzheimer's disease, Parkinson's disease, Huntington's disease,

CC amyotrophic lateral sclerosis, and Shy-Drager syndrome). The products can

CC also be used for detection, diagnosis and prognosis.

XX

SQ Sequence 240 AA;

Query Match 100.0%; Score 252; DB 21; Length 240;

Best Local Similarity 100.0%; Pred. No. 4.2e-20;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCCTCRHHPCPPGQGVQSGKFSFGFCI 40

DB 80 cvqpfhcgdpccctcrhhpcppgqgvsgkfsfgfqi 119

RESULT 7

AAW37839

ID AAW37839 standard; Protein; 241 AA.

XX

XX AAW37839;

XX

XX (GETH ) GENENTECH INC.

XX PA

XX PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;

XX PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;

XX PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

XX WPI: 2000-572271/53.

DR N-PSDB; AAC58596.

XX

XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of

PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid

PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -

XX Claim 33; Fig 36; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can

CC be used in the treatment of immune related diseases. The human PRO

CC proteins, anti-PRO antibodies, agonists and antagonists are useful for

CC treating and diagnosing immune related disorders. The disorders are

CC selected from systemic lupus erythematosus, rheumatoid arthritis,

CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,

CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's

CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic

CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,

CC immune-mediated renal disease, demyelinating diseases of the central

CC and peripheral nervous systems, hepatobiliary diseases, inflammatory

CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,

CC auto-immune or immune-mediated skin diseases, allergic diseases,

CC immunological diseases of the lung, and transplantation associated

CC diseases including graft rejection and graft-versus-host-disease.

CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used

CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and

CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein

CC sequences given in the exemplification of the present invention.

XX

SQ Sequence 241 AA;

Query Match 100.0%; Score 252; DB 21; Length 241;

Best Local Similarity 100.0%; Pred. No. 4.2e-20;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCCTCRHHPGPPGQGVQSGQKFSFGQCI 40

Db 74 cvqpefhcgdpccctcrhpcppgpgvgqgkfsfgqci 113

RESULT 11

AAAY95880

XX ID AAY95880 standard; Protein: 241 AA.

XX AC AAY95880;

XX DT 20-NOV-2000 (first entry)

XX DE Human tumour necrosis factor receptor-like protein TR11SV1.

XX KW TR11SV1; human; tumour necrosis factor receptor-like protein;

XX KW immunodeficiency; autoimmune disease; rheumatoid arthritis;

XX KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;

XX KW dermatological; antiinflammatory; therapy; diagnosis.

XX OS Homo sapiens.

XX

XX Key Location/Qualifiers

XX Domain 1...162

XX Domain /label= Extracellular\_domain

XX Domain 163...179

XX Domain /label= Transmembrane\_domain

XX Domain 180...241

XX Domain /label= Intracellular\_domain

XX Modified-site 146

FT Domain

FT /note= "N-glycosylated"

FT 51..61

FT /note= "conserved domain CD-I"

FT 72..81

FT /note= "conserved domain CD-II"

FT 85..94

FT /note= "conserved domain CD-III"

FT 108..115

FT /note= "conserved domain CD-IV"

FT 128..134

FT /note= "conserved domain CD-V"

FT 153..160

FT /note= "conserved domain CD-VI"

FT 176..186

FT /note= "conserved domain CD-VII"

FT 195..201

FT /note= "conserved domain CD-VIII"

FT 211..216

FT /note= "conserved domain CD-IX"

FT 231..240

FT /note= "conserved domain CD-X"

FT 2..10

FT /note= "epitope-bearing region"

FT 11..19

FT /note= "epitope-bearing region"

FT 27..35

FT /note= "epitope-bearing region"

FT 38..46

FT /note= "epitope-bearing region"

FT 42..50

FT /note= "epitope-bearing region"

FT 31..46

FT /note= "epitope-bearing region"

FT 61..69

FT /note= "epitope-bearing region"

FT 99..107

FT /note= "epitope-bearing region"

FT 125..133

FT /note= "epitope-bearing region"

FT 143..151

FT /note= "epitope-bearing region"

FT 156..164

FT /note= "epitope-bearing region"

FT 196..204

FT /note= "epitope-bearing region"

FT 209..217

FT /note= "epitope-bearing region"

FT 229..237

FT /note= "epitope-bearing region"

XX WO200050459-A1.

XX 31-AUG-2000.

XX 23-FEB-2000; 2000WO-US04572.

XX 24-FEB-1999; 99US-0121648.

XX 13-MAY-1999; 99US-0134172.

XX 16-JUL-1999; 99US-0144076.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, NI J;

XX WPI: 2000-572072/53.

DR N-PSDB; AAA50305.

XX Human tumor necrosis factor receptor-like proteins useful for

PT diagnosis, prevention and treatment of disease states associated with

PT aberrant cell survival such as autoimmune disease and rheumatoid

PT arthritis -

XX Claim 14(1); Fig 2A-B; 278pp; English.

```

XX AAB27651;
AC 26-JAN-2001 (first entry)
DT Human protein PRO364.
DE
DE
XX Cardiovascular; endothelial; angiogenic disorder; PRO179;
KW PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333;
KW PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;
KW gene therapy.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Peptide 1..25
FT /label= "Signal peptide"
XX WO200053757-A2.
XX 14-SEP-2000.
XX 24-FEB-2000; 2000WO-US05004.
XX 08-MAR-1999; 99WO-US05028.
XX 12-MAR-1999; 99US-0123957.
XX 02-JUN-1999; 99WO-US12252.
XX 20-JUL-1999; 99US-0144758.
XX 26-JUL-1999; 99US-0145698.
XX 01-SEP-1999; 99WO-US20111.
XX 15-SEP-1999; 99WO-US21090.
XX 30-NOV-1999; 99WO-US28313.
XX 30-NOV-1999; 99WO-US28409.
XX 02-DEC-1999; 99WO-US28565.
XX 18-FEB-2000; 2000WO-US04342.
XX 22-FEB-2000; 2000WO-US04414.
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;
PI Goddard A, Gurney AL, Hillan KJ, Marsters SA, Paoni NF, Pitti RM;
PI Watanabe CK, Williams PM, Wood WI;
XX
XX WPI: 2000-611444/58.
XX N-PSDB; AAA99903.
XX
XX Novel PRO polypeptides and agonists and antagonists of them, used to
PT diagnose and treat cardiovascular, endothelial and angiogenic disorders
PT
XX
XX Claim 71; Fig 6; 181pp; English.
XX
XX The present invention relates to methods for stimulating or inhibiting
CC angiogenesis and cardiovascularization. The methods involve the use of
CC pharmaceutical compositions based on the following proteins, PRO179,
CC PRO238, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333,
CC PRO840, PRO877, PRO878, PRO879, PRO882, PRO885 or PRO887. These
CC proteins were identified by isolating cDNA clones encoding secreted
CC proteins. The proteins of the invention may be used to diagnose and
CC treat cardiovascular, endothelial or angiogenic disorders. The present
CC sequence is one of the proteins of the invention.
XX
SQ Sequence 241 AA;

```

```

Query Match 100.0%; Score 252; DB 21; Length 241;
Best Local Similarity 100.0%; Pred. No. 4, 2e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CVQPEFHCGDPCCTTCRRHPCPPGGVQSGKFSFGQCI 40
Db 74 cvqpefhcgdpctcttrhpcppggvqsgkfsfgfqi 113

```

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RESULT 10
AAB33431
ID AAB33431 standard; Protein; 241 AA.
XX
XX AC AAB33431;
XX
XX 29-JAN-2001 (first entry)
DE Human PRO364 protein UNQ319 SEQ ID NO:92.
XX
XX Human; immune related disease; diagnosis; inflammatory; cardiant;
KW dermatological; antiarthritic; antifneumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.
XX
XX Homo sapiens.
XX
XX WO200053758-A2.
XX 14-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US05841.
XX 08-MAR-1999; 99WO-US05028.
XX 10-MAR-1999; 99US-0123618.
XX 12-MAR-1999; 99US-0123957.
XX 23-MAR-1999; 99US-0125775.
XX 12-APR-1999; 99US-0128849.
XX 20-APR-1999; 99WO-US08615.
XX 28-APR-1999; 99US-0131445.
XX 04-MAY-1999; 99US-0132371.
XX 14-MAY-1999; 99US-0134287.
XX 02-JUN-1999; 99WO-US12252.
XX 23-JUN-1999; 99US-0141037.
XX 20-JUL-1999; 99US-0144758.
XX 28-JUL-1999; 99US-0145698.
XX 28-JUL-1999; 99US-0146222.
XX 01-SEP-1999; 99WO-US20111.
XX 08-SEP-1999; 99WO-US20594.
XX 13-SEP-1999; 99WO-US20944.
XX 13-SEP-1999; 99WO-US21090.
XX 15-SEP-1999; 99WO-US21547.
XX 05-OCT-1999; 99WO-US23089.
XX 29-OCT-1999; 99US-0162506.
XX 28-NOV-1999; 99WO-US28214.
XX 30-NOV-1999; 99WO-US28313.
XX 30-NOV-1999; 99WO-US28409.
XX 01-DEC-1999; 99WO-US28301.
XX 01-DEC-1999; 99WO-US28634.
XX 02-DEC-1999; 99WO-US28551.
XX 02-DEC-1999; 99WO-US28564.
XX 02-DEC-1999; 99WO-US28565.
XX 16-DEC-1999; 99WO-US30095.
XX 20-DEC-1999; 99WO-US30999.
XX 30-DEC-1999; 99WO-US31274.
XX 05-JAN-2000; 2000WO-US00219.
XX 06-JAN-2000; 2000WO-US00277.
XX 11-FEB-2000; 2000WO-US03565.
XX 18-FEB-2000; 2000WO-US04341.
XX 18-FEB-2000; 2000WO-US04342.
XX 22-FEB-2000; 2000WO-US04414.

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PR 13-SEP-1999; 99WO-US20944.
PR 13-SEP-1999; 99WO-US21090.
PR 13-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-OCT-1999; 99US-0162506.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;
XX Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NP, Smith V;
XX Watanabe CK, Williams PM, Wood WI;
XX
XX WPI; 2000-412154/35.
XX N-PSDB; AAA77604.
XX
XX Nucleic acids encoding PRO polypeptides useful for preventing,
XX diagnosing and treating diagnosing a cardiovascular, endothelial or
XX angiogenic disorders in mammals
XX
XX Claim 72; Fig 44; 315pp; English.
XX
XX The present invention describes nucleic acids encoding PRO polypeptides
XX useful for preventing, diagnosing and treating diagnosing a
XX cardiovascular, endothelial or angiogenic disorder in mammals by
XX modulating cell proliferation, angiogenesis and cardiovascularisation,
XX and for identifying agonists and antagonists of these processes. The
XX nucleic acids and the proteins they encode may be used in the
XX prevention, treatment and diagnosis of diseases associated with
XX inappropriate PRO expression such as cardiovascular, endothelial or
XX angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
XX cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors
XX containing them and the PRO polypeptide may be used to treat disorders
XX associated with decreased PRO expression. AAA77510 to AAA77721 and
XX AAB24388 to AAB24435 represent nucleotide and protein sequences used in
XX the exemplification of the present invention.
XX
XX Sequence 241 AA;
XX
XX Query Match 100.0%; Score 252; DB 21; Length 241;
XX Best Local Similarity 100.0%; Pred. No. 4.2e-20;
XX Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 CVQPEFHCGDPCCTTCRHHPCPPGQVGSQKFSFGFCI 40
Db 74 cvqpefhcgdpcccttrhhpcppgpgvgsgqkfsfgfc 113

RESULT 14
AA771467
ID AA771467 standard; Protein: 241 AA.
XX
XX AA771467;
XX
XX 08-NOV-2000 (first entry)
XX
XX Human PRO364 protein.
XX
XX PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;
XX neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;
XX breast; prostate; colon; lung; renal; ovarian; central nervous system;
XX CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue;
XX tumour necrosis factor receptor; GTR protein homologue.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..25
XX /label= Signal_peptide
XX Modified-site 5..11
XX /note= "N-myristoylation site"
XX Modified-site 8..14
XX /note= "N-myristoylation site"

```

```

FT Modified-site 25..31
FT /note= "N-myristoylation site"
FT Protein 26..241
FT /label= Mature_PRO364_protein
FT Modified-site 30..36
FT /note= "N-myristoylation site"
FT Modified-site 33..39
FT /note= "N-myristoylation site"
FT Modified-site 118..124
FT /note= "N-myristoylation site"
FT Modified-site 122..128
FT /note= "N-myristoylation site"
FT Modified-site 146..150
FT /note= "Asn is N-glycosylated"
FT Modified-site 156..162
FT /note= "N-myristoylation site"
FT Domain 163..183
FT /label= Transmembrane_domain
FT Binding-site 166..177
FT /note= "Prokaryotic membrane lipoprotein lipid
FT attachment site"
FT Region 171..193
FT /note= "Leucine zipper pattern"
XX
XX WO200032778-A2.
XX
XX 08-JUN-2000.
XX
XX 30-NOV-1999; 99WO-US28409.
XX
XX 01-DEC-1998; 98WO-US25108.
XX 16-DEC-1998; 98US-0112850.
XX 22-DEC-1998; 98US-0113296.
XX 20-JUL-1999; 99US-0144758.
XX 26-JUL-1999; 99US-0145698.
XX
XX (GETH ) GENENTECH INC.
XX
XX Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;
XX WPI; 2000-412325/35.
XX N-PSDB; AAD01240.
XX
XX New composition useful for inhibiting neoplastic cell growth and for
XX treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or
XX their antagonists
XX
XX Claim 31; Fig 4; 108pp; English.
XX
XX The present sequence is the human PRO364 protein, encoded by the cDNA
XX clone, designated as DNA47365-1206. It is isolated from human small
XX intestine tissue cDNA library, identified using probes based on the
XX consensus sequence DNA44825, relative to the Incyte expressed sequence
XX tag (EST) 3003460. This EST has homology to tumour necrosis factor
XX receptor (TNFR) family of polypeptides. PRO364 sequence also shows
XX homology to members of the TNFR family, and mouse GTR protein.
XX This clone is assigned the ATCC deposit No: 209436. PRO364 functions as
XX a neoplastic cell growth inhibitor and is used for treating tumours
XX using an effective amount of PRO655, PRO364 and PRO344. This composition
XX is especially useful for treatment of human cancers such as breast,
XX prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.
XX
XX Sequence 241 AA;
XX
XX Query Match 100.0%; Score 252; DB 21; Length 241;
XX Best Local Similarity 100.0%; Pred. No. 4.2e-20;
XX Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 CVQPEFHCGDPCCTTCRHHPCPPGQVGSQKFSFGFCI 40
Db 74 cvqpefhcgdpcccttrhhpcppgpgvgsgqkfsfgfc 113

```

XX The present sequence is that of human tumour necrosis factor  
 CC receptor-like protein TR11SV1, a novel 26 kDa protein which shows  
 CC 58.6% identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The sequence was deduced from  
 CC cDNA (see AA50305) discovered in a PHA-stimulated T-cell library.  
 CC The invention provides TR11, TR11SV1 and TR11SV2 nucleic acids  
 CC (see AA50304-06) and highly conserved encoded proteins (see  
 CC AAY95879-81), as well as vectors, host cells and recombinant methods for  
 CC their production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an  
 CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.  
 XX Sequence 241 AA;  
 SQ

Query Match 100.0%; Score 252; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-20;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCTCRHHPCPPGQVSGQKFSFGFCI 40  
 ||||||||||||||||||||||||||||||||||||  
 Db 74 cvqpefhcgdpctctcrhhpcppgvgqgkfsfgfqi 113

RESULT 12  
 AAY95895  
 ID AAY95895 standard; Protein; 241 AA.  
 XX  
 AC AAY95895;  
 XX  
 DT 20-NOV-2000 (first entry).  
 XX  
 DE Human tumour necrosis factor receptor-like protein TR11 mutein.  
 XX  
 KW TR11; human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
 KW dermatological; antiinflammatory; therapy; diagnosis; mutein;  
 KW mutant.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200050459-A1.  
 XX  
 PD 31-AUG-2000.  
 XX  
 PF 23-FEB-2000; 2000WO-US04572.  
 XX  
 PR 24-FEB-1999; 99US-0121648.  
 PR 13-MAY-1999; 99US-0134172.  
 PR 16-JUL-1999; 99US-0144076.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Ni J;  
 XX  
 DR WPI; 2000-572072/53.  
 XX  
 PT Human tumor necrosis factor receptor-like proteins useful for  
 PT diagnosis, prevention and treatment of disease states associated with  
 PT aberrant cell survival such as autoimmune disease and rheumatoid

PT arthritis  
 XX  
 PS Disclosure; 294-295; 278pp; English.  
 XX  
 CC The present sequence is that of human tumour necrosis factor  
 CC receptor-like protein TR11 (see also AAY95879), a novel protein  
 CC showing identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The invention provides  
 CC highly conserved TR11, TR11SV1 and TR11SV2 proteins (see AAY95879-81),  
 CC as well as vectors, host cells and recombinant methods for their  
 CC production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an  
 CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunoglobulin  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.  
 XX Sequence 241 AA;  
 SQ

Query Match 100.0%; Score 252; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-20;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCTCRHHPCPPGQVSGQKFSFGFCI 40  
 ||||||||||||||||||||||||||||||||||||  
 Db 74 cvqpefhcgdpctctcrhhpcppgvgqgkfsfgfqi 113

RESULT 13  
 AAB24409  
 ID AAB24409 standard; Protein; 241 AA.  
 XX  
 AC AAB24409;  
 XX  
 DT 07-NOV-2000 (first entry)  
 XX  
 DE Human PRO364 protein sequence SEQ ID NO:117.  
 XX  
 KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
 KW cytostatic; gene therapy; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200032221-A2.  
 XX  
 PD 08-JUN-2000.  
 XX  
 PF 30-NOV-1999; 99WO-US28313.  
 XX  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 16-DEC-1998; 98US-0112850.  
 PR 12-JAN-1999; 99US-0115554.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 28-APR-1999; 99US-0131445.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.

---

## RESULT 15

AAV52159  
ID AAV52159 standard; Protein; 241 AA.

XX AC AAV52159;

XX DT 01-FEB-2000 (first entry)

XX DE TR1LSV1 amino acid sequence.

XX KW Tumour necrosis factor receptor-like protein; TR1L; TR1LSV1; TR1LSV2;  
KW G1FR; growth; differentiation; cell death; immune deficiency disorder;  
KW Digeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia;  
KW Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes;  
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;  
KW inflammatory condition.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domain 1..162

FT FT /note= "Extracellular domain"

FT FT 163..179

FT FT /note= "Transmembrane domain"

FT FT 180..241

FT FT /note= "Intracellular domain"

XX PN W09920758-A1.

XX XX

XX PD 29-APR-1999.

XX PF 21-OCT-1998; 98WO-US22085.

XX PR 21-OCT-1997; 97US-0063212.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ni J, Ruben SM;

XX DR WPI; 2000-061922/05.

XX DR N-PSDB; AAZ37763.

XX PT New tumour necrosis factor receptor-like polypeptides used to, e.g.  
treat Digeorge syndrome -

XX PS Claim 14; Fig 2; 167pp; English.

XX This is the amino acid sequence of the human tumour necrosis factor  
XX receptor-like protein splice variant 1 (TR1LSV1 receptor). The invention  
XX relates to TR1L and two splice variants TR1LSV1 and TR1LSV2. The  
XX nucleotide sequences were determined by sequencing cloned cDNAs  
XX AAZ37765-37766. The TR1L receptor and its splice variants show homology  
XX to the murine glucocorticoid-induced tumour necrosis factor receptor  
XX family related gene (G1FR). TR1L, TR1LSV1 and TR1LSV2 polypeptides may  
XX be involved in the regulation of cell-type specific receptor-mediated  
XX cell growth, differentiation, and ultimately, cell death. They can be  
XX used for screening for agonists/antagonists. The polypeptides, agonists  
XX or antagonists can be used for treating a disease state associated with  
XX aberrant cell survival. They can be used for treating immune deficiency  
XX disorders, Digeorge syndrome, HIV infection, severe combined  
XX immunodeficiency (SCID), Wiskott-Aldrich disorder, blood coagulation  
XX disorders, blood platelet disorders or wounds resulting from trauma or  
XX surgery. They can also be used to treat heart attacks, strokes,  
XX Addison's disease, haemolytic anaemia, rheumatoid arthritis, Goodpastures  
XX syndrome, Grave's disease, multiple sclerosis, myasthenia gravis,  
XX Stiff-Man syndrome, systemic lupus erythematosus, Guillain-Barre  
XX syndrome, insulin dependent diabetes mellitus or autoimmune inflammatory  
XX eye disease, anaphylaxis, hypersensitivity to an antigenic molecule,  
XX organ rejection or graft versus host disease, inflammatory conditions,  
XX ischaemia-reperfusion injury, complement-mediated hyperacute rejection,  
XX nephritis, cytokine or chemokine induced lung injury, inflammatory bowel  
XX disease, Crohn's disease, hyperproliferative disorders, or infections.

CC They can also be used to repair, replace, or protect tissue damaged by  
CC congenital defects, trauma, age, disease, surgery, including cosmetic  
CC plastic surgery, fibrosis, reperfusion injury, peripheral nerve  
CC injuries, neuropathies, and central nervous system disease (e.g.  
CC Alzheimer's disease, Parkinson's disease, Huntington's disease,  
CC anyotrophic lateral sclerosis, and Shy-Drager syndrome). The products can  
CC also be used for detection, diagnosis and prognosis.

XX SQ Sequence 241 AA;

Query Match 100.0%; Score 252; DB 21; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4.2e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCTCRHHPCPPGGVQSGKFSFGFCI 40

|||||

Db 74 cvqpefhcgdpccctcrhhpcppggvgsgkfsfgfc 113

Search completed: September 4, 2001, 15:56:24

Job time: 341 sec



PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 XX other T cell disorders  
 PS Disclosure: Pages 61-62; 71pp; English.  
 CC This is the amino acid sequence of the truncated human 312C2 T cell  
 CC protein from clone A8. The 312C2 proteins are expressed in thymus  
 CC cells and are induced on T cells and spleen cells following activation.  
 CC Engagement of 312C2 stimulates proliferation of T cell clones,  
 CC antigen-specific proliferation and cytokine production by T-cells, and  
 CC potentiates T cell expansion or apoptosis. The products can be used  
 CC in the treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX SQ Sequence 228 AA;

Query Match 100.0%; Score 255; DB 19; Length 228;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41  
 ||||||||||||||||||||||||||||||||||||||||  
 Db 27 GCGPGRLLLTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 67

RESULT 2  
 AAW37841  
 ID AAW37841 standard; Protein: 232 AA.  
 AC AAW37841;  
 DT 28-JUL-1998 (first entry)  
 XX Human 312C2 protein from clone\_A5 amino acid sequence.  
 DE Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 KW antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
 KW autoimmune disorders.  
 XX Homo sapiens.  
 OS  
 PN WO9806842-A1.  
 XX  
 PD 19-FEB-1998.  
 XX  
 PF 14-AUG-1997; 97WO-US13931.  
 PR 07-OCT-1996; 96US-0027901.  
 PR 16-AUG-1996; 96US-0689943.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 XX  
 PI Gorman DM, Randall TD, Zlotnik A;  
 XX  
 DR WPI; 1998-159534/14.  
 XX  
 XX Isolated 312C2 T cell gene - used to develop products for treating,  
 PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 PT other T cell disorders  
 PS Disclosure: Pages 62-63; 71pp; English.  
 CC This is the amino acid sequence of the human 312C2 T cell protein from  
 CC clone\_A5, which is identical to sequence AAW37838 for the first 105  
 CC amino acid residues. It is thought that divergence may be due to  
 CC an unspliced intron. The 312C2 proteins are expressed in thymus  
 CC cells and are induced on T cells and spleen cells following activation.  
 CC Engagement of 312C2 stimulates proliferation of T cell clones,

CC antigen-specific proliferation and cytokine production by T-cells, and  
 CC potentiates T cell expansion or apoptosis. The products can be used  
 CC in the treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX SQ Sequence 232 AA;

Query Match 100.0%; Score 255; DB 19; Length 232;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 41  
 ||||||||||||||||||||||||||||||||||||||||  
 Db 27 GCGPGRLLLTGTDARCCRVHTTRCCRDYPGEECCSEWDCM 67

RESULT 3  
 AAY95879  
 ID AAY95879 standard; Protein: 234 AA.  
 XX  
 AC AAY95879;  
 XX  
 DT 20-NOV-2000 (first entry)  
 XX Human tumour necrosis factor receptor-like protein TR11.  
 DE Human tumour necrosis factor receptor-like protein TR11.  
 XX TR11; human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
 KW dermatological; antiinflammatory; therapy; diagnosis.  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT /label= Signal\_peptide  
 FT Protein 26..234  
 FT /label= Mature\_protein  
 FT Domain 26..162  
 FT /label= Extracellular\_domain  
 FT Domain 163..179  
 FT /label= Transmembrane\_domain  
 FT Domain 180..234  
 FT /label= Intracellular\_domain  
 FT Modified-site 146  
 FT /note= "N-glycosylated"  
 FT Domain 72..81  
 FT /note= "conserved domain CD-II"  
 FT Domain 84..93  
 FT /note= "conserved domain CD-III"  
 FT Domain 107..113  
 FT /note= "conserved domain CD-IV"  
 FT Domain 128..134  
 FT /note= "conserved domain CD-V"  
 FT Domain 153..160  
 FT /note= "conserved domain CD-VI"  
 FT Domain 176..186  
 FT /note= "conserved domain CD-VII"  
 FT Domain 204..209  
 FT /note= "conserved domain CD-IX"  
 FT Domain 224..233  
 FT /note= "conserved domain CD-X"  
 FT Region 27..36  
 FT /note= "epitope-bearing region"  
 FT Region 43..51  
 FT /note= "epitope-bearing region"  
 FT Region 59..67  
 FT /note= "epitope-bearing region"  
 FT Region 56..64

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:56:23 ; Search time 126.12 Seconds  
(without alignments)  
19.708 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_33\_73

Perfect score: 255

Sequence: 1 GCGPGKLLGTGTARCCRV.....TTRCCRDYPGECCSEWDCM 41

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*

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21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*

22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	255	100.0	228	AAW37840	Truncated human 31
2	255	100.0	232	AAW37841	Human 312C2 protei
3	255	100.0	234	AAAY95879	Human tumour necro
4	255	100.0	234	AAAY52158	Tumour necrosis fa
5	255	100.0	235	AAAY44825	Human molecule ass
6	255	100.0	241	AAW37839	Amino acid sequenc
7	255	100.0	241	AAAY06605	Human TNF receptor
8	255	100.0	241	AAAB27651	Human protein PRO3
9	255	100.0	241	AAAB33431	Human PRO364 prote
10	255	100.0	241	AAAY95895	Human tumour necro
11	255	100.0	241	AAAB24409	Human PRO364 prote

12	255	100.0	241	21	AAV71467	Human PRO364 prote
13	255	100.0	241	22	AAAB20115	Human immunostimul
14	255	100.0	241	22	AAAB47054	Human PRO364. Hom
15	255	100.0	241	22	AAAB50910	Human PRO364 prote
16	255	100.0	241	22	AAAB50982	Human PRO364 prote
17	255	100.0	241	22	AAAB53090	Human angiogenesis
18	255	100.0	311	19	AAW37842	Human 312C2 protei
19	255	100.0	316	22	AAAB47055	Polypeptide encode
20	255	100.0	317	20	AAAY06645	PRO364-related EST
21	239	93.7	240	21	AAAY95881	Human tumour necro
22	239	93.7	240	21	AAAY52160	TR11SV2 amino acid
23	87.5	34.3	89	21	AAV76013	Murine TNF-alpha f
24	87.5	34.3	89	22	AAAB55952	Skin cell protein,
25	87.5	34.3	222	19	AAW49018	Mouse glucocortico
26	87.5	34.3	228	19	AAW49016	Mouse glucocortico
27	87.5	34.3	228	19	AAW37838	Amino acid sequenc
28	87.5	34.3	294	19	AAW49017	Mouse glucocortico
29	81.5	32.0	241	21	AAAY95880	Human tumour necro
30	81.5	32.0	241	21	AAAY52159	TR11SV1 amino acid
31	65.5	25.7	150	20	AAW98148	TRAIN-R short, sol
32	65.5	25.7	328	20	AAAY06400	Human NTR-5 recept
33	65.5	25.7	417	19	AAW70386	Amino acid sequenc
34	65.5	25.7	417	20	AAW98146	Human TRAIN-R. Ho
35	65.5	25.7	417	21	AAAB33474	Human PRO4333 prot
36	65.5	25.7	423	19	AAW70387	Amino acid sequenc
37	65.5	25.7	423	20	AAW85724	Novel protein (Clo
38	65.5	25.7	423	20	AAW93581	Human hAPO4-alpha
39	65.5	25.7	423	21	AAAB23547	Human Troy protein
40	64	25.1	109	17	AAW84086	T-lymphocyte stimu
41	64	25.1	443	18	AAW27441	Oil seed rape cyst
42	62	24.3	127	21	AAAB51446	Human secreted pro
43	62	24.3	127	21	AAAB51450	Human secreted pro
44	61.5	24.1	150	20	AAAY06523	Mouse STRIPE2 (Tan
45	61.5	24.1	150	20	AAAY22224	Mouse TNFR superfa

#### ALIGNMENTS

RESULT 1

AAW37840  
ID AAW37840 standard; Protein; 228 AA.

XX AC AAW37840;

XX DT 28-JUL-1998 (first entry)

XX Truncated human 312C2 protein from clone\_A8 amino acid sequence.

DE DE Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
KW antigen-specific T cell proliferation; cytokine production by T-cell;  
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
KW autoimmune disorders.

XX OS Homo sapiens.

XX PN WO9806842-A1.

XX PD 19-FEB-1998.

XX PF 14-AUG-1997; 97WO-US13931.

XX PR 07-OCT-1996; 96US-0027901.

XX PR 16-AUG-1996; 96US-0689943.

XX PA (SCHE ) SCHERING CORP.

XX PI Gorman DM, Randall TD, Zlotnik A;

XX DR WPI; 1998-159534/14.

XX DR N-PSDB; AAV19154.

XX PT Isolated 312C2 T cell gene - used to develop products for treating,

CC haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's  
 CC disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome,  
 CC systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent  
 CC diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,  
 CC hypersensitivity to an antigenic molecule, organ rejection or graft  
 CC versus host disease, inflammatory conditions, ischaemia-reperfusion  
 CC injury, complement-mediated hyperacute rejection, nephritis, cytokine or  
 CC chemokine induced lung injury, inflammatory bowel disease, Crohn's  
 CC disease, hyperproliferative disorders, or infections. They can also be  
 CC used to repair, replace, or protect tissue damaged by congenital  
 CC defects, trauma, age, disease, surgery, including cosmetic plastic  
 CC surgery, fibrosis, reperfusion injury, peripheral nerve injuries,  
 CC neuropathies, and central nervous system disease (e.g. Alzheimer's  
 CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral  
 CC sclerosis, and Shy-Drager syndrome). The products can also be used for  
 CC detection, diagnosis and prognosis.

XX  
 XX  
 SQ Sequence 234 AA;

Query Match 100.0%; Score 255; DB 21; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTDARCCRVHTTRCCRDYPGECCSEWDCM 41  
 Db 33 gcgpgrrlllgtgdarcrcrvhttrccrdypgeccsewdcm 73  
 |||||

RESULT 5  
 AAY44825  
 ID AAY44825 standard; Protein: 235 AA.  
 AC AAY44825;  
 XX  
 XX 18-MAY-2000 (first entry)  
 XX Human molecule associated with cell proliferation, MACP-5.  
 XX Human; molecule associated with cell proliferation; MACP-5;  
 KW Incyte clone 2809903; antiarteriosclerotic; hepatotropic; cytostatic;  
 KW anti-inflammatory; antipsoriatic; anti-HIV; antiasthmatic; anaemia;  
 KW dermatological; antidiabetic; nephrotropic; antithyroid; thyromimetic;  
 KW immunosuppressive; osteopathic; antiarthritic; uropathic; antiulcer;  
 KW ophthalmological; diagnosis; treatment; prevention; immune disorder;  
 KW cell proliferative disorder; actinic keratosis; arteriosclerosis;  
 KW atherosclerosis; bursitis; hepatitis; Crohn's disease; amyloidosis.

XX  
 OS Homo sapiens.  
 XX  
 XX Location/Qualifiers  
 FH Key 1..19  
 FT Region /label= Signature\_sequence  
 FT Region 68..96  
 FT Region /label= Signature\_sequence  
 FT Region 109..147  
 FT Region /label= Signature\_sequence  
 FT Region 122..129  
 FT Region /label= Signature\_sequence  
 FT Region 157..175  
 FT Region /label= Signature\_sequence  
 FT Region 165..186  
 FT Region /label= Signature\_sequence  
 FT Modified-site 37  
 FT /note= "Potential phosphorylation site"  
 FT Modified-site 48  
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 FT Modified-site 82  
 FT /note= "Potential phosphorylation site"  
 FT Modified-site 205  
 FT /note= "Potential phosphorylation site"

ET Modified-site 223  
 FT /note= "Potential phosphorylation site"  
 FT Modified-site 140  
 FT /note= "N-glycosylated"  
 XX  
 XX WO200005374-A2.  
 PN 03-FEB-2000.  
 PD 21-JUL-1999; 99WO-US16637.  
 PF 22-JUL-1998; 98US-0093827.  
 PR (INCY-) INCYTE PHARM INC.  
 XX  
 XX Tang YT, Lal P, Hillman JL, Corley NC, Patterson C, Baughn MR;  
 PI WPI: 2000-182699/16.  
 XX N-PSDB: AAZ49948.  
 DR  
 XX Polypeptides and polynucleotides useful for treating and detecting cell  
 PT proliferation disorders e.g. actinic keratosis, and immune disorders  
 PT e.g. Crohn's disease  
 XX  
 PS Claim 1; Pages 64-65; 67pp; English.  
 XX  
 CC The present sequence is a molecule associated with cell  
 CC proliferation, MACP-5 from Incyte clone 2809903 isolated from TLYMN0T06  
 CC CDNA library. This sequence is expressed in cardiovascular and  
 CC haematopoietic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV,  
 CC hepatotropic, antiinflammatory, antipsoriatic, cytostatic, antiasthmatic,  
 CC dermatological, antidiabetic, nephrotropic, antithyroid, thyromimetic,  
 CC immunosuppressive, osteopathic, antiarthritic, uropathic, antiulcer,  
 CC and ophthalmological activities. The present sequence is useful in the  
 CC diagnosis treatment and prevention of cell proliferative disorders e.g.  
 CC actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and  
 CC hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and  
 CC anaemia.  
 XX  
 SQ Sequence 235 AA;

Query Match 100.0%; Score 255; DB 21; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTDARCCRVHTTRCCRDYPGECCSEWDCM 41  
 Db 27 gcgpgrrlllgtgdarcrcrvhttrccrdypgeccsewdcm 67  
 |||||

RESULT 6  
 AAW37839  
 ID AAW37839 standard; Protein: 241 AA.  
 XX  
 XX AAW37839;  
 XX  
 XX 28-JUL-1998 (first entry)  
 XX  
 XX Amino acid sequence of the human 312C2 T cell protein.  
 DE Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 XX antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
 KW autoimmune disorders.  
 XX  
 XX Homo sapiens.  
 OS  
 XX Location/Qualifiers  
 FH Key 1..726  
 FT CDS /\*tag= a  
 FT /product= "human 312C2 protein"  
 XX

FT	Region	/note= "epitope-bearing region"
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FT	FT	/note= "epitope-bearing region"
FT	99..107	
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FT	125..133	
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FT	143..151	
FT	FT	/note= "epitope-bearing region"
FT	156..164	
FT	FT	/note= "epitope-bearing region"
FT	203..211	
FT	FT	/note= "epitope-bearing region"
FT	222..230	
FT	FT	/note= "epitope-bearing region"
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PX	W0200050459-A1.	
XX		
PD	31-AUG-2000.	
XX		
PF	23-FEB-2000; 2000WO-US04572.	
XX		
PR	24-FEB-1999; 99US-0121648.	
PR	13-MAY-1999; 99US-0134172.	
PR	16-JUL-1999; 99US-0144076.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Ruben SM, NI J;	
XX		
DR	WPI; 2000-572072/53.	
DR	N-PSDB; AAA50304.	
XX		
PT	Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid arthritis -	
PT		
XX		
PS	Claim 14(c); Fig 1A-B; 278pp; English.	
XX		
CC	The present sequence is that of human tumour necrosis factor receptor-like protein TRIL1, a novel 25 kDa protein which shows 58.6% identity to murine glucocorticoid induced tumour necrosis factor receptor family-related gene. The sequence was deduced from a cDNA clone (see AAA50304) discovered in a T-helper cell library.	
CC	TRIL1 activated NF-kappaB through a TRAF2-mediated mechanism.	
CC	Expression is activation-inducible. The TRIL1 ligand is constitutively expressed in an endothelial cell line. This suggests that TRIL1 and its ligand may be involved in activated T-cell trafficking.	
CC	The invention provides TRIL1, TRILSV1 and TRILSV2 nucleic acids (see AAA50304-06) and highly conserved encoded proteins (see AA95879-81), as well as vectors, host cells and recombinant methods for their production. TRIL1, TRILSV1 and/or TRILSV2 polypeptides are useful for treating, preventing, prognosis and/or diagnosis of an immunodeficiency, especially common variable immunodeficiency, X-linked agammaglobulinemia, severe combined immunodeficiency (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin deficiency with hyper IgM. TRIL1, TRILSV1 and/or TRILSV2 antagonists (e.g. antibodies) are used to treat, prevent, prognose and/or diagnose an autoimmune disease, especially rheumatoid arthritis, systemic lupus erythematosus, thrombocytopenia purpura or IGA nephropathy. The polypeptides, polynucleotides and/or antibodies can be administered to cells in vitro, ex vivo or in vivo or to a multicellular organism. Soluble forms of the polypeptides may also be used. Methods for screening for agonist/antagonist compounds are also provided.	
XX		
SQ	Sequence 234 AA;	
	Query Match 100.0%; Score 255; DB 21; Length 234;	
	Best Local Similarity 100.0%; Pred. No. 6.3e-20;	
	Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

QY	1	GC	GPGRLLTGTGDARCCRVHTTTCRCRDYPGECCSEWDQM	41
Db	33	gc	gpggrlllgtgdarccrvhtttcrdrpygeccsewdcm	73
RESULT	4			
AA52158				
ID	AA52158 standard; Protein; 234 AA.			
XX				
AC	AA52158;			
XX				
DT	01-FEB-2000 (first entry)			
XX				
DE	Tumour necrosis factor receptor-like protein (TRIL1) amino acid sequence.			
XX				
KW	Tumour necrosis factor receptor-like protein; TRIL1; TRILSV1; TRILSV2; GITR; growth; differentiation; cell death; immune deficiency disorder; Digeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia; Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes; Alzheimer's disease; Parkinson's disease; Huntington's disease; inflammatory condition.			
OS	Homo sapiens.			
XX				
FH	Key	Location/Qualifiers		
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FT	Protein	/label= Signal_peptide		
FT		26..234		
FT		/label= TRIL1		
FT	Domain	26..162		
FT		/note= "Extracellular domain"		
FT	Domain	163..179		
FT		/note= "Transmembrane domain"		
FT	Domain	180..234		
FT		/note= "Intracellular domain"		
XX				
PN	WO9920758-A1.			
XX				
PD	29-APR-1999.			
XX				
PF	21-OCT-1998; 98WO-US22085.			
XX				
PR	21-OCT-1997; 97US-0063212.			
XX				
PA	(HUMA-) HUMAN GENOME SCI INC.			
XX				
PI	NI J, Ruben SM;			
XX				
DR	WPI; 2000-061922/05.			
DR	N-PSDB; AA237762.			
XX				
PT	New tumour necrosis factor receptor-like polypeptides used to, e.g. treat Digeorge syndrome -			
XX				
PS	Claim 14; Fig 1; 167pp; English.			
XX				
CC	This is the amino acid sequence of the human tumour necrosis factor receptor-like protein (TRIL1 receptor). The invention relates to TRIL1 and two splice variants TRILSV1 and TRILSV2. The nucleotide sequences were determined by sequencing cloned cDNAs AA237765-237766. The TRIL1 receptor and its splice variants show homology to the murine glucocorticoid induced tumour necrosis factor receptor family-related gene (GITR).			
CC	TRIL1, TRILSV1 and TRILSV2 polypeptides may be involved in the regulation of cell-type specific receptor-mediated cell growth, differentiation, and ultimately, cell death. They can be used for screening for agonists/antagonists. The polypeptides, agonists or antagonists can be used for treating a disease state associated with aberrant cell survival. They can be used for treating immune deficiency disorders, Digeorge syndrome, HIV infection, severe combined immunodeficiency (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood platelet disorders or wounds resulting from trauma or surgery. They can also be used to treat heart attacks, strokes, Addison's disease,			

```

FT XX /label= "Signal peptide"
PN XX WO200053757-A2.
XX PD 14-SEP-2000.
XX PF 24-FEB-2000; 2000WO-US05004.
XX PR 08-MAR-1999; 99WO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 02-JUN-1999; 99WO-US12252.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28565.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
XX PA (GETH ) GENENTECH INC.
XX PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;
PI Goddard A, Gurney AL, Hillan KJ, Marsters SA, Paoni NF, Pitti RM;
PI Watanabe CK, Williams PM, Wood WI;
XX WPI: 2000-611444/58.
DR DR N-PSDB; AAA99903.
XX PT Novel PRO polypeptides and agonists and antagonists of them, used to
PT diagnose and treat cardiovascular, endothelial and angiogenic disorders
XX PS Claim 71; Fig 6; 181pp; English.
XX CC The present invention relates to methods for stimulating or inhibiting
CC angiogenesis and cardiovascularization. The methods involve the use of
CC pharmaceutical compositions based on the following proteins, PRO179,
CC PRO238, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333,
CC PRO840, PRO877, PRO878, PRO882, PRO885 or PRO887. These
CC proteins were identified by isolating cDNA clones encoding secreted
CC proteins. The proteins of the invention may be used to diagnose and
CC treat cardiovascular, endothelial or angiogenic disorders. The present
CC sequence is one of the proteins of the invention.
XX SQ Sequence 241 AA;

Query Match 100.0%; Score 255; DB 21; Length 241;
Best Local Similarity 100.0%; Pred. NO. 6.4e-20;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTDARCRVHTTRCCRDYFGECCEWDCM 41
Db 33 gcgpgrrlllgtgdarcrcrvhttrccrdyfgceccwdc 73

RESULT 9
AAB33431
ID AAB33431 standard; Protein; 241 AA.
XX AC AAB33431;
XX DT 29-JAN-2001 (first entry)
XX DE Human PRO364 protein UNQ319 SEQ ID NO:92.
XX KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW dermatological; antiarthritic; antiirchumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;

```

osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;  
idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
autoimmune thrombocytopaenia; immune-mediated renal disease;  
demyelinating disease; hepatobiliary disease; Whipple's disease;  
inflammatory bowel disease; gluten-sensitive enteropathy;  
autoimmune disease; immune-mediated skin disease; allergic disease;  
immunological disease; transplantation associated disease;  
graft rejection; graft-versus-host-disease.

Homo sapiens.

WO200053758-A2.

14-SEP-2000.

02-MAR-2000; 2000WO-US05841.

08-MAR-1999; 99WO-US05028.  
10-MAR-1999; 99US-0123618.  
12-MAR-1999; 99US-0123957.  
23-MAR-1999; 99US-0125775.  
12-APR-1999; 99US-0128849.  
20-APR-1999; 99WO-US08615.  
28-APR-1999; 99US-0131445.  
04-MAY-1999; 99US-0132371.  
14-MAY-1999; 99US-0134287.  
02-JUN-1999; 99WO-US12252.  
23-JUN-1999; 99US-0141037.  
20-JUL-1999; 99US-0144758.  
26-JUL-1999; 99US-0145698.  
28-JUL-1999; 99US-0146222.  
01-SEP-1999; 99WO-US20111.  
08-SEP-1999; 99WO-US20594.  
13-SEP-1999; 99WO-US20944.  
15-SEP-1999; 99WO-US21090.  
15-SEP-1999; 99WO-US21547.  
05-OCT-1999; 99WO-US23089.  
29-OCT-1999; 99US-0162506.  
29-NOV-1999; 99WO-US28214.  
30-NOV-1999; 99WO-US28313.  
30-NOV-1999; 99WO-US28409.  
01-DEC-1999; 99WO-US28301.  
01-DEC-1999; 99WO-US28634.  
02-DEC-1999; 99WO-US28551.  
02-DEC-1999; 99WO-US28564.  
02-DEC-1999; 99WO-US28565.  
16-DEC-1999; 99WO-US30095.  
20-DEC-1999; 99WO-US30999.  
30-DEC-1999; 99WO-US31274.  
05-JAN-2000; 2000WO-US00219.  
06-JAN-2000; 2000WO-US00277.  
06-JAN-2000; 2000WO-US00376.  
11-FEB-2000; 2000WO-US03565.  
18-FEB-2000; 2000WO-US04341.  
18-FEB-2000; 2000WO-US04342.  
22-FEB-2000; 2000WO-US04414.

(GETH ) GENENTECH INC.

Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;  
WPI: 2000-572271/53.  
N-PSDB: AAC58596.

Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
arthritis, osteoarthritis, thyroiditis and diabetes mellitus -

Claim 33; Fig 36; 309pp; English.

PN WO9806842-A1.  
 XX  
 PD 19-FEB-1998.  
 XX  
 PF 14-AUG-1997; 97WO-US13931.  
 XX  
 PR 07-OCT-1996; 96US-0027901.  
 XX  
 PR 16-AUG-1996; 96US-0689943.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 XX  
 PI Gorman DM, Randall TD, Zioltnik A;  
 XX  
 PI WPI; 1998-159534/14.  
 XX  
 DR N-PSDB; AAV19153.  
 DR  
 PT Isolated 312C2 T cell gene - used to develop products for treating,  
 XX e.g. cancers, auto-immune disorders, transplantation rejection and  
 PT other T cell disorders  
 XX  
 PS Claim 2; Pages 59-60; 71pp; English.  
 XX  
 CC This is the amino acid sequence encoding the human 312C2 T cell  
 CC protein. The 312C2 proteins are expressed in thymus cells and are  
 CC induced on T cells and spleen cells following activation. Engagement  
 CC of 312C2 stimulates proliferation of T cell clones, antigen-specific  
 CC proliferation and cytokine production by T-cells, and potentiates T  
 CC cell expansion or apoptosis. The products can be used in the  
 CC treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX  
 SQ Sequence 241 AA;  
 XX  
 Query Match 100.0%; Score 255; DB 19; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCGPGRLLGTGDARCCRVHTTRCCRDYPGECCECCSEWDCM 41  
 DB 33 gcgpgrrllgtgdarccrvhttrccrdypgeccsewdcmm 73  
 RESULT 7  
 ID AAY06605 standard; Protein; 241 AA.  
 XX  
 AC AAY06605;  
 XX  
 DT 26-OCT-1999 (first entry)  
 XX  
 DE Human TNF receptor homologue PRO364.  
 XX  
 KW PRO364; tumour necrosis factor receptor; human; apoptosis;  
 KW inflammation; antiinflammatory; NF-KB activation;  
 KW autoimmune disease; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT Peptide 1..25  
 FT /note= "signal peptide"  
 FT Protein 26..241  
 FT /note= "mature protein"  
 FT Modified-site 146  
 FT /note= "N-glycosylated"  
 FT Domain 162..180  
 FT /note= "transmembrane domain"  
 XX  
 PN WO9940196-A1.

XX  
 PD 12-AUG-1999.  
 XX  
 PF 09-FEB-1999; 99WO-US02642.  
 XX  
 PR 09-FEB-1998; 98US-0024087.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;  
 PI Pitti RM, Wood WI;  
 XX  
 DR WPI; 1999-494296/41.  
 DR N-PSDB; AAX87670.  
 XX  
 PT Tumour necrosis factor receptor homologue - useful for, e.g.  
 PT modulating apoptosis and NF-KB activation and proinflammatory or  
 PT autoimmune responses  
 XX  
 PS Claim 17; Fig 2A; 104pp; English.  
 XX  
 CC The present sequence represents human PRO364, a novel member of the  
 CC tumour necrosis factor receptor family. The sequence was deduced  
 CC from a bone marrow cDNA clone (see AAX87670). Methods for the  
 CC recombinant production of PRO364 polypeptides, e.g. in CHO,  
 CC Escherichia coli or yeast host cells, are provided. Claimed  
 CC polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the  
 CC mature protein) and 26-X of the present sequence, where X is any  
 CC one of amino acid residues 157-167 of PRO364. PRO364 polypeptides  
 CC are useful for modulating apoptosis, NF-KB activation and  
 CC proinflammatory or autoimmune responses in mammalian cells  
 CC (claimed). Chimeric molecules comprising a PRO364 polypeptide  
 CC fused to a heterologous sequence such as epitope tag or  
 CC immunoglobulin Fc region are also claimed. PRO364 can be used in  
 CC assays to identify other proteins or molecules involved in binding  
 CC interactions. This is useful for identifying inhibitors or  
 CC agonists of receptor/ligand binding. The PRO364 polypeptides may  
 CC also be combined with an agent that is cytotoxic, chemotherapeutic  
 CC or a growth inhibitor. PRO364 antibodies are useful in diagnostic  
 CC methods, purification methods and also in therapy, e.g. as  
 CC inhibitors.  
 XX  
 SQ Sequence 241 AA;  
 XX  
 Query Match 100.0%; Score 255; DB 20; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCGPGRLLGTGDARCCRVHTTRCCRDYPGECCECCSEWDCM 41  
 DB 33 gcgpgrrllgtgdarccrvhttrccrdypgeccsewdcmm 73  
 RESULT 8  
 AAB27651  
 ID AAB27651 standard; Protein; 241 AA.  
 XX  
 AC AAB27651;  
 XX  
 DT 26-JAN-2001 (first entry)  
 XX  
 DE Human protein PRO364.  
 XX  
 KW Cardiovascular; endothelial; angiogenic disorder; PRO179;  
 KW PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333;  
 KW PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;  
 KW gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT Peptide 1..25

FT	Modified-site	30..36	/note= "N-myristoylation site"
FT	Modified-site	33..39	/note= "N-myristoylation site"
FT	Modified-site	118..124	/note= "N-myristoylation site"
FT	Modified-site	122..128	/note= "N-myristoylation site"
FT	Modified-site	146..150	/note= "Asn is N-glycosylated"
FT	Modified-site	156..162	/note= "N-myristoylation site"
FT	Domain	163..183	/label= Transmembrane_domain
FT	Binding-site	166..177	/note= "Prokaryotic membrane lipoprotein lipid attachment site"
FT	Region	171..193	/note= "Leucine zipper pattern"
XX	WO200032778-A2.		
PN	08-JUN-2000.		
XX			
PD			
PF	30-NOV-1999;	99WO-US28409.	
PR	01-DEC-1998;	98WO-US25108.	
PR	16-DEC-1998;	98US-0112850.	
PR	22-DEC-1998;	98US-0113296.	
PR	20-JUL-1999;	99US-0144758.	
PR	26-JUL-1999;	99US-0145698.	
XX			
PA	(GETH ) GENENTECH INC.		
XX			
PI	Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;		
XX			
DR	WPI; 2000-412325/35.		
XX	N-PSDB; AAD01240.		
DR			
XX			
PT	New composition useful for inhibiting neoplastic cell growth and for treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or their antagonists -		
PT			
XX			
PS	Claim 31; Fig 4; 108pp; English.		
XX			
CC	The present sequence is the human PRO364 protein, encoded by the cDNA clone, designated as DNA47365-1206. It is isolated from human small intestine tissue cDNA library, identified using probes based on the consensus sequence DNA44825, relative to the Incyte expressed sequence tag (EST) 3003460. This EST has homology to tumour necrosis factor receptor (TNFR) family of polypeptides. PRO364 sequence also shows homology to members of the TNFR family and mouse G1TR protein.		
CC	This clone is assigned the ATCC deposit No: 209436. PRO364 functions as a neoplastic cell growth inhibitor and is used for treating tumours, using an effective amount of PRO655, PRO364 and PRO344. This composition is especially useful for treatment of human cancers such as breast, prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.		
XX			
SQ	Sequence	241 AA;	
Query Match 100.0%; Score 255; DB 21; Length 241;			
Best Local Similarity 100.0%; Pred. No. 6.4e-20;			
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	CGCGRLLLGTTGTGTCARCCRVHTTRCCRDYPGEECCSEWDCM 41	
Db	33	gcgpglllgtdarccrvhttrccrdypgeccsewdcm 73	
RESULT 13			
AAB20115			
ID AAB20115 standard; Protein: 241 AA.			

CC The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are  
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
 CC autoimmune or immune-mediated skin diseases, allergic diseases,  
 CC immunological diseases of the lung, and transplantation associated  
 CC diseases including graft rejection and graft-versus-host-disease.  
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.

XX Sequence 241 AA;

Query Match 100.0%; Score 255; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGPGRLLGTGDARCCRVHTTRCCRDYPGECCECCSEWDCM 41  
 |||||  
 Db 33 gcgpgrrllgtgdarcrcrvhttrccrdypgeccsewdcm 73

RESULT 10

AAY95895  
 ID AAY95895 standard; Protein; 241 AA.

XX  
 AC AAY95895;

XX 20-NOV-2000 (first entry)

XX Human tumour necrosis factor receptor-like protein TR11 mutein.

XX TR11; human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
 KW dermatological; antiinflammatory; therapy; diagnosis; mutain;  
 KW mutant.

XX Homo sapiens.

XX WO200050459-A1.

XX 31-AUG-2000.

XX 23-FEB-2000; 2000WO-US04572.

XX 24-FEB-1999; 99US-0121648.

XX 13-MAY-1999; 99US-0134172.

XX 16-JUL-1999; 99US-0144076.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, NI J;

XX WPI; 2000-572072/53.

XX Human tumor necrosis factor receptor-like proteins useful for  
 PT diagnosis, prevention and treatment of disease states associated with  
 PT aberrant cell survival such as autoimmune disease and rheumatoid  
 PT arthritis

XX Disclosure; 294-295; 278pp; English.

CC The present sequence is that of human tumour necrosis factor  
 CC receptor-like protein TR11 (see also AAY95879), a novel protein  
 CC showing identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The invention provides  
 CC highly conserved Tril1, TrilSV1 and TrilSV2 proteins (see AAY95879-81),  
 CC as well as vectors, host cells and recombinant methods for their  
 CC production. Tril1, TrilSV1 and/or TrilSV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an  
 CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. Tril1, TrilSV1 and/or TrilSV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IGA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.

XX Sequence 241 AA;

Query Match 100.0%; Score 255; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGPGRLLGTGDARCCRVHTTRCCRDYPGECCECCSEWDCM 41  
 |||||  
 Db 33 gcgpgrrllgtgdarcrcrvhttrccrdypgeccsewdcm 73

RESULT 11

AAB24409

ID AAB24409 standard; Protein; 241 AA.

XX  
 AC AAB24409;

XX 07-NOV-2000 (first entry)

XX Human PRO364 protein sequence SEQ ID NO:117.

XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
 KW cytostatic; gene therapy; vaccine.

XX Homo sapiens.

XX WO200032221-A2.

XX 08-JUN-2000.

XX 30-NOV-1999; 99WO-US28313.

XX 01-DEC-1998; 98WO-US25108.

XX 16-DEC-1998; 98US-0112850.

XX 12-JAN-1999; 99US-0115554.

XX 08-MAR-1999; 99WO-US05028.

XX 12-MAR-1999; 99US-0123957.

XX 28-APR-1999; 99US-0131445.

XX 14-MAY-1999; 99US-0134287.

XX 02-JUN-1999; 99WO-US12252.

XX 23-JUN-1999; 99US-0141037.

XX 20-JUL-1999; 99US-014758.

XX 26-JUL-1999; 99US-0145698.

XX 01-SEP-1999; 99WO-US20111.

XX 08-SEP-1999; 99WO-US20594.

XX 13-SEP-1999; 99WO-US20944.

XX 15-SEP-1999; 99WO-US21090.

XX 15-SEP-1999; 99WO-US21547.

XX 05-OCT-1999; 99WO-US23089.



FT /note= "Potential transmembrane domain"  
 PN W0200103720-A2.  
 XX 18-JAN-2001.  
 XX 11-JUL-2000; 2000WO-US18867.  
 XX 12-JUL-1999; 99US-0143304.  
 PR (GETH ) GENENTECH INC.  
 PA Williams PM, Gerritsen ME;  
 PI WPI; 2001-138257/14.  
 XX N-PSDB; AAC85433.  
 DR Composition for diagnosing and treating cardiovascular, endothelial and  
 XX angiogenic disorders, comprises a PRO364 or PRO175 polypeptide -  
 PT Claim 1; Fig 1; 76pp; English.  
 PS This sequence represents PRO364 polypeptide, which is a human gluco-  
 CC corticoid-induced tumor necrosis factor receptor (hGTR). The  
 CC corresponding ligand (hGTRL), PRO175, is given in AAB47056.  
 CC PRO364 and PRO175 may be used in a mixture with a cardiovascular,  
 CC endothelial, angiogenic or angiostatic agent for the treatment of a  
 CC cardiovascular, endothelial, angiogenic or angiostatic disorder. The  
 CC PRO364 CDNA sequence was isolated from an expressed sequence tag (EST)  
 CC database as having homology to members of the tumour necrosis factor  
 CC receptor (TNFR) family of polypeptides. The PRO175 cDNA sequence was  
 CC isolated from a library of cDNA fragments derived from human umbilical  
 CC vein endothelial cells (HUVEC). Administering an effective amount of  
 CC PRO364 or PRO175 or their antagonists is useful for treating cardiac  
 CC hypertrophy (which is initiated by myocardial infarction and  
 CC characterized by the presence of an elevated level of PGE<sub>2</sub>alpha),  
 CC trauma, a cancer, or age-related macular degeneration in a human.  
 CC Administering a therapeutically effective amount of an antibody that  
 CC binds PRO364 or PRO175 is useful for inhibiting angiogenesis induced  
 CC by PRO364 or PRO175 in a human suffering from a tumor or a retinal  
 CC disorder. PRO364 or PRO175, or their antagonists, are useful for  
 CC vascular-related drug targeting or as therapeutic targets for the  
 CC treatment or prevention of atherosclerosis, hypertension, inflammatory  
 CC vasculitides, Reynaud's disease, aneurysms, arterial restenosis,  
 CC thrombophlebitis, tumor angiogenesis, gut protection or regeneration  
 CC and treatment of lung or liver fibrosis, periodontal diseases,  
 CC attraction of bone-forming cells, central and peripheral nervous  
 CC system disease and neuropathies and rheumatoid arthritis.  
 XX  
 SQ Sequence 241 AA;

Query Match 100.0%; Score 255; DB 22; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-20;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLGTGTGTCRCRVTTCRCRDYPCGECSCSEWDCM 41  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 33 GCGPGRLLGTGTGTCRCRVTTCRCRDYPCGECSCSEWDCM 73

RESULT 15

AAB50910

ID AAB50910 standard; Protein; 241 AA.

XX AC AAB50910;

XX DT 21-MAR-2001 (first entry)

XX DE Human PRO364 protein.

XX KW Human; PRO; antiinflammatory; dermatological; antiarthritic;

XX KW antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;

KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;  
 KW antiallergic; antiasthmatic; immune related disorder;  
 XX hepatobiliary disease; autoimmune disease; allergy.  
 OS Homo sapiens.

XX W0200073452-A2.  
 XX 07-DEC-2000.  
 XX 02-JUN-2000; 2000WO-US15264.

XX 02-JUN-1999; 99WO-US12252.  
 PR 20-JUL-1999; 99US-0144732.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.

(GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;  
 PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;  
 PI Wood WI;

WPI; 2001-025253/03.  
 N-PSDB; AAC91469.

XX Thirty three nucleic acids encoding PRO polypeptides which are useful  
 PT in the diagnosis and treatment of immune related disorders, e.g.  
 PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 PT thyroiditis and diabetes mellitus -

Claim 58; Fig 18; 218pp; English.

The present sequence is one of thirty three novel PRO polypeptides.  
 The PRO polypeptides, anti-PRO antibodies, agonists and  
 antagonists are useful for treating and diagnosing immune related  
 disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
 osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,  
 immune-mediated renal disease, demyelinating diseases of the central  
 and peripheral nervous systems (such as multiple sclerosis, idiopathic  
 demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic  
 inflammatory demyelinating polyneuropathy), hepatobiliary diseases  
 (such as infectious, autoimmune chronic active hepatitis, primary  
 biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
 inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
 disease, autoimmune or immune-mediated skin diseases (such as bullous  
 skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
 allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
 food hypersensitivity and urticaria), immunological diseases of the

XX AAB201115;  
AC 30-APR-2001 (first entry)  
DT Human immunostimulant PRO364.  
DE  
XX PRO364; UNQ319; human; immune disease; autoimmune disease;  
KW antirheumatic; antiarthritic; antiinflammatory; antianemic;  
KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;  
KW hepatotropic; virucide; dermatological; antipsoriatic;  
KW antiasthmatic; antiallergic; immunostimulant.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..25  
FT Protein /label= Signal\_peptide  
FT 26..241  
FT Domain /label= Mature\_protein  
FT 163..183  
FT Modified-site /note= "transmembrane domain"  
FT 5..11  
FT Modified-site /note= "N-myristoylation site"  
FT 8..14  
FT Modified-site /note= "N-myristoylation site"  
FT 25..31  
FT Modified-site /note= "N-myristoylation site"  
FT 30..36  
FT Modified-site /note= "N-myristoylation site"  
FT 33..39  
FT Modified-site /note= "N-myristoylation site"  
FT 118..124  
FT Modified-site /note= "N-myristoylation site"  
FT 122..128  
FT Modified-site /note= "N-myristoylation site"  
FT 156..162  
FT Modified-site /note= "N-myristoylation site"  
FT 146..150  
FT Modified-site /note= "Asn is N-glycosylated"  
FT 166..177  
FT Peptide /note= "prokaryotic membrane lipoprotein lipid  
FT attachment site"  
FT 171..193  
FT Peptide /note= "leucine zipper pattern"  
XX  
PN WO200105972-A1.  
XX  
XX 25-JAN-2001.  
XX  
XX 15-MAR-2000; 2000WO-US06884.  
XX  
XX 20-JUL-1999; 99US-0144758.  
XX  
XX (GETH) GENENTECH INC.  
XX PA  
XX Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;  
XX Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK;  
XX Wood WI;  
XX WPI; 2001-103149/11.  
XX N-PSDB; AAF30057.  
XX  
XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
XX diagnosing and treating immune-related disorders, such as multiple  
XX sclerosis, rheumatoid arthritis and diabetes -  
XX  
XX Claim 20; Fig 16; 127pp; English.  
XX  
XX The present sequence is that of novel human immunomodulator PRO364  
XX (UNQ319), as deduced from cDNA (see AAF30057) isolated from a  
XX small intestine library. PRO364 (26 kDa, pI 6.34) shows sequence  
XX homology to mouse G1NR protein and may be its human counterpart.

CC The invention provides polynucleotides (see AAF30050-62) encoding  
CC novel human PRO proteins (see AAB20108-20) including PRO364.  
CC Claimed compositions comprising these proteins or their agonists  
CC are useful for increasing infiltration of inflammatory cells into  
CC a tissue of a mammal, stimulating or enhancing an immune  
CC response, or increasing the proliferation of T-lymphocytes in a  
CC mammal in response to an antigen. Claimed compositions comprising  
CC a PRO polypeptide or its antagonist have the opposite effect. A  
CC claimed method for treating an immune related disorder, such as a T  
CC cell disorder, involves administering a PRO polypeptide, an agonist  
CC antibody or an antagonist antibody. The disorder is selected from  
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
CC juvenile chronic arthritis, spondyloarthritis, systemic sclerosis,  
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
CC thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated  
CC renal disease, demyelinated diseases (such as multiple sclerosis),  
CC autoimmune chronic active hepatitis, primary biliary cirrhosis,  
CC granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel  
CC disease (ulcerative colitis and Crohn's disease), gluten-sensitive  
CC enteropathy, Whipple's disease, (auto)immune-mediated skin diseases  
CC (such as bullous skin disease, erythema multiforme and psoriasis),  
CC allergic diseases (such as asthma, allergic rhinitis, atopic  
CC dermatitis, food hypersensitivity and urticaria), immunologic  
CC diseases of the lung and transplantation associated diseases (such  
CC as graft rejection and graft-versus-host disease) (all claimed).  
CC Claimed methods of diagnosing these disorders comprise detecting  
CC the level of expression of the PRO gene. Also claimed are a method  
CC of identifying a compound capable of inhibiting the expression or  
CC activity of the PRO polypeptide, vectors, host cells, antibodies,  
CC and a method of stimulating the proliferation of T lymphocytes  
CC using PRO364.  
XX  
XX Sequence 241 AA;

Query Match 100.0%; Score 255; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 6.4e-20;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGRLLLGCTDARCCRVHTTCCRDYPGEECCSEWDCM 41  
|||||  
Db 33 gcgpglllgtgttdarccrvhttrccrdypgeccsewdcm 73

RESULT 14  
AAB47054  
ID AAB47054 standard; Protein; 241 AA.  
XX  
AC AAB47054;

DT 08-MAY-2001 (first entry)  
XX  
XX Human PRO364.

PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;  
KW hG1TR; ligand; hG1TRL; PRO175; tumor necrosis factor receptor; TNFR;  
KW human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;  
KW myocardial infarction; PGF\_2alpha; trauma; cancer; angiogenesis;  
KW age-related macular degeneration; antibody; periodontal disease;  
KW vascular-related drug targeting; atherosclerosis; hypertension;  
KW inflammatory vasculitides; Reynaud's disease; aneurysm;  
KW arterial restenosis; thrombophlebitis; tumor angiogenesis;  
KW lung; liver; fibrosis; neuropathy; rheumatoid arthritis.  
XX  
OS Homo sapiens.

XX Key Location/Qualifiers  
FH Peptide 1..26  
FT /note= "Potential signal peptide"  
FT Modified-site 146  
FT /note= "N-glycosylated"  
FT Domain 162..180

Sequence 241 AA;  
SQ

QY I GCGPGRLELGGTGDARCCRVHTTRCCRDYPGEECCSEWDCM 41  
|||||

Job time: 341 sec

CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
CC antagonists (e.g. antibodies) are used to treat, prevent, prognose  
CC and/or diagnose an autoimmune disease, especially rheumatoid  
CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
CC antibodies can be administered to cells in vitro, ex vivo or in  
CC vivo or to a multicellular organism. Soluble forms of the  
CC polypeptides may also be used. Methods for screening for  
CC agonist/antagonist compounds are also provided.  
XX  
SQ Sequence 234 AA;

Query Match 100.0%; Score 753; DB 21; Length 234;  
Best Local Similarity 100.0%; Pred. No. 2.8e-55;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTGDARCCRVHTTRCCRDYDYGEECCSEWDCMCVQPFHCGDPCCTTCRHH 60  
DB |||||  
DB 33 GCGPGRLLLTGTGDARCCRVHTTRCCRDYDYGEECCSEWDCMCVQPFHCGDPCCTTCRHH 92  
QY 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTCTQFGFLTVPFGNKTNAV 120  
DB |||||  
DB 93 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTCTQFGFLTVPFGNKTNAV 152  
QY 121 CV 122  
DB ||  
DB 153 CV 154

RESULT 3  
AAV52158  
ID AAY52158 standard; Protein; 234 AA.  
XX  
AC AAY52158;  
XX  
DT 01-FEB-2000 (first entry)  
XX  
DE Tumour necrosis factor receptor-like protein (TR11) amino acid sequence.  
XX  
KW Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2;  
KW GTR; growth; differentiation; cell death; immune deficiency disorder;  
KW Digeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia;  
KW Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes;  
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;  
KW inflammatory condition.  
XX  
OS Homo sapiens.

Key Location/Qualifiers  
FT 1..25 /label= Signal\_peptide  
FT 26..234 /label= TR11  
FT 26..162 /note= "Extracellular domain"  
FT 163..179 /note= "Transmembrane domain"  
FT 180..234 /note= "Intracellular domain"  
FT  
FT  
XX WO9920758-A1.  
XX  
XX 29-APR-1999.  
XX  
XX 21-OCT-1998; 98WO-US22085.  
XX  
XX 21-OCT-1997; 97US-0063212.  
PR  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX N1 J, Ruben SM;

XX  
DR WPI; 2000-061922/05.  
DR N-PSDB; AA237762.  
XX  
PT New tumour necrosis factor receptor-like polypeptides used to, e.g.  
PT treat Digeorge syndrome -  
XX  
PS Claim 14; Fig 1; 167pp; English.  
XX  
XX This is the amino acid sequence of the human tumour necrosis factor  
CC receptor-like protein (TR11 receptor). The invention relates to TR11 and  
CC two splice variants TR11SV1 and TR11SV2. The nucleotide sequences were  
CC determined by sequencing cloned cDNAs AA237765-237766. The TR11 receptor  
CC and its splice variants show homology to the murine glucocorticoid  
CC induced tumour necrosis factor receptor family-related gene (GTR).  
CC TR11, TR11SV1 and TR11SV2 polypeptides may be involved in the regulation  
CC of cell-type specific receptor-mediated cell growth, differentiation,  
CC and ultimately, cell death. They can be used for screening for  
CC agonists/antagonists. The polypeptides, agonists or antagonists can be  
CC used for treating a disease state associated with aberrant cell  
CC survival. They can be used for treating immune deficiency disorders,  
CC Digeorge syndrome, HIV infection, severe combined immunodeficiency  
CC (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood  
CC platelet disorders or wounds resulting from trauma or surgery. They can  
CC also be used to treat heart attacks, strokes, Addison's disease,  
CC haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's  
CC disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome,  
CC systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent  
CC diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,  
CC hypersensitivity to an antigenic molecule, organ rejection or graft  
CC versus host disease, inflammatory conditions, ischaemia-reperfusion  
CC injury, complement-mediated hyperacute rejection, nephritis, cytokine or  
CC chemokine induced lung injury, inflammatory bowel disease, Crohn's  
CC disease, hyperproliferative disorders, or infections. They can also be  
CC used to repair, replace, or protect tissue damaged by congenital  
CC defects, trauma, age, disease, surgery, including cosmetic plastic  
CC surgery, fibrosis, reperfusion injury, peripheral nerve injuries,  
CC neuropathies, and central nervous system disease (e.g. Alzheimer's  
CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral  
CC sclerosis, and Shy-Drager syndrome). The products can also be used for  
CC detection, diagnosis and prognosis.  
XX  
SQ Sequence 234 AA;

Query Match 100.0%; Score 753; DB 21; Length 234;  
Best Local Similarity 100.0%; Pred. No. 2.8e-55;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTGDARCCRVHTTRCCRDYDYGEECCSEWDCMCVQPFHCGDPCCTTCRHH 60  
DB |||||  
DB 33 GCGPGRLLLTGTGDARCCRVHTTRCCRDYDYGEECCSEWDCMCVQPFHCGDPCCTTCRHH 92  
QY 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTCTQFGFLTVPFGNKTNAV 120  
DB |||||  
DB 93 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTCTQFGFLTVPFGNKTNAV 152  
QY 121 CV 122  
DB ||  
DB 153 CV 154

RESULT 4  
AAV44825  
ID AAY44825 standard; Protein; 235 AA.  
XX  
AC AAY44825;  
XX  
DT 18-MAY-2000 (first entry)  
XX  
DE Human molecule associated with cell proliferation, MACP-5.  
XX  
XX Human; molecule associated with cell proliferation; MACP-5;  
KW

KW Incyte clone 2809903; antiarteriosclerotic; hepatotropic; cytostatic;  
 KW anti-inflammatory; antiproliferative; anti-HIV; antitumor; anemic;  
 KW dermatological; antidiabetic; nephrotropic; antithyroid; thyromimetic;  
 KW immunosuppressive; osteopathic; antiarthritic; uropathic; antitumor;  
 KW ophthalmological; diagnosis; treatment; prevention; immune disorder;  
 KW cell proliferative disorder; actinic keratosis; arteriosclerosis;  
 KW atherosclerosis; bursitis; hepatitis; Crohn's disease; amyloidosis.  
 XX  
 XX Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
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 FT /label= Signature\_sequence  
 FT 68..96  
 FT /label= Signature\_sequence  
 FT 109..147  
 FT /label= Signature\_sequence  
 FT 122..129  
 FT /label= Signature\_sequence  
 FT 157..175  
 FT /label= Signature\_sequence  
 FT 165..186  
 FT /label= Signature\_sequence  
 FT 37  
 FT /note= "Potential phosphorylation site"  
 FT 48  
 FT /note= "Potential phosphorylation site"  
 FT 62  
 FT /note= "Potential phosphorylation site"  
 FT 82  
 FT /note= "Potential phosphorylation site"  
 FT 205  
 FT /note= "Potential phosphorylation site"  
 FT 223  
 FT /note= "Potential phosphorylation site"  
 FT 140  
 FT /note= "N-glycosylated"  
 XX  
 XX WO200005374-A2.  
 XX  
 XX PD 03-FEB-2000.  
 XX  
 XX PF 21-JUL-1999; 99WO-US16637.  
 XX  
 XX PR 22-JUL-1998; 98US-0093827.  
 XX  
 XX PA (INCY-) INCYTE PHARM INC.  
 XX  
 XX PI Tang YT, Lal P, Hillman JL, Corley NC, Patterson C, Baughn MR;  
 XX WPI; 2000-182699/16.  
 XX N-PSDB; AA249948.  
 DR  
 DR Polypeptides and polynucleotides useful for treating and detecting cell  
 PT proliferation disorders e.g. actinic keratosis, and immune disorders  
 PT e.g. Crohn's disease  
 XX  
 XX Claim 1; Pages 64-65; 67pp; English.  
 XX  
 XX The present sequence is a molecule associated with cell  
 CC proliferation, MACP-5 from incyte clone 2809903 isolated from TLYMN0706  
 CC CDNA library. This sequence is expressed in cardiovascular and  
 CC haematopoietic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV,  
 CC hepatotropic, antiinflammatory, antiproliferative, cytostatic, antitumor,  
 CC dermatological, antidiabetic, nephrotropic, antithyroid, thyromimetic,  
 CC immunosuppressive, osteopathic, antiarthritic, uropathic, antitumor,  
 CC and ophthalmological activities. The present sequence is useful in the  
 CC diagnosis, treatment and prevention of cell proliferative disorders e.g.  
 CC actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and  
 CC hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and  
 CC anaemia.  
 XX  
 XX Sequence 235 AA;

Query Match 100.0%; Score 753; DB 21; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-55;  
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GCGPRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60  
 Db 27 GCGPRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 86  
 Qy 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTCTQFGFLTVPFGNKTHNAV 120  
 Db 87 PCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTCTQFGFLTVPFGNKTHNAV 146  
 Qy 121 CV 122  
 Db 147 CV 148  
 RESULT 5  
 AAW37839  
 ID AAW37839 standard; Protein; 241 AA.  
 XX  
 AC AAW37839;  
 XX  
 XX 28-JUL-1998 (first entry)  
 XX  
 DE Amino acid sequence of the human 312C2 T cell protein.  
 XX  
 KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 KW antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
 KW auto-immune disorders.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..726  
 FT /\*tag= a  
 FT /product= "human 312C2 protein"  
 XX  
 XX WO9806842-A1.  
 XX  
 XX PD 19-FEB-1998.  
 XX  
 XX PF 14-AUG-1997; 97WO-US13931.  
 XX  
 XX PR 07-OCT-1996; 96US-0027901.  
 XX PR 16-AUG-1996; 96US-0689943.  
 XX  
 XX PA (SCHE) SCHERING CORP.  
 XX  
 XX Gorman DM, Randall TD, Zlotnik A;  
 XX WPI; 1998-159534/14.  
 XX DR N-PSDB; AAV19153.  
 XX  
 XX Isolated 312C2 T cell gene - used to develop products for treating,  
 PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 PT other T cell disorders  
 XX  
 XX Claim 2; Pages 59-60; 71pp; English.  
 XX  
 XX This is the amino acid sequence encoding the human 312C2 T cell  
 CC protein. The 312C2 proteins are expressed in thymus cells and are  
 CC induced on T cells and spleen cells following activation. Engagement  
 CC of 312C2 stimulates proliferation of T cell clones, antigen-specific  
 CC proliferation and cytokine production by T-cells, and potentiates T  
 CC cell expansion or apoptosis. The products can be used in the  
 CC treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells

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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:56:23 ; Search time 136.12 Seconds  
(without alignments)  
58.644 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_33\_154

Perfect score: 753

Sequence: 1 GCGPRLLLGTGTARCCRV.....TQGFGLTVFGNKTHNAVCV 122

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_0601.\*

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- 3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*
- 4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*
- 5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*
- 6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*
- 7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*
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- 14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.\*
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- 19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*
- 20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*
- 21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*
- 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	753	100.0	228	19 AAW37840	Truncated human 31
2	753	100.0	234	21 AAY95879	Human tumour necro
3	753	100.0	234	21 AAY52158	Tumour necrosis fa
4	753	100.0	235	21 AAY44825	Human molecule ass
5	753	100.0	241	19 AAW37839	Amino acid sequenc
6	753	100.0	241	20 AAY06605	Human TNF receptor
7	753	100.0	241	21 AAB27651	Human protein PRO3
8	753	100.0	241	21 AAB33431	Human PRO364 prote
9	753	100.0	241	21 AAY95895	Human tumour necro
10	753	100.0	241	21 AAB24409	Human PRO364 prote
11	753	100.0	241	21 AAY71467	Human PRO364 prote

12	753	100.0	241	22 AAB20115	Human immunostimul
13	753	100.0	241	22 AAB47054	Human PRO364. Hom
14	753	100.0	241	22 AAB50910	Human PRO364. Hom
15	753	100.0	241	22 AAB50982	Human PRO364. Hom
16	753	100.0	241	22 AAB53090	Human anglogenesis
17	753	100.0	311	19 AAW37842	Human 312C2 protel
18	737	97.9	240	21 AAY95881	Human tumour necro
19	737	97.9	240	21 AAY52160	Human tumour necro
20	703	93.4	316	22 AAB47055	TR11SV2 amino acid
21	703	93.4	317	20 AAY06645	POLYPEPTIDE ENCODE
22	579.5	77.0	241	21 AAY95880	PRO364-related EST
23	579.5	77.0	241	21 AAY52159	Human tumour necro
24	468	62.2	232	19 AAW37841	TR11SV1 amino acid
25	445.5	59.2	222	19 AAW49018	Human 312C2 protel
26	445.5	59.2	228	19 AAW49016	Mouse glucocorticoid
27	445.5	59.2	228	19 AAW37838	Mouse glucocorticoid
28	445.5	59.2	294	19 AAW49017	Amino acid sequenc
29	212.5	28.2	89	21 AAY76013	Mouse glucocorticoid
30	212.5	28.2	89	22 AAB55952	Murine TNF-alpha f
31	164	21.8	206	16 AAR81881	Skin cell protein,
32	164	21.8	206	16 AAW48977	Mouse type-II memb
33	164	21.8	438	16 AAR81882	Mouse OX40 extrace
34	164	21.8	438	19 AAW48976	Plasmid pDC406/OX4
35	154	20.5	300	21 AAB03622	OX40/Fc mutein. C
36	154	20.5	300	21 AAB03623	Monkey Fas ligand
37	152.5	20.3	255	16 AAR70977	Human Fas ligand i
38	152.5	20.3	255	16 AAR64197	H4-11B receptor pr
39	152.5	20.3	255	18 AAW26658	Human 4-11B polype
40	152.5	20.3	255	20 AAY33214	Human 4-11B recept
41	152.5	20.3	255	20 AAY28688	Human CD137 protel
42	152.5	20.3	255	22 AAB50521	Human receptor pro
43	151.5	20.1	132	21 AAY94714	Human tumour necro
44	151	20.1	300	21 AAB19710	Tumour necrosis fa
45	151	20.1	300	21 AAY96597	Human Fas ligand i
					Human FLINT. Homo

ALIGNMENTS

RESULT 1  
AAW37840  
ID AAW37840 standard; Protein; 228 AA.  
XX  
AC AAW37840;  
XX  
DT 28-JUL-1998 (first entry)  
XX  
DE Truncated human 312C2 protein from clone\_A8 amino acid sequence.  
XX  
KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
KW antigen-specific T cell proliferation; cytokine production by T-cell;  
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
KW autoimmune disorders.  
XX  
OS Homo sapiens.  
XX  
PN WO9806842-A1.  
XX  
PD 19-FEB-1998.  
XX  
PF 14-AUG-1997; 97WO-US13931.  
XX  
PR 07-OCT-1996; 96US-0027901.  
PR 16-AUG-1996; 96US-0689943.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Gorman DM, Randall TD, Zlotnik A;  
XX  
DR WPI; 1998-159534/14.  
DR N-PSDB; AAV19154.  
XX  
PT Isolated 312C2 T cell gene - used to develop products for treating,

PT	e.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders
XX	Disclosure; Pages 61-62; 71pp; English.
XX	This is the amino acid sequence of the truncated human 312C2 T cell protein from clone A8. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation.
XX	CC Engagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders.
XX	Sequence 228 AA;
XX	Query Match 100.0%; Score 753; DB 19; Length 228;
XX	Best Local Similarity 100.0%; Pred. No. 2.8e-55;
XX	Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GCGPRLLLGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTCRHH 60
DB	27 GCGPRLLLGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTCRHH 86
QY	61 PCPPGQVQSGKSFQFCIDCAGTFSGGHEGCKRPWTDCTQFGFLTVPFGNKTNAV 120
DB	87 PCPPGQVQSGKSFQFCIDCAGTFSGGHEGCKRPWTDCTQFGFLTVPFGNKTNAV 146
QY	121 CV 122
DB	147 CV 148
RESULT	2
AAAY95879	
ID	AAAY95879 standard; Protein; 234 AA.
XX	AAAY95879;
XX	20-NOV-2000 (first entry)
XX	Human tumour necrosis factor receptor-like protein TR11.
XX	Tr11; human; tumour necrosis factor receptor-like protein; immunodeficiency; autoimmune disease; rheumatoid arthritis; immunosuppressive; antirheumatic; antiarthritic; haemostatic; dermatological; antiinflammatory; therapy; diagnosis.
XX	Homo sapiens.
XX	Key Location/Qualifiers
FT	Peptide 1..25
FT	/label= Signal_peptide
FT	26..234
FT	/label= Mature_protein
FT	26..162
FT	/label= Extracellular_domain
FT	163..179
FT	/label= Transmembrane_domain
FT	180..234
FT	/label= Intracellular_domain
FT	Modified-site 146
FT	/note= "N-glycosylated"
FT	Domain 72..81
FT	/note= "conserved domain CD-II"
FT	Domain 84..93
FT	/note= "conserved domain CD-III"
FT	Domain 107..113
FT	/note= "conserved domain CD-IV"

PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 XX (GETH ) GENENTECH INC.  
 XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL; Gurney AL; Hebert C, Hienzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK; Wood WI;  
 XX WPI; 2001-025253/03.  
 DR N-PSDB; AAC91469.  
 XX Thirty three nucleic acids encoding PRO polypeptides which are useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
 XX Claim 58; Fig 18; 218pp; English.  
 XX The present sequence is one of thirty three novel PRO polypeptides.  
 CC The PRO polypeptides, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems (such as multiple sclerosis, idiopathic demyelinating polynuropathy or Guillain-Barre syndrome, and chronic inflammatory demyelinating polynuropathy), hepatobiliary diseases (such as infectious, autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis), inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases (such as bullous skin diseases, erythema multiforme, contact dermatitis, psoriasis), allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria), immunological diseases of the lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonitis), transplantation associated diseases including graft rejection and graft-versus-host diseases.  
 XX Sequence 241 AA;  
 SQ  
 Query Match 100.0%; Score 753; DB 22; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-55;  
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CGCGPRLLLGTGDARCCRVHTRCCRDYPGECCEWDCMCVQPFHCGDPCCTCRHH 60  
 Db |||||  
 33 gcgpglllgtgdarcrcrvhtrccrdypgeccsewdcmcvqpfhcgdpccctcrhh 92  
 Qy 61 PCPPQGVQSQGKSFQFCIDACSTGSGHGHCCKPWTDCFTQCFGLVFPGNKTHNAV 120  
 Db |||||  
 93 pcppqgvqsgkqkfsgfqcldcasgftfsgghgchckpwcddctqfglvfpgnkchnav 152  
 Qy 121 CV 122  
 Db ||  
 153 cv 154  
 RESULT 15  
 AAB50982  
 ID AAB50982 standard; Protein; 241 AA.  
 AC AAB50982;  
 XX  
 XX 21-MAR-2001 (first entry)  
 DT  
 XX Human PRO364 protein.

XX Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive; vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic; vulnery; antiangular; gene therapy; cardiovascular disease; endothelial disorder; angiogenic disorder; cancer; periodontal disease; wound healing.  
 XX Homo sapiens.  
 OS  
 PN WO200073445-A2.  
 XX  
 XX 07-DEC-2000.  
 XX  
 XX 17-MAY-2000; 2000WO-US13705.  
 XX  
 XX 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 15-MAR-2000; 2000WO-US06319.  
 PR 21-MAR-2000; 2000WO-US06884.  
 PR 30-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 XX (GETH ) GENENTECH INC.  
 XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME; Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA; Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
 XX WPI; 2001-025251/03.  
 DR N-PSDB; AAC90566.  
 XX Seventeen nucleic acids encoding PRO polypeptides which are useful in diagnosis and treatment of cardiovascular, endothelial or angiogenic disorders in a mammal -  
 XX Claim 71; Fig 8; 182pp; English.  
 XX The present sequence is one of seventeen novel PRO polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating cardiovascular, endothelial or angiogenic disorders in a mammal. Examples of these disorders include cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and antagonists are also used to prevent tumour angiogenesis and for treating periodontal diseases. They are also used to stimulate wound healing and tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO antibodies are useful for diagnosing a cardiovascular, endothelial or angiogenic disorder.  
 XX Sequence 241 AA;  
 SQ

Query Match 100.0%; Score 753; DB 22; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-55;  
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CGCGPRLLLGTGDARCCRVHTRCCRDYPGECCEWDCMCVQPFHCGDPCCTCRHH 60  
 Db |||||  
 33 gcgpglllgtgdarcrcrvhtrccrdypgeccsewdcmcvqpfhcgdpccctcrhh 92



Qy	61	PCPGQVQSGKSFQFCIDCA	SGTFSGCGHGHCKPWT	CTQFGFLTVFPGNKTHNAV	120
Db	93	PCPPGQVQSGKFSFGICD	CSGTFSGHGHCKPWT	CTQFGFLTVFPGNKTHNAV	152
Qy	121	CV	122		
Db	153	CV	154		

Search completed: September 4, 2001, 15:56:23  
Job time: 340 sec



Db 153 cv 154  
RESULT 13  
AAB47054  
ID AAB47054 standard; Protein; 241 AA.  
XX AAB47054;  
AC AAB47054;  
XX  
XX 08-MAY-2001 (first entry)  
DT  
XX Human PRO364.  
DE  
XX PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;  
KW hGTR; ligand; hGTR; PRO175; tumour necrosis factor receptor; TNFR;  
KW human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;  
KW myocardial infarction; PGF\_2alpha; trauma; cancer; angiogenesis;  
KW age-related macular degeneration; antibody; periodontal disease;  
KW vascular-related drug targeting; atherosclerosis; hypertension;  
KW inflammatory vasculitides; Reynaud's disease; aneurysm;  
KW arterial restenosis; thrombophlebitis; tumor angiogenesis;  
KW lung; liver; fibrosis; neuropathy; rheumatoid arthritis.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..26  
FT /note= "Potential signal peptide"  
FT Modified-site 146  
FT /note= "N-glycosylated"  
FT Domain 162..180  
FT /note= "Potential transmembrane domain"  
XX  
XX WO200103720-A2.  
XX  
XX 18-JAN-2001.  
XX  
XX 11-JUL-2000; 2000WO-US18867.  
XX  
XX 12-JUL-1999; 99US-0143304.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Williams PM, Gerritsen ME;  
XX  
XX WPI: 2001-138257/14.  
XX  
XX N-PSDB; AAC85433.  
XX  
XX Composition for diagnosing and treating cardiovascular, endothelial and  
XX PT angiogenic disorders, comprises a PRO364 or PRO175 polypeptide -  
XX  
XX Claim 1; Fig 1; 76pp; English.  
XX  
XX This sequence represents PRO364 polypeptide, which is a human gluco-  
XX CC corticoid-induced tumor necrosis factor receptor (hGTR). The  
XX CC corresponding ligand (hGTR), PRO175, is given in AAB47056.  
XX CC PRO364 and PRO175 may be used in a mixture with a cardiovascular,  
XX CC endothelial, angiogenic or angiostatic agent for the treatment of a  
XX CC cardiovascular, endothelial, angiogenic or angiostatic disorder. The  
XX CC PRO364 cDNA sequence was isolated from an expressed sequence tag (EST)  
XX CC database as having homology to members of the tumour necrosis factor  
XX CC receptor (TNFR) family of polypeptides. The PRO175 cDNA sequence was  
XX CC isolated from a library of cDNA fragments derived from human umbilical  
XX CC vein endothelial cells (HUVEC). Administering an effective amount of  
XX CC PRO364 or PRO175 or their antagonists is useful for treating cardiac  
XX CC hypertrophy (which is initiated by myocardial infarction and  
XX CC characterized by the presence of an elevated level of PGF\_2alpha),  
XX CC trauma, a cancer, or age-related macular degeneration in a human.  
XX CC Administering a therapeutically effective amount of an antibody that  
XX CC binds PRO364 or PRO175 is useful for inhibiting angiogenesis induced  
XX CC by PRO364 or PRO175 in a human suffering from a tumor or a retinal  
XX CC disorder. PRO364 or PRO175, or their antagonists, are useful for

CC vascular-related drug targeting or as therapeutic targets for the  
CC treatment or prevention of atherosclerosis, hypertension, inflammatory  
CC vasculitides, Reynaud's disease, aneurysms, arterial restenosis,  
CC thrombophlebitis, tumor angiogenesis, gut protection or regeneration  
CC and treatment of lung or liver fibrosis, periodontal diseases,  
CC attraction of bone-forming cells, central and peripheral nervous  
CC system disease and neuropathies and rheumatoid arthritis.  
XX  
XX Sequence 241 AA;  
SQ  
Query Match 100.0%; Score 753; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2.9e-55;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCGPRLGLLTGTARCCRVHTTRCCRDYPGECSCSEWDCMCVQPEFHGDCPCCTTCRHH 60  
|||||  
Db 33 gcgprlllgtgdarcervhttrccrdypgeccsewdcmcvqefhgdcpccttcrhh 92  
|||||  
Qy 61 PCPPGGVQVSGGKFSFGFCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVPFGNKTHNAV 120  
|||||  
Db 93 pcppggvqvggkfsfgfcidcasgtfsggheghckpwtctqfgfltvpfgnkthnav 152  
|||||  
Qy 121 CV 122  
||  
Db 153 cv 154  
RESULT 14  
AAB50910  
ID AAB50910 standard; Protein; 241 AA.  
XX AAB50910;  
XX  
XX 21-MAR-2001 (first entry)  
DT  
XX Human PRO364 protein.  
DE  
XX Human; PRO; antiinflammatory; dermatological; antiarthritic;  
KW antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;  
KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;  
KW antiallergic; antiasthmatic; immune related disorder;  
KW hepatobiliary disease; autoimmune disease; allergy.  
XX  
XX Homo sapiens.  
XX  
XX OS  
XX WO200073452-A2.  
XX  
XX 07-DEC-2000.  
XX  
XX 02-JUN-2000; 2000WO-US15264.  
XX  
XX 02-JUN-1999; 99WO-US12252.  
XX 20-JUL-1999; 99US-0144732.  
XX 28-JUL-1999; 99US-0144736.  
XX 01-SEP-1999; 99US-0146222.  
XX 15-SEP-1999; 99WO-US20111.  
XX 15-SEP-1999; 99WO-US21090.  
XX 15-SEP-1999; 99WO-US21547.  
XX 29-OCT-1999; 99US-0162506.  
XX 30-NOV-1999; 99WO-US28313.  
XX 01-DEC-1999; 99WO-US28634.  
XX 09-DEC-1999; 99US-0170262.  
XX 20-DEC-1999; 99WO-US30911.  
XX 05-JAN-2000; 2000WO-US00219.  
XX 06-JAN-2000; 2000WO-US00376.  
XX 11-FEB-2000; 2000WO-US03565.  
XX 18-FEB-2000; 2000WO-US04341.  
XX 22-FEB-2000; 2000WO-US04342.  
XX 24-FEB-2000; 2000WO-US04414.  
XX 15-MAR-2000; 2000WO-US04914.  
XX 20-MAR-2000; 2000WO-US06884.  
XX 20-MAR-2000; 2000WO-US07377.

anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AAC58397 to AAC58578 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAC33414 to AAB33477 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.

Sequence 241 AA;

Query Match 100.0%; Score 753; DB 21; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2.9e-55;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGPGRLLLTGTDCRCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60  
|||||  
Db 33 gcgprlllgtgdarcrcrvhttrccrdypgeccsewdcmcvqpefhcgdpccctcrhh 92

Qy 61 PCPPGGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTCTQFGFLTVFPGNKTHNAV 120  
|||||  
Db 93 pcppggvqsgkfsgfsgfcidcasgtfsgghegchkpwtcdctqfgfltvfpgnkthnav 152

Qy 121 CV 122

Db 153 CV 154

RESULT 9

AAY95895  
ID AAY95895 standard; Protein; 241 AA.

AC AAY95895;

DT 20-NOV-2000 (first entry)

DE Human tumour necrosis factor receptor-like protein TR11 mutein.

XX TR11; human; tumour necrosis factor receptor-like protein;  
KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
KW dermatological; antiinflammatory; therapy; diagnosis; mutein;  
KW mutant.

XX Homo sapiens.

XX WO200050459-A1.

XX PD 31-AUG-2000.

XX PF 23-FEB-2000; 2000WO-US04572.

XX PR 24-FEB-1999; 99US-0121648.

XX PR 13-MAY-1999; 99US-0134172.

XX PR 16-JUL-1999; 99US-0144076.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, NI J;

XX DR WPI; 2000-572072/53.

XX Human tumor necrosis factor receptor-like proteins useful for  
PT diagnosis, prevention and treatment of disease states associated with  
PT aberrant cell survival such as autoimmune disease and rheumatoid  
PT arthritis

XX Disclosure; 294-295; 278pp; English.

CC The present sequence is that of human tumour necrosis factor  
CC receptor-like protein TR11 (see also AAY95879), a novel protein  
CC showing identity to murine glucocorticoid induced tumour necrosis  
CC factor receptor family-related gene. The invention provides  
CC highly conserved TR11, TR11SV1 and TR11SV2 proteins (see AAY95879-81),  
CC as well as vectors, host cells and recombinant methods for their  
CC production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful  
CC for treating, preventing, prognosis and/or diagnosis of an  
CC immunodeficiency, especially common variable immunodeficiency,  
CC X-linked agammaglobulinemia, severe combined immunodeficiency  
CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
CC and/or diagnose an autoimmune disease, especially rheumatoid  
CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
CC or IGA nephropathy. The polypeptides, polynucleotides and/or  
CC antibodies can be administered to cells in vitro, ex vivo or in  
CC vivo or to a multicellular organism. Soluble forms of the  
CC polypeptides may also be used. Methods for screening for  
CC agonist/antagonist compounds are also provided.

Sequence 241 AA;

Query Match 100.0%; Score 753; DB 21; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2.9e-55;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGPGRLLLTGTDCRCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHH 60  
|||||  
Db 33 gcgprlllgtgdarcrcrvhttrccrdypgeccsewdcmcvqpefhcgdpccctcrhh 92

Qy 61 PCPPGGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTCTQFGFLTVFPGNKTHNAV 120  
|||||  
Db 93 pcppggvqsgkfsgfsgfcidcasgtfsgghegchkpwtcdctqfgfltvfpgnkthnav 152

Qy 121 CV 122

Db 153 CV 154

RESULT 10

AAB24409

ID AAB24409 standard; Protein; 241 AA.

XX AAB24409;

XX 07-NOV-2000 (first entry)

XX Human PRO364 protein sequence SEQ ID NO:117.

XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
KW cytostatic; gene therapy; vaccine.

XX Homo sapiens.

XX WO200032221-A2.

XX PD 08-JUN-2000.

XX PF 30-NOV-1999; 99WO-US28313.

XX PR 01-DEC-1998; 98WO-US25108.

XX PR 16-DEC-1998; 98US-0112850.

XX PR 12-JAN-1999; 99US-0115554.

XX PR 08-MAR-1999; 99WO-US05028.

XX PR 12-MAR-1999; 99US-0123957.

XX PR 28-APR-1999; 99US-0131445.

XX PR 14-MAY-1999; 99US-0134287.

XX PR 02-JUN-1999; 99WO-US12252.

XX PR 23-JUN-1999; 99US-0141037.



PR 30-NOV-1999; 99WO-US28409.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
 PI Goddard A, Gurney AL, Hillan KJ, Marsters SA, Paoni NF, Pitti RM;  
 PI Watanabe CK, Williams PM, Wood WI;  
 XX  
 DR WPI: 2000-611444/58.  
 DR N-PSDB; AAA99903.  
 XX  
 PT Novel PRO polypeptides and agonists and antagonists of them, used to  
 PT diagnose and treat cardiovascular, endothelial and angiogenic disorders  
 PT -  
 XX  
 PS Claim 71; Fig 6; 181pp; English.  
 XX  
 CC The present invention relates to methods for stimulating or inhibiting  
 CC angiogenesis and cardiovascularization. The methods involve the use of  
 CC pharmaceutical compositions based on the following proteins, PRO179,  
 CC PRO338, PRO364, PRO846, PRO1760, PRO205, PRO321, PRO333,  
 CC PRO840, PRO877, PRO878, PRO879, PRO882, PRO885 or PRO887. These  
 CC proteins were identified by isolating cDNA clones encoding secreted  
 CC proteins. The proteins of the invention may be used to diagnose and  
 CC treat cardiovascular, endothelial or angiogenic disorders. The present  
 CC sequence is one of the proteins of the invention.  
 XX  
 SQ Sequence 241 AA;

Query Match 100.0%; Score 753; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-55;  
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPRLLLGTGTDAKRCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCCTCRHH 60  
 |||||  
 Db 33 gcgpglllgtgtdarccrvhttrccrdygeccsewdcmcvqpefhcgdpccctcrhh 92  
 |||||  
 QY 61 PCPCGCGVQSGKFGFGQICDASGTFSGHGCHKRPWDTCTQFGFLTVPFGNKTHNAV 120  
 |||||  
 Db 93 pcpggvgvsgqkfsfgfqcldcasgtfsgghgchpwtcdtqgtlvtvfgnkthnav 152  
 |||||  
 QY 121 CV 122  
 ||  
 Db 153 cv 154

RESULT 8  
 AAB33431  
 ID AAB33431 standard; Protein; 241 AA.  
 XX  
 AC AAB33431;  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 DE Human PRO364 protein UNQ319 SEQ ID NO:92.  
 XX  
 KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
 KW dermatological; antiarthritic; antirheumatic; immunosuppressive;  
 KW haemostatic; antithyroid; antidiabetic; neuroprotective;  
 KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;  
 KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
 KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;  
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
 KW autoimmune thrombocytopaenia; immune-mediated renal disease;  
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
 KW inflammatory bowel disease; gluten-sensitive enteropathy;  
 KW autoimmune disease; immune-mediated skin disease; allergic disease;  
 KW immunological disease; transplantation associated disease;

KW graft rejection; graft-versus-host-disease.  
 OS Homo sapiens.  
 XX WO2000053758-A2.  
 PN  
 XX 14-SEP-2000.  
 PD  
 XX 02-MAR-2000; 2000WO-US05841.  
 XX 08-MAR-1999; 99WO-US05028.  
 PR 10-MAR-1999; 99US-0123618.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 23-MAR-1999; 99US-0125775.  
 PR 12-APR-1999; 99US-0128849.  
 PR 20-APR-1999; 99WO-US08615.  
 PR 28-APR-1999; 99US-0131445.  
 PR 04-MAY-1999; 99US-0132371.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR  
 XX  
 PA (GETH ) GENENTECH INC.

(GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

WPI: 2000-572271/53.

N-PSDB; AAC58596.

XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -

PS Claim 33; Fig 36; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are  
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthritis,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic

CC which affect immunological responses, e.g. autoimmune disorders.

SQ Sequence 241 AA; Query Match 100.0%; Score 753; DB 19; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-55; Mismatches 0; Indels 0; Gaps 0;  
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCGPGRLLLTGTDAACRCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCTTCRHH 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 33 GCGPGRLLLTGTDAACRCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCTTCRHH 92  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGHGHCCKPWTDCQFGFLTVFPGNKTHNAV 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 93 PCPPGQGVQSGKFSFGFCIDCASGTFSGHGHCCKPWTDCQFGFLTVFPGNKTHNAV 152  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 121 CV 122  
 ||  
 Db 153 cv 154

RESULT 6

AA05605 ID AAY06605 standard; Protein; 241 AA.

XX AC AAY06605;

XX DT 26-OCT-1999 (first entry)

XX DE Human TNF receptor homologue PRO364.

XX KW PRO364; tumour necrosis factor receptor; human; apoptosis;  
 KW inflammation; antiinflammatory; NF-KB activation;  
 KW autoimmune disease; therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 FT Peptide 1..25 /note= "signal peptide"  
 FT Protein 26..241 /note= "mature protein"  
 FT Modified-site 146 /note= "N-glycosylated"  
 FT Domain 162..180 /note= "transmembrane domain"

XX PN WO9940196-A1.

XX PD 12-AUG-1999.

XX PF 09-FEB-1999; 99WO-US02642.

XX PR 09-FEB-1998; 98US-0024087.

XX PA (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;

PI Pitti RM, Wood WI;

XX WPI; 1999-494296/41.

XX DR N-PSDB; AAX87670.

XX PT Tumour necrosis factor receptor homologue - useful for, e.g.  
 PT modulating apoptosis and NF-KB activation and proinflammatory or  
 PT autoimmune responses

PS Claim 17; Fig 2A; 104pp; English.

XX CC The present sequence represents human PRO364, a novel member of the  
 CC tumour necrosis factor receptor family. The sequence was deduced  
 CC from a bone marrow cDNA clone (see AAX87670). Methods for the

CC recombinant production of PRO364 polypeptides, e.g. in CHO,  
 CC Escherichia coli or yeast host cells, are provided. Claimed  
 CC polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the  
 CC mature protein) and 26-X of the present sequence, where X is any  
 CC one of amino acid residues 157-167 of PRO364. PRO364 polypeptides  
 CC are useful for modulating apoptosis, NF-KB activation and  
 CC proinflammatory or autoimmune responses in mammalian cells  
 CC (claimed). Chimeric molecules comprising a PRO364 polypeptide  
 CC fused to a heterologous sequence such as epitope tag or  
 CC immunoglobulin Fc region are also claimed. PRO364 can be used in  
 CC assays to identify other proteins or molecules involved in binding  
 CC interactions. This is useful for identifying inhibitors or  
 CC agonists of receptor/ligand binding. The PRO364 polypeptides may  
 CC also be combined with an agent that is cytotoxic, chemotherapeutic  
 CC or a growth inhibitor. PRO364 antibodies are useful in diagnostic  
 CC methods, purification methods and also in therapy, e.g. as  
 CC inhibitors.

XX SQ Sequence 241 AA;

Query Match 100.0%; Score 753; DB 20; Length 241;

Best Local Similarity 100.0%; Pred. No. 2.9e-55;

Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTDAACRCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCTTCRHH 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 33 GCGPGRLLLTGTDAACRCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCTTCRHH 92  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 PCPPGQGVQSGKFSFGFCIDCASGTFSGHGHCCKPWTDCQFGFLTVFPGNKTHNAV 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 93 PCPPGQGVQSGKFSFGFCIDCASGTFSGHGHCCKPWTDCQFGFLTVFPGNKTHNAV 152  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 CV 122

||

Db 153 cv 154

RESULT 7

AA027651 ID AAB27651 standard; Protein; 241 AA.

XX AC AAB27651;

XX DT 26-JAN-2001 (first entry)

XX DE Human protein PRO364.

XX KW Cardiovascular; endothelial; angiogenic disorder; PRO179;  
 KW PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333;  
 KW PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;  
 KW gene therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..25 /label= "signal peptide"

XX PN WO200053757-A2.

XX PD 14-SEP-2000.

XX PF 24-FEB-2000; 2000WO-US05004.

XX PR 08-MAR-1999; 99WO-US05028.

PR 12-MAR-1999; 99US-0123957.

PR 02-JUN-1999; 99WO-US12252.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 01-SEP-1999; 99WO-US20111.

PR 15-SEP-1999; 99WO-US21090.

PR 30-NOV-1999; 99WO-US28313.

PT e.g. cancers, auto-immune disorders, transplantation rejection and  
PT other T cell disorders  
XX  
PS Disclosure: Pages 61-62; 71pp; English.  
XX  
CC This is the amino acid sequence of the truncated human 312C2 T cell  
CC protein from clone A8. The 312C2 proteins are expressed in thymus  
CC cells and are induced on T cells and spleen cells following activation.  
CC Engagement of 312C2 stimulates proliferation of T cell clones,  
CC antigen-specific proliferation and cytokine production by T-cells, and  
CC potentiates T cell expansion or apoptosis. The products can be used  
CC in the treatment of conditions associated with abnormal physiology or  
CC development, including abnormal proliferation, e.g. cancerous  
CC conditions or degenerative conditions. They can be used in the  
CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
CC which affect immunological responses, e.g. autoimmune disorders.  
XX  
XX  
SQ Sequence 228 AA;

Query Match 100.0%; Score 737; DB 19; Length 228;  
Best Local Similarity 100.0%; Pred. NO. 4.9e-54;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DARCCRVHTTRCCRDYPCBECSSWDKVCQPEFHCGDPCTTCAHHPCPPGQGVQSGK 60  
Db 40 darccrvhttrccrdypgeccsswdkvcqpefhcgdpcttcrhpcppggvgsgk 99  
QY 61 FSGFGCIDCASGTFSGGHCCHKPWTCTQFGTLVFPGNKTHNAVCPGSPPAEPLG 119  
Db 100 fsfgfcidcasgtfsggheghckpwtctqfgtlvfpgnkthnavcvgpsppaeplg 158

RESULT 2  
ID AAY95879  
XX AAY95879 standard; Protein; 234 AA.  
AC AAY95879;  
XX  
DT 20-NOV-2000 (first entry)  
XX  
DE Human tumour necrosis factor receptor-like protein TR11.  
XX  
KW TR11; human; tumour necrosis factor receptor-like protein;  
KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
KW dermatological; antiinflammatory; therapy; diagnosis.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..25  
FT /label= Signal\_peptide  
FT Protein 26..234  
FT /label= Mature\_protein  
FT Domain 26..162  
FT /label= Extracellular\_domain  
FT Domain 163..179  
FT /label= Transmembrane\_domain  
FT Domain 180..234  
FT /label= Intracellular\_domain  
FT Modified-site 146  
FT /note= "N-glycosylated"  
FT Domain 72..81  
FT /note= "conserved domain CD-II"  
FT Domain 84..93  
FT /note= "conserved domain CD-III"  
FT Domain 107..113  
FT /note= "conserved domain CD-IV"  
FT Domain 128..134  
FT /note= "conserved domain CD-V"  
FT Domain 153..160  
FT /note= "conserved domain CD-VI"

FT Domain 176..186  
FT /note= "conserved domain CD-VII"  
FT Domain 204..209  
FT /note= "conserved domain CD-IX"  
FT Domain 224..233  
FT /note= "conserved domain CD-X"  
FT Region 27..36  
FT /note= "epitope-bearing region"  
FT Region 43..51  
FT /note= "epitope-bearing region"  
FT Region 59..67  
FT /note= "epitope-bearing region"  
FT Region 56..64  
FT /note= "epitope-bearing region"  
FT Region 66..71  
FT /note= "epitope-bearing region"  
FT Region 99..107  
FT /note= "epitope-bearing region"  
FT Region 125..133  
FT /note= "epitope-bearing region"  
FT Region 143..151  
FT /note= "epitope-bearing region"  
FT Region 156..164  
FT /note= "epitope-bearing region"  
FT Region 203..211  
FT /note= "epitope-bearing region"  
FT Region 222..230  
FT /note= "epitope-bearing region"  
XX  
XX WO2000050459-A1.  
XX  
XX 31-AUG-2000.  
XX  
XX 23-FEB-2000; 2000WO-US04572.  
XX  
XX 24-FEB-1999; 99US-0121648.  
XX 13-MAY-1999; 99US-0134172.  
XX 16-JUL-1999; 99US-0144076.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Ruben SM, NI J;  
XX  
XX WPI; 2000-572072/53.  
XX N-PSDB; AAA50304.  
XX  
XX Human tumor necrosis factor receptor-like proteins useful for  
XX diagnosis, prevention and treatment of disease states associated with  
XX aberrant cell survival such as autoimmune disease and rheumatoid  
XX arthritis  
XX  
XX Claim 14(c); Fig 1A-B; 278pp; English.  
XX  
XX The present sequence is that of human tumour necrosis factor  
XX receptor-like protein TR11, a novel 25 kDa protein which shows  
XX 58.6% identity to murine glucocorticoid induced tumour necrosis  
XX factor receptor family-related gene. The sequence was deduced from  
XX a cDNA clone (see AAA50304) discovered in a T-helper cell library.  
XX TR11 activated NF-kappaB through a TRAF2-mediated mechanism.  
XX Expression is activation-inducible. The TR11 ligand is constitutively  
XX expressed in an endothelial cell line. This suggests that TR11 and  
XX its ligand may be involved in activated T-cell trafficking.  
XX The invention provides TR11, TR11SV1 and TR11SV2 nucleic acids  
XX (see AAA50304-06) and highly conserved encoded proteins (see  
XX AAY95879-81), as well as vectors, host cells and recombinant methods for  
XX their production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful  
XX for treating, preventing, prognosis and/or diagnosis of an  
XX immunodeficiency, especially common variable immunodeficiency,  
XX x-linked agammaglobulinemia, severe combined immunodeficiency  
XX (SCID), Wiskott-Aldrich syndrome or x-linked immunoglobulin  
XX deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
XX antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
XX and/or diagnose an autoimmune disease, especially rheumatoid



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:56:23 ; Search time 126.12 Seconds  
(without alignments)  
57.202 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_46\_164

Perfect score: 737

Sequence: 1 DARCCRVHTTRCCRDYPGEE.....GNKTHNAVCPGSPAEPPLG 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A\_Geneseq\_0601.\*

1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
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21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	737	100.0	228	19 AAW37840	Truncated human 31
2	737	100.0	234	21 AAY95879	Human tumour necro
3	737	100.0	234	21 AAY52158	Tumour necrosis fa
4	737	100.0	235	21 AAY44825	Human molecule ass
5	737	100.0	241	19 AAW37839	Amino acid sequenc
6	737	100.0	241	20 AAY05605	Human TNF receptor
7	737	100.0	241	21 AAB27651	Human protein PRO3
8	737	100.0	241	21 AAB33431	Human PRO364 prote
9	737	100.0	241	21 AAY95895	Human tumour necro
10	737	100.0	241	21 AAB24409	Human PRO364 prote
11	737	100.0	241	21 AAY71467	Human PRO364 prote

12	737	100.0	241	22 AAB20115	Human immunostimul
13	737	100.0	241	22 AAB47054	Human PRO364. Hom
14	737	100.0	241	22 AAB50910	Human PRO364 prote
15	737	100.0	241	22 AAB50982	Human PRO364 prote
16	737	100.0	241	22 AAB53090	Human angiogenesis
17	737	100.0	311	19 AAW37842	Human 312C2 protei
18	721	97.8	240	21 AAY95881	Human tumour necro
19	721	97.8	240	21 AAY52160	TR11SV2 amino acid
20	636	86.3	241	21 AAY95880	Human tumour necro
21	636	86.3	241	21 AAY52159	TR11SV1 amino acid
22	632.5	85.8	316	22 AAB47055	Polypeptide encode
23	632.5	85.8	317	20 AAY06645	PRO364-related EST
24	425.5	57.7	222	19 AAW49018	Mouse glucocortico
25	425.5	57.7	228	19 AAW49016	Mouse glucocortico
26	425.5	57.7	228	19 AAW37838	Amino acid sequenc
27	425.5	57.7	294	19 AAW49017	Mouse glucocortico
28	395	53.6	232	19 AAW37841	Human 312C2 protei
29	175.5	23.8	89	21 AAY76013	Murine TNF-alpha f
30	175.5	23.8	89	22 AAB55952	Skin cell protein,
31	159.5	21.6	255	16 AAR70977	H4-1BB receptor pr
32	159.5	21.6	255	16 AAR64197	Human 4-1BB polype
33	159.5	21.6	255	18 AAW26658	Human 4-1BB recept
34	159.5	21.6	255	20 AAY33214	Human CD137 protei
35	159.5	21.6	255	20 AAY28688	Human receptor pro
36	159.5	21.6	255	22 AAB50521	Human tumour necro
37	158.5	21.5	219	18 AAW31759	A novel human h4-1
38	158.5	21.5	219	20 AAW92523	Human h4-1BBSV rec
39	158	21.4	206	16 AAR81881	Mouse type-II memb
40	158	21.4	206	19 AAW48977	Mouse OX40 extrace
41	158	21.4	438	16 AAR81882	Plasmid pDC406/OX4
42	158	21.4	438	19 AAW48976	OX40/FC mutein. C
43	154.5	21.0	219	20 AAW92524	Human h4-1BBSV rec
44	154	20.9	273	20 AAV42185	Human mFLINT #2 pr
45	154	20.9	277	16 AAR76996	Deduced sequence e

#### ALIGNMENTS

RESULT 1  
AAW37840  
ID AAW37840 standard; Protein; 228 AA.  
XX  
AC AAW37840;  
XX  
DT 28-JUL-1998 (first entry)  
XX  
DE Truncated human 312C2 protein from clone\_A8 amino acid sequence.  
XX  
KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
KW antigen-specific T cell proliferation; cytokine production by T-cell;  
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
KW autoimmune disorders.  
OS Homo sapiens.  
XX  
XX  
PN W09806842-A1.  
XX  
PD 19-FEB-1998.  
XX  
PF 14-AUG-1997; 97WO-US19331.  
XX  
PR 07-OCT-1996; 96US-0027901.  
PR 16-AUG-1996; 96US-0689943.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Gorman DM, Randall TD, Zlotnik A;  
XX  
XX WPI; 1998-159534/14.  
DR N-PSDB; AAV19154.  
XX  
PT Isolated 312C2 T cell gene - used to develop products for treating,

FT FT /label= Signature\_sequence  
68..96  
FT FT /label= Signature\_sequence  
109..147  
FT FT /label= Signature\_sequence  
122..129  
FT FT /label= Signature\_sequence  
157..175  
FT FT /label= Signature\_sequence  
165..186  
FT FT /label= Signature\_sequence  
37  
FT FT /note= "Potential phosphorylation site"  
48  
FT FT /note= "Potential phosphorylation site"  
62  
FT FT /note= "Potential phosphorylation site"  
82  
FT FT /note= "Potential phosphorylation site"  
205  
FT FT /note= "Potential phosphorylation site"  
223  
FT FT /note= "Potential phosphorylation site"  
140  
FT FT /note= "N-glycosylated"  
XX  
PN WO200005374-A2.  
XX  
XX 03-FEB-2000.  
XX  
XX 21-JUL-1999; 99WO-US16637.  
XX  
XX 22-JUL-1998; 98US-0093827.  
XX  
XX (INCY-) INCYTE PHARM INC.  
XX  
XX Tang YT, Lal P, Hillman JL, Corley NC, Patterson C, Baughn MR;  
XX  
XX WPI; 2000-182699/16.  
DR N-PSDB; AA49948.  
XX  
XX Polypeptides and polynucleotides useful for treating and detecting cell  
PT proliferation disorders e.g. actinic keratosis, and immune disorders  
PT e.g. Crohn's disease  
XX  
XX Claim 1; Pages 64-65; 67pp; English.  
XX  
XX The present sequence is a molecule associated with cell  
CC proliferation, MACP-5 from incyte clone 2809903 isolated from TLYMN0706  
CC cDNA library. This sequence is expressed in cardiovascular and  
CC haematopoietic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV,  
CC hepatotropic, antiinflammatory, antipsoriatic, cytostatic, antiasthmatic,  
CC dermatological, antidiabetic, nephrotropic, antithyroid, thyromimetic,  
CC immunosuppressive, osteopathic, antiarthritic, uropathic, antitumor,  
CC and ophthalmological activities. The present sequence is useful in the  
CC diagnosis, treatment and prevention of cell proliferative disorders e.g.  
CC actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and  
CC hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and  
XX anaemia.  
XX  
SQ Sequence 235 AA;

Query Match 100.0%; Score 737; DB 21; Length 235;  
Best Local Similarity 100.0%; Pred. No. 5.1e-54;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DARCCRVHTRCCRDYPGECCSEWDCMCVQPFHCGDPCCTTCRRHPCPPGQGVQSGK 60  
DB 40 darccrvhtrccrdypgeccsewdcmcvqpfhcgdpcttcrhpcpppggvgsgk 99  
QY 61 FSGFGQCIDCASGTFSGGHEGHCKPWTDCQFGFLTVFPGNKNTHNAVVCVPSPPAEPLG 119  
DB 119

Db 100 fsfgfqidcasgtfsggheghckpwtcdtqfgfltvfpgnknthnavcvpgspaeplg 158

RESULT 5  
AAW37839  
ID AAW37839 standard; Protein; 241 AA.  
XX  
AC AAW37839;  
XX  
DT 28-JUL-1998 (first entry)  
XX  
DE Amino acid sequence of the human 312C2 T cell protein.  
XX  
KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
KW antigen-specific T cell proliferation; cytokine production by T-cell;  
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
KW autoimmune disorders.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..726  
FT /\*tag= a  
FT /product= "human 312C2 protein"  
XX  
PN WO9806842-A1.  
XX  
PD 19-FEB-1998.  
XX  
PF 14-AUG-1997; 97WO-US13931.  
XX  
PR 07-OCT-1996; 96US-0027901.  
PR 16-AUG-1996; 96US-0689943.  
XX  
XX (SCHE ) SCHERING CORP.  
XX  
XX Gorman DM, Randall TD, Zlotnik A;  
XX  
XX WPI; 1998-159534/14.  
DR N-PSDB; AAV19153.  
XX  
XX Isolated 312C2 T cell gene - used to develop products for treating,  
PT e.g. cancers, auto-immune disorders, transplantation rejection and  
PT other T cell disorders  
XX  
XX Claim 2; Pages 59-60; 71pp; English.  
XX  
XX This is the amino acid sequence encoding the human 312C2 T cell  
CC protein. The 312C2 proteins are expressed in thymus cells and are  
CC induced on T cells and spleen cells following activation. Engagement  
CC of 312C2 stimulates proliferation of T cell clones, antigen-specific  
CC proliferation and cytokine production by T-cells, and potentiates T  
CC cell expansion or apoptosis. The products can be used in the  
CC treatment of conditions associated with abnormal physiology or  
CC development, including abnormal proliferation, e.g. cancerous  
CC conditions or degenerative conditions. They can be used in the  
CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
CC which affect immunological responses, e.g. autoimmune disorders.  
XX  
SQ Sequence 241 AA;

Query Match 100.0%; Score 737; DB 19; Length 241;  
Best Local Similarity 100.0%; Pred. No. 5.2e-54;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DARCCRVHTRCCRDYPGECCSEWDCMCVQPFHCGDPCCTTCRRHPCPPGQGVQSGK 60  
DB 46 darccrvhtrccrdypgeccsewdcmcvqpfhcgdpcttcrhpcpppggvgsgk 105  
QY 61 FSGFGQCIDCASGTFSGGHEGHCKPWTDCQFGFLTVFPGNKNTHNAVVCVPSPPAEPLG 119  
DB 106 fsfgfqidcasgtfsggheghckpwtcdtqfgfltvfpgnknthnavcvpgspaeplg 164



CC PRO840, PRO877, PRO878, PRO879, PRO882, PRO885 or PRO887. These  
 CC proteins were identified by isolating cDNA clones encoding secreted  
 CC proteins. The proteins of the invention may be used to diagnose and  
 CC treat cardiovascular, endothelial or angiogenic disorders. The present  
 CC sequence is one of the proteins of the invention.  
 XX  
 SQ Sequence 241 AA;

Query Match 100.0%; Score 737; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-54;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQVQSOGK 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 46 darccrvhttrccrdypgeccsewdcmvcqpefhcgdpctcttrhhpcppggvgvsgk 105

QY 61 FSFGFCIDCASGTFSGGHEGCKPWTCTQFGFLTVPFGKNTNNAVCPGSPPAEPLG 119  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 106 fsfgfcidcasgtfsggheghckpwtcdctqfgfltvfgnktnavcvcpsppaepig 164

## RESULT 8

AAB33431  
 ID AAB33431 standard; Protein: 241 AA.

AC AAB33431;

DT 29-JAN-2001 (first entry)

XX Human PRO364 protein UNQ319 SEQ ID NO:92.

XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
 KW dermatological; antiarthritic; antirheumatic; immunosuppressive;  
 KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;  
 KW antianaemic; hepatotropic; virucide; antipsoriatic; anti allergic;  
 KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
 KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;  
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
 KW autoimmune thrombocytopaenia; immune-mediated renal disease;  
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
 KW inflammatory bowel disease; gluten-sensitive enteropathy;  
 KW autoimmune disease; immune-mediated skin disease; allergic disease;  
 KW immunological disease; transplantation associated disease;  
 KW graft rejection; graft-versus-host-disease.

XX Homo sapiens.

OS  
 XX WO200053758-A2.

PN  
 XX

PD  
 XX

XX 14-SEP-2000.

PF 02-MAR-2000; 2000WO-US05841.

XX 08-MAR-1999; 99WO-US05028.

PR 10-MAR-1999; 99US-0123618.

PR 12-MAR-1999; 99US-0123957.

PR 23-MAR-1999; 99US-0125775.

PR 12-APR-1999; 99US-0128849.

PR 20-APR-1999; 99WO-US08615.

PR 28-APR-1999; 99US-0131445.

PR 04-MAY-1999; 99US-0132371.

PR 14-MAY-1999; 99US-0134287.

PR 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 26-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 28-JUL-1999; 99US-0146222.

PR 01-SEP-1999; 99WO-US20111.

PR 08-SEP-1999; 99WO-US20594.

PR 13-SEP-1999; 99WO-US20944.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.

(GETH ) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
 XX Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;  
 XX

DR WPI: 2000-572271/53.

DR N-PSDB; AAC58596.

XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -

PS Claim 33; Fig 36; 309pp: English.

XX The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are  
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
 CC autoimmune or immune-mediated skin diseases, allergic diseases,  
 CC immunological diseases of the lung, and transplantation associated  
 CC diseases including graft rejection and graft-versus-host-disease.  
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.

XX Sequence 241 AA;

Query Match 100.0%; Score 737; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-54;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQVQSOGK 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 46 darccrvhttrccrdypgeccsewdcmvcqpefhcgdpctcttrhhpcppggvgvsgk 105

QY 61 FSFGFCIDCASGTFSGGHEGCKPWTCTQFGFLTVPFGKNTNNAVCPGSPPAEPLG 119  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 106 fsfgfcidcasgtfsggheghckpwtcdctqfgfltvfgnktnavcvcpsppaepig 164

RESULT 6  
ID AAY06605  
XX AAY06605 standard; Protein; 241 AA.  
AC AAY06605;  
XX 26-OCT-1999 (first entry)  
DT Human TNF receptor homologue PRO364.  
DE  
XX PRO364; tumour necrosis factor receptor; human; apoptosis;  
KW inflammation; antiinflammatory; NF-KB activation;  
KW autoimmune disease; therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..25  
FT /note= "signal peptide"  
FT Protein 26..241  
FT /note= "mature protein"  
FT Modified-site 146  
FT /note= "N-glycosylated"  
FT Domain 162..180  
FT /note= "transmembrane domain"  
XX WO9940196-A1.  
PN  
XX 12-AUG-1999.  
PD  
XX  
XX 09-FEB-1999; 99WO-US02642.  
PF  
XX  
XX 09-FEB-1998; 98US-0024087.  
PR  
XX  
XX (GETH ) GENENTECH INC.  
PA  
XX  
XX Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;  
PI Pitti RM, Wood WI;  
PI  
XX WPI; 1999-494296/41.  
DR N-PSDB; AAX87670.  
XX  
XX Tumour necrosis factor receptor homologue - useful for, e.g.  
PT modulating apoptosis and NF-KB activation and proinflammatory or  
PT autoimmune responses  
XX  
XX Claim 17; Fig 2A; 104pp; English.  
XX  
XX The present sequence represents human PRO364, a novel member of the  
CC tumour necrosis factor receptor family. The sequence was deduced  
CC from a bone marrow cDNA clone (see AAX87670). Methods for the  
CC recombinant production of PRO364 polypeptides, e.g. in CHO,  
CC Escherichia coli or yeast host cells, are provided. Claimed  
CC polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the  
CC mature protein) and 26-X of the present sequence, where X is any  
CC one of amino acid residues 157-167 of PRO364. PRO364 polypeptides  
CC are useful for modulating apoptosis, NF-KB activation and  
CC proinflammatory or autoimmune responses in mammalian cells  
CC (claimed). Chimeric molecules comprising a PRO364 polypeptide  
CC fused to a heterologous sequence such as epitope tag or  
CC immunoglobulin Fc region are also claimed. PRO364 can be used in  
CC assays to identify other proteins or molecules involved in binding  
CC interactions. This is useful for identifying inhibitors or  
CC antagonists of receptor/ligand binding. The PRO364 polypeptides may  
CC also be combined with an agent that is cytotoxic, chemotherapeutic  
CC or a growth inhibitor. PRO364 antibodies are useful in diagnostic  
CC methods, purification methods and also in therapy, e.g. as  
CC inhibitors.  
XX  
XX Sequence 241 AA;

Query Match 100.0%; Score 737; DB 20; Length 241;  
Best Local Similarity 100.0%; Pred. No. 5.2e-54;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DARCCRVHTTRCCRDYPGECCSEWDCMCVQPEFHCGDPCCTTCRRHPCPPGGQVQSQGK 60  
|||||  
Db 46 darccrvhttrccrdypgeccsewdcmcvqpefhcgdpccctcrhhpcppggvqsggk 105  
|||||  
QY 61 FSFGFCIDCASGTFSGGHEGCHKPMTDCTQFGFLTVPFGNKTNAVCVPGSPPAEPLG 119  
|||||  
Db 106 fsfgfcidcasgtfsgghegchkpwtcdctqfgfltvpfgnktnavcvpgspaeplg 164  
|||||  
RESULT 7  
AAB27651  
ID AAB27651 standard; Protein; 241 AA.  
XX  
XX AAB27651;  
AC  
XX  
XX 26-JAN-2001 (first entry)  
DT  
XX  
XX Human protein PRO364.  
DE  
XX  
XX Cardiovascular; endothelial; angiogenic disorder; PRO179;  
KW PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333;  
KW PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;  
KW gene therapy.  
XX  
XX Homo sapiens.  
OS  
XX  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..25  
FT /label= "Signal peptide"  
FT  
XX  
XX WO200053757-A2.  
PN  
XX  
XX 14-SEP-2000.  
PD  
XX  
XX 24-FEB-2000; 2000WO-US05004.  
PF  
XX  
XX 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 02-JUN-1999; 99WO-US12252.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 30-NOV-1999; 99WO-US28313.  
PR 02-DEC-1999; 99WO-US28565.  
PR 30-NOV-1999; 99WO-US28409.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gershtsen ME;  
PI Goddard A, Gurney AL, Hillan KJ, Marsters SA, Paoni NF, Pitti RM;  
PI Watanabe CK, Williams PM, Wood WI;  
XX  
XX WPI; 2000-611444/58.  
DR N-PSDB; AAA99903.  
XX  
XX Novel PRO polypeptides and agonists and antagonists of them, used to  
PT diagnose and treat cardiovascular, endothelial and angiogenic disorders  
PT  
XX  
XX Claim 71; Fig 6; 181pp; English.  
PS  
XX  
XX The present invention relates to methods for stimulating or inhibiting  
CC angiogenesis and cardiovascularization. The methods involve the use of  
CC pharmaceutical compositions based on the following proteins, PRO179,  
CC PRO238, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333,

CC associated with decreased PRO expression. AAA77510 to AAA77721 and  
CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in  
CC the exemplification of the present invention.

SQ Sequence 241 AA;

Query Match 100.0%; Score 737; DB 21; Length 241;

Best Local Similarity 100.0%; Pred. No. 5.2e-54;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPFHCGDPCCTTCRHHPCPPGQGVQSGK 60

Db 46 darccrvhttrccrdypgeecsewdcmvqpfhcgdpccctcrhhpcppgpgvgsgk 105

QY 61 FSGFGQICDASGTFSGGHEGCHKPWTDCTQFGELTVFPGNKTHNAVCPGSPPAEPLG 119

Db 106 fsfgqicdcasgtfsggheghckpwtcdctqfgfltvpgnktthnavcvpgspppaeplg 164

RESULT 11

AAV71467

ID AAY71467 standard; Protein; 241 AA.

AC AAY71467;

DT 08-NOV-2000 (first entry)

XX Human PRO364 protein.

XX PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;

KW neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;

KW breast; prostate; colon; lung; renal; ovarian; central nervous system;

KW CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue;

KW tumour necrosis factor receptor; GTR protein homologue.

OS Homo sapiens.

XX Key

FX Location/Qualifiers

FT Peptide 1..25

FT /label= Signal\_peptide

FT Modified-site 5..11 "N-myristoylation site"

FT /note=

FT Modified-site 8..14 "N-myristoylation site"

FT /note=

FT Modified-site 25..31 "N-myristoylation site"

FT /note=

FT Protein 26..241

FT /label= Mature\_PRO364\_protein

FT /note=

FT Modified-site 30..36

FT /note= "N-myristoylation site"

FT Modified-site 33..39

FT /note= "N-myristoylation site"

FT Modified-site 118..124

FT /note= "N-myristoylation site"

FT Modified-site 122..128

FT /note= "N-myristoylation site"

FT Modified-site 146..150

FT /note= "Asn is N-glycosylated"

FT Modified-site 156..162

FT /note= "N-myristoylation site"

FT Domain 163..183

FT /label= Transmembrane\_domain

FT Binding-site 166..177

FT /note= "Prokaryotic membrane lipoprotein lipid attachment site"

FT Region 171..193

FT /note= "Leucine zipper pattern"

XX W0200032778-A2.

XX 08-JUN-2000.

XX

PF 30-NOV-1999; 99WO-US28409.

XX 01-DEC-1998; 98WO-US25108.

PR 16-DEC-1998; 98US-0112850.

PR 22-DEC-1998; 98US-0113296.

PR 20-JUL-1999; 99US-0144758.

XX 26-JUL-1999; 99US-0145698.

PA (GETH ) GENENTECH INC.

XX

XX Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;

XX WPI; 2000-412325/35.

DR N-ESDB; AAD01240.

XX

XX New composition useful for inhibiting neoplastic cell growth and for

XX treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or

XX their antagonists -

XX

XX Claim 31; Fig 4; 108pp; English.

XX

XX The present sequence is the human PRO364 protein, encoded by the cDNA

XX clone, designated as DNA47365-1206. It is isolated from human small

XX intestine tissue cDNA library, identified using probes based on the

XX consensus sequence DNA4825, relative to the Incyte expressed sequence

XX tag (EST) 3003460. This EST has homology to tumour necrosis factor

XX receptor (TNFR) family of polypeptides. PRO364 sequence also shows

XX homology to members of the TNFR family and mouse GTR protein.

XX This clone is assigned the ATCC deposit No: 209436. PRO364 functions as

XX a neoplastic cell growth inhibitor and is used for treating tumours,

XX using an effective amount of PRO655, PRO364 and PRO344. This composition

XX is especially useful for treatment of human cancers such as breast,

XX prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.

XX

SQ Sequence 241 AA;

Query Match 100.0%; Score 737; DB 21; Length 241;

Best Local Similarity 100.0%; Pred. No. 5.2e-54;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPFHCGDPCCTTCRHHPCPPGQGVQSGK 60

Db 46 darccrvhttrccrdypgeecsewdcmvqpfhcgdpccctcrhhpcppgpgvgsgk 105

QY 61 FSGFGQICDASGTFSGGHEGCHKPWTDCTQFGELTVFPGNKTHNAVCPGSPPAEPLG 119

Db 106 fsfgqicdcasgtfsggheghckpwtcdctqfgfltvpgnktthnavcvpgspppaeplg 164

RESULT 12

AAB20115

ID AAB20115 standard; Protein; 241 AA.

XX

AC AAB20115;

XX

DT 30-APR-2001 (first entry)

XX

DE Human immunostimulant PRO364.

XX

KW PRO364; UNQ319; human; immune disease; autoimmune disease;

KW antirheumatic; antiarthritic; antiinflammatory; antianaemic;

KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;

KW hepatotropic; virucide; dermatological; antipsoriatic;

KW antiasthmatic; antiallergic; immunostimulant.

XX

OS Homo sapiens.

XX

FX Key

FX Location/Qualifiers

FX 1..25

FX /label= Signal\_peptide

FX Protein 26..241

FX /label= Mature\_protein



XX	Composition for diagnosing and treating cardiovascular, endothelial and
PT	angiogenic disorders, comprises a PRO364 or PRO175 polypeptide -
XX	
PS	Claim 1; Fig 1; 76pp; English.
XX	
CC	This sequence represents PRO364 polypeptide, which is a human gluco-
CC	corticoid-induced tumor necrosis factor receptor (hGTR). The
CC	corresponding ligand (hGTRL), PRO175, is given in ABA47056.
CC	PRO364 and PRO175 may be used in a mixture with a cardiovascular,
CC	endothelial, angiogenic or angiostatic agent for the treatment of a
CC	cardiovascular, endothelial, angiogenic or angiostatic disorder. The
CC	PRO364 cDNA sequence was isolated from an expressed sequence tag (EST)
CC	database as having homology to members of the tumour necrosis factor
CC	receptor (TNFR) family of polypeptides. The PRO175 cDNA sequence was
CC	isolated from a library of cDNA fragments derived from human umbilical
CC	vein endothelial cells (HUVEC). Administering an effective amount of
CC	PRO364 or PRO175 or their antagonists is useful for treating cardiac
CC	hypertrophy (which is initiated by myocardial infarction and
CC	characterized by the presence of an elevated level of Pgf-2alpha),
CC	trauma, a cancer, or age-related macular degeneration in a human.
CC	Administering a therapeutically effective amount of an antibody that
CC	binds PRO364 or PRO175 is useful for inhibiting angiogenesis induced
CC	by PRO364 or PRO175 in a human suffering from a tumor or a retinal
CC	disorder. PRO364 or PRO175, or their antagonists, are useful for
CC	vascular-related drug targeting or as therapeutic targets for the
CC	treatment or prevention of atherosclerosis, hypertension, inflammatory
CC	vasculitides, Reynaud's disease, aneurysms, arterial restenosis,
CC	thrombophlebitis, tumor angiogenesis, gut protection or regeneration
CC	and treatment of lung or liver fibrosis, periodontal diseases,
CC	attraction of bone-forming cells, central and peripheral nervous
CC	system disease and neuropathies and rheumatoid arthritis.
XX	
XX	Sequence 241 AA:
XX	

Query Match	100.0%	Score 737;	DB 22;	Length 241;
Best Local Similarity	100.0%	Pred. No. 5.2e-54;		
Matches 119;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps	0;			

QY	1	DARCCRVHTRCCRDY	PGEBCCSEWDCMCVQPFHCGDCCCTCRHHPCPPGGVQSQK	60
Db	46	darccrvhtrccrdypge	bccsewdcmcvqpfhcgdpccctcrhhpcppggvgvsqk	105
QY	61	FSFGQCIDCASCTFSGSHGCHKPMTDCTQGFGLTVFPGNKTHNAVCPGSPASPLG	119	
Db	106	fsfgqcidcasatfaaghechckpwtcdtafaflvfpankthnavcvvgspsaeqla	164	

RESULT	14	
AAB50910		
ID	AAB50910	standard; Protein: 241 AA.
XX	AC	
XX	AAB50910;	
XX	AC	
XX	XX	
DT	21-MAR-2001	(first entry)
XX	Human	PRO364 protein.
XX		
KW	Human:	PRO: antiinflammatory; dermatological; antiarthritic;
KW	antiinflammatory;	cardiac; antianaemic; immunosuppressive; antithyroid;
KW	antidiabetic;	neotropic; neuroprotective; hepatotropic; virucide;
KW	antiallergic;	antisthmatic; immune related disorder;
KW	hepatobiliary disease;	autoimmune disease; allergy.

OS Homo sapiens.  
XX  
XX  
PN WO200073452-A2.  
XX  
PD 07-DEC-2000.  
XX  
PF 02-JUN-2000; 2000WO-US15264.  
XX

PR	02-JUN-1999;	99WO-US12252.
PR	20-JUL-1999;	99US-0144732.
PR	20-JUL-1999;	99US-0144758.
PR	28-JUL-1999;	99US-0146222.
PR	01-SEP-1999;	99WO-US20111.
PR	15-SEP-1999;	99WO-US21090.
PR	15-SEP-1999;	99WO-US21547.
PR	29-OCT-1999;	99US-0162506.
PR	30-NOV-1999;	99WO-US28313.
PR	01-DEC-1999;	99WO-US28634.
PR	09-DEC-1999;	99US-0170262.
PR	20-DEC-1999;	99WO-US30911.
PR	03-JAN-2000;	2000WO-US00219.
PR	06-JAN-2000;	2000WO-US00376.
PR	11-FEB-2000;	2000WO-US03565.
PR	18-FEB-2000;	2000WO-US04341.
PR	18-FEB-2000;	2000WO-US04342.
PR	22-FEB-2000;	2000WO-US04414.
PR	24-FEB-2000;	2000WO-US04914.
PR	15-MAR-2000;	2000WO-US06884.
PR	20-MAR-2000;	2000WO-US07377.
PR	21-MAR-2000;	2000WO-US07532.
PR	30-MAR-2000;	2000WO-US08439.
PR	17-MAY-2000;	2000WO-US13705.
PR	22-MAY-2000;	2000WO-US14042.
XX		
XX		
PA	( GETH ) GENENTECH INC.	
XX		
XX	Ashkenazi AJ, Baker KP, Chan B,	Goddard A, Godowski PJ, Gurney AL;
PI	Hebert C, Henzel W, Kabakoff RC,	Shelton DL, Tumas D, Watanabe CK;
PI	Wood WI;	
XX		
XX	WPI; 2001-025253/03.	
DR	N-PSDB: AAC91469.	

Thirty three nucleic acids encoding PRO polypeptides which are useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus -

PS Claim 58; Fig 18; 218pp; English.

The present sequence is one of thirty three novel PRO polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic chronic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems (such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic inflammatory demyelinating polyneuropathy), hepatobiliary diseases (such as infectious, autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis), inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases (such as bullous skin diseases, erythema multiforme, contact dermatitis, psoriasis), allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, lung hypersensitivity and urticaria), immunological diseases of the food (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonitis), transplantation associated diseases including graft rejection and graft-versus-host diseases.

Sequence 241 AA:

Query Match	100.0%;	Score 737;	DB 22;	Length 241;
Best Local Similarity	100.0%;	Pred. No. 5.2e-54;		
Matches 119:	Conservative 0;	Mismatches 0;	Indels 0;	

0v 1 DARCCRVHTTRCCRDYPGEECCSEWDCMCVOPEFHCGDPCCCTTCRHHPCPPGOGVOSGK 60



FT Domain 163..183  
 FT Modified-site /note= "transmembrane domain"  
 FT 5..11  
 FT Modified-site /note= "N-myristoylation site"  
 FT 8..14  
 FT Modified-site /note= "N-myristoylation site"  
 FT 25..31  
 FT Modified-site /note= "N-myristoylation site"  
 FT 30..36  
 FT Modified-site /note= "N-myristoylation site"  
 FT 33..39  
 FT Modified-site /note= "N-myristoylation site"  
 FT 118..124  
 FT Modified-site /note= "N-myristoylation site"  
 FT 122..128  
 FT Modified-site /note= "N-myristoylation site"  
 FT 156..162  
 FT Modified-site /note= "N-myristoylation site"  
 FT 146..150  
 FT Modified-site /note= "Asn is N-glycosylated"  
 FT 166..177  
 FT Peptide /note= "prokaryotic membrane lipoprotein lipid attachment site"  
 FT 171..193  
 FT Peptide /note= "leucine zipper pattern"  
 FT WO200105972-A1.  
 FT 25-JAN-2001.  
 FT 15-MAR-2000; 2000WO-US06884.  
 FT 20-JUL-1999; 99US-0144758.  
 FT (GETH ) GENENTECH INC.  
 FT Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;  
 FT Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK;  
 FT Wood WT;  
 FT WPI: 2001-103149/11.  
 FT N-PSDB: AAF30057.  
 FT  
 FT New PRO polypeptides, nucleic acids and (ant)agonists.\*useful for  
 FT diagnosing and treating immune-related disorders, such as multiple  
 FT sclerosis, rheumatoid arthritis and diabetes -  
 FT  
 FT Claim 20; Fig 16; 127pp; English.  
 FT  
 FT The present sequence is that of novel human immunomodulator PRO364  
 FT (UNQ319), as deduced from cDNA (see AAF30057) isolated from a  
 FT small intestine library. PRO364 (26 kDa, PI 6.34) shows sequence  
 FT homology to mouse GITR protein and may be its human counterpart.  
 FT The invention provides polynucleotides (see AAF30050-62) encoding  
 FT novel human PRO proteins (see AAB20108-20) including PRO364.  
 FT Claimed compositions comprising these proteins or their agonists  
 FT are useful for increasing infiltration of inflammatory cells into  
 FT a tissue of a mammal, stimulating or enhancing an immune  
 FT response, or increasing the proliferation of T-lymphocytes in a  
 FT mammal in response to an antigen. Claimed compositions comprising  
 FT a PRO polypeptide or its antagonist have the opposite effect. A  
 FT claimed method for treating an immune related disorder, such as a T  
 FT cell disorder, involves administering a PRO polypeptide, an agonist  
 FT antibody or an antagonist antibody. The disorder is selected from  
 FT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 FT juvenile chronic arthritis, spondyloarthritis, systemic sclerosis,  
 FT idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 FT vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 FT thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated  
 FT renal disease, demyelinated diseases (such as multiple sclerosis),  
 FT autoimmune chronic active hepatitis, primary biliary cirrhosis,  
 FT granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel  
 FT disease (ulcerative colitis and Crohn's disease), gluten-sensitive

CC enteropathy, Whipple's disease, (auto)immune-mediated skin diseases  
 CC (such as bullous skin disease, erythema multiforme and psoriasis),  
 CC allergic diseases (such as asthma, allergic rhinitis, atopic  
 CC dermatitis, food hypersensitivity and urticaria), immunologic  
 CC diseases of the lung and transplantation associated diseases (such  
 CC as graft rejection and graft-versus-host disease) (all claimed).  
 CC Claimed methods of diagnosing these disorders comprise detecting  
 CC the level of expression of the PRO gene. Also claimed are a method  
 CC of identifying a compound capable of inhibiting the expression or  
 CC activity of the PRO polypeptide, vectors, host cells, antibodies,  
 CC and a method of stimulating the proliferation of T lymphocytes  
 CC using PRO364.  
 XX  
 SQ Sequence 241 AA;  
 Query Match 100.0%; Score 737; DB 22; Length 241;  
 Best Local Similarity 100.0%; Pred. NO. 5.2e-34;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DARCVRHTTRCCRDYPGECCSEWDCMCVQPEFHGCGPCCTTCRHHPCPPGQGVQSGK 60  
 Db 46 darcvrhttrccrdypgeccsewdcmcvqpefhgcpcttcrrhhpcppgqvsgsk 105  
 QY 61 FSGFGQCIDCASGTFSGGHEGHCXKRWTDCTQFGFLTVPNGKTHNAVCPGSPPAEPLG 119  
 Db 106 fsfgfqcidasgtfsggheghckpwtcdtqfgfltvpngkthnavcvgpsppaeplg 164  
 RESULT 13  
 AAB47054  
 ID AAB47054 standard; Protein: 241 AA.  
 XX  
 AC AAB47054;  
 XX  
 DT 08-MAY-2001 (first entry)  
 XX  
 DE Human PRO364.  
 XX  
 KW PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;  
 KW hGTR; ligand; hGTRL; PRO175; tumour necrosis factor receptor; TNFR;  
 KW human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;  
 KW myocardial infarction; PGF-2alpha; trauma; cancer; angiogenesis;  
 KW age-related macular degeneration; antibody; periodontal disease;  
 KW vascular-related drug targeting; atherosclerosis; hypertension;  
 KW inflammatory vasculitides; Reynaud's disease; aneurysm;  
 KW arterial restenosis; thrombophlebitis; tumor angiogenesis;  
 KW lung; liver; fibrosis; neuropathy; rheumatoid arthritis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..26  
 FT /note= "Potential signal peptide"  
 FT Modified-site 146  
 FT /note= "N-glycosylated"  
 FT Domain 162..180  
 FT /note= "Potential transmembrane domain"  
 XX  
 WO200103720-A2.  
 XX  
 PN 18-JAN-2001.  
 XX  
 PD 11-JUL-2000; 2000WO-US18867.  
 XX  
 PF 12-JUL-1999; 99US-0143304.  
 XX  
 PR (GETH ) GENENTECH INC.  
 XX  
 PA Williams PM, Gerritsen ME;  
 XX WPI: 2001-138257/14.  
 XX N-PSDB: AAC85433.  
 DR

---

Db 46 darcrrvhttrccrdypgeccsewcmcvqpfhcgdpcttcrhpcppggvsggk 105  
QY 61 FSGFGQCIDCASGTFSGGHEGCHKPWTDTQFGFLTVFPGNKTHNAVCPGSPPAEPLG 119  
Db 106 fsfgqcidcasgtfsgghegchckpwtddctqfgfltvfpgnkthnavcvpgspaeplg 164

RESULT 15  
AAB50982  
ID AAB50982 standard; Protein; 241 AA.  
XX AAB50982;  
AC AAB50982;  
XX 21-MAR-2001 (first entry)  
XX Human PRO364 protein.  
XX Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive;  
KW vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;  
KW vulnery; antianginal; gene therapy; cardiovascular disease;  
KW endothelial disorder; angiogenic disorder; cancer; periodontal disease;  
KW wound healing.  
XX Homo sapiens.  
OS  
XX  
XX WO200073445-A2.  
XX  
XX 07-DEC-2000.  
XX  
XX PF 17-MAY-2000; 2000WO-US13705.  
XX  
XX 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 28-JUL-1999; 99US-0146222.  
PR 01-SEP-1999; 99WO-US20111.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
XX  
XX (GETH ) GENENTECH INC.  
PA  
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;  
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
XX  
XX WPI; 2001-025251/03.  
DR  
DR N-PSDB; AAC90566.  
XX  
XX Seventeen nucleic acids encoding PRO polypeptides which are useful in  
PT diagnosis and treatment of cardiovascular, endothelial or angiogenic  
PT disorders in a mammal -  
XX  
XX Claim 71; Fig 8; 182pp; English.  
XX  
XX The present sequence is one of seventeen novel PRO polypeptides. The PRO  
CC nucleic acids, polypeptides, agonists and antagonists are useful for  
CC treating cardiovascular, endothelial or angiogenic disorders in a mammal.  
CC Examples of these disorders include cardiac hypertrophy, trauma, cancer,  
CC age-related macular degeneration, atherosclerosis, hypertension, arterial  
CC restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial

CC infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and  
CC antagonists are also used to prevent tumour angiogenesis and for treating  
CC periodontal diseases. They are also used to stimulate wound healing and  
CC tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO  
CC antibodies are useful for diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder.  
XX  
SQ Sequence 241 AA;  
  
Query Match 100.0%; Score 737; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 5.2e-54;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DARCRRVHTTRCCRDYPGEECCSEWDCMCVQPFHCGDPCTTCRHHPCPPGGVSGGK 60  
Db 46 darcrrvhttrccrdypgeccsewcmcvqpfhcgdpcttcrhpcppggvsggk 105  
  
QY 61 FSGFGQCIDCASGTFSGGHEGCHKPWTDTQFGFLTVFPGNKTHNAVCPGSPPAEPLG 119  
Db 106 fsfgqcidcasgtfsgghegchckpwtddctqfgfltvfpgnkthnavcvpgspaeplg 164

Search completed: September 4, 2001, 15:56:23  
Job time: 340 sec

FT Domain 107..113 /note= "conserved domain CD-IV"  
 FT Domain 128..134 /note= "conserved domain CD-V"  
 FT Domain 153..160 /note= "conserved domain CD-VI"  
 FT Domain 176..186 /note= "conserved domain CD-VII"  
 FT Domain 204..209 /note= "conserved domain CD-IX"  
 FT Domain 224..233 /note= "conserved domain CD-X"  
 FT Region 27..36 /note= "epitope-bearing region"  
 FT Region 43..51 /note= "epitope-bearing region"  
 FT Region 59..67 /note= "epitope-bearing region"  
 FT Region 56..64 /note= "epitope-bearing region"  
 FT Region 66..71 /note= "epitope-bearing region"  
 FT Region 99..107 /note= "epitope-bearing region"  
 FT Region 125..133 /note= "epitope-bearing region"  
 FT Region 143..151 /note= "epitope-bearing region"  
 FT Region 156..164 /note= "epitope-bearing region"  
 FT Region 203..211 /note= "epitope-bearing region"  
 FT Region 222..230 /note= "epitope-bearing region"  
 FT Region 277..285 /note= "epitope-bearing region"  
 XX  
 PN WO200050459-A1.  
 XX  
 PD 31-AUG-2000.  
 XX  
 XX 23-FEB-2000; 2000WO-US04572.  
 XX  
 PR 24-FEB-1999; 99US-0121648.  
 PR 13-MAY-1999; 99US-0134172.  
 PR 16-JUL-1999; 99US-0144076.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, NI J;  
 XX  
 DR WPI; 2000-572072/53.  
 DR N-PSDB; AAA50304.  
 XX  
 XX Human tumor necrosis factor receptor-like proteins useful for  
 PT diagnosis, prevention and treatment of disease states associated with  
 PT aberrant cell survival such as autoimmune disease and rheumatoid  
 PT arthritis -  
 XX  
 PS Claim 14(c); Fig 1A-B; 278pp; English.  
 XX  
 CC The present sequence is that of human tumour necrosis factor  
 CC receptor-like protein TR11, a novel 25 kDa protein which shows  
 CC 58.6% identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The sequence was deduced from  
 CC a cDNA clone (see AAA50304) discovered in a T-helper cell library.  
 CC TR11 activated NF-kappaB through a TRAF2-mediated mechanism.  
 CC Expression is activation-inducible. The TR11 ligand is constitutively  
 CC expressed in an endothelial cell line. This suggests that TR11 and  
 CC its ligand may be involved in activated T-cell trafficking.  
 CC The invention provides TR11, TR11SV1 and TR11SV2 nucleic acids  
 CC (see AAA50304-06) and highly conserved encoded proteins (see  
 CC IAY95879-81), as well as vectors, host cells and recombinant methods for  
 CC their production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an

CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognose  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.  
 XX  
 SQ Sequence 234 AA;  
 Query Match 100.0%; Score 979; DB 21; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-70;  
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MAQHGMAGAFRALCGLALCALSLGORPTGGCGPGRLLLTGTGDARCRVHTTRCCRD 60  
 Db 1 maqhgmagafraleglallcalslgqrptggpgcpggrlllgtgdarccrvhttrccrd 60  
 Qy 61 YPGEECCSEWDCMCVQPFHCGDPCTTCRRHPCPPGQGVQSGKFSFGQCIDCASGTF 120  
 Db 61 ypgeeccsewdcmcvqpfhcgdpcttcrhpcppgqgvqsgkfsfgqcidcasgtf 120  
 Qy 121 SGGHEGCHKPWTDCQTQFGFLTVPGNKTHNAVCPGSPPAEPLG 164  
 Db 121 sgghegchkpwtcdqtfqfgfltvpgnknthnavcvpgspaeplg 164  
 RESULT 2  
 RAY52158  
 ID AAY52158 standard; Protein; 234 AA.  
 XX  
 AC AAY52158;  
 XX  
 DT 01-FEB-2000 (first entry)  
 XX  
 DE Tumour necrosis factor receptor-like protein (TR11) amino acid sequence.  
 XX  
 KW Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2;  
 KW G1TR; growth; differentiation; cell death; immune deficiency disorder;  
 KW Digeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia;  
 KW Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes;  
 KW Alzheimer's disease; Parkinson's disease; Huntingdon's disease;  
 KW inflammatory condition.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..25 /label= Signal\_peptide  
 FT Protein 26..234 /label= TR11  
 FT Domain 26..162 /note= "Extracellular domain"  
 FT Domain 163..179 /note= "Transmembrane domain"  
 FT Domain 180..234 /note= "Intracellular domain"  
 XX  
 PN WO9920758-A1.  
 XX  
 XX 29-APR-1999.  
 XX  
 XX 21-OCT-1998; 98WO-US22085.  
 XX  
 XX 21-OCT-1997; 97US-0063212.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.

Result No.	Score	Query Match	Length	DB	ID	Description
1	979	100.0	234	21	AA95879	Human tumour necro
2	979	100.0	234	21	AA52158	Tumour necrosis fa
3	979	100.0	241	19	AA37839	Amino acid sequenc
4	979	100.0	241	20	AA06605	Human TNF receptor
5	979	100.0	241	21	AA27651	Human protein PRO3
6	979	100.0	241	21	AA33431	Human PRO364 prote
7	979	100.0	241	21	AA95895	Human tumour necro
8	979	100.0	241	21	AA24409	Human PRO364 prote
9	979	100.0	241	21	AA71467	Human PRO364 prote
10	979	100.0	241	22	AA20115	Human immunostimul
11	979	100.0	241	22	AA847054	Human PRO364. Hom

FI domain  
84...93  
/note="conserved domain CD-III"



XX Ni J, Ruben SM;  
 XX WPI; 2000-061922/05.  
 DR N-PSDB; AA237762.  
 XX  
 PT New tumour necrosis factor receptor-like polypeptides used to, e.g.  
 PT treat Digeorge syndrome -  
 XX  
 PS Claim 14; Fig 1; 167pp; English.  
 XX  
 CC This is the amino acid sequence of the human tumour necrosis factor  
 CC receptor-like protein (Trll receptor). The invention relates to Trll and  
 CC two splice variants TrllSV1 and TrllSV2. The nucleotide sequences were  
 CC determined by sequencing cloned cDNAs AA237765-237766. The Trll receptor  
 CC and its splice variants show homology to the murine glucocorticoid  
 CC induced tumour necrosis factor receptor family-related gene (GTRF).  
 CC Trll, TrllSV1 and TrllSV2 polypeptides may be involved in the regulation  
 CC of cell-type specific receptor-mediated cell growth, differentiation,  
 CC and ultimately, cell death. They can be used for screening for  
 CC agonists/antagonists. The polypeptides, agonists or antagonists can be  
 CC used for treating a disease state associated with aberrant cell  
 CC survival. They can be used for treating immune deficiency disorders,  
 CC Digeorge syndrome, HIV infection, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood  
 CC platelet disorders or wounds resulting from trauma or surgery. They can  
 CC also be used to treat heart attacks, strokes, Addison's disease,  
 CC haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's  
 CC disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome,  
 CC systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent  
 CC diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,  
 CC hypersensitivity to an antigenic molecule, organ rejection or graft  
 CC versus host disease, inflammatory conditions, ischaemia-reperfusion  
 CC injury, complement-mediated hyperacute rejection, nephritis, cytokine or  
 CC chemokine induced lung injury, inflammatory bowel disease, Crohn's  
 CC disease, hyperproliferative disorders, or infections. They can also be  
 CC used to repair, replace, or protect tissue damaged by congenital  
 CC defects, trauma, age, disease, surgery, including cosmetic plastic  
 CC surgery, fibrosis, reperfusion injury, peripheral nerve injuries,  
 CC neuropathies, and central nervous system disease (e.g. Alzheimer's  
 CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral  
 CC sclerosis, and Shy-Drager syndrome). The products can also be used for  
 CC detection, diagnosis and prognosis.  
 XX Sequence 234 AA;  
 SQ  
 Query Match 100.0%; Score 979; DB 21; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-70;  
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAQHGMAGAFRALCGLLCALSLGQRTGPGCGPGRLLLTGTDCRCRVRHTTCCRD 60  
 DB 1 maqhgmgafrafcgllalcalsglrptggpgcgprlllgtgdarccrvhttrccrd 60  
 QY 61 YPGECCSEWDCMVCQPEHFCGDPCTTCRHPCPPGQGVQSGKFSFGQCIDCASGTF 120  
 DB 61 ypgeccsewdcmcvqpefhcgdpcttcrrhpcppgqgvqsgkfsfgqcidcasgtf 120  
 QY 121 SGGHEGCHKPWTDCQFGFLTVFPGNKTHNAVCPVGPSPAPPLG 164  
 DB 121 sgghegchckpwtcdqfgfltvfpgnkthnavcvpsppaepig 164  
 RESULT 3  
 ID AAW37839  
 XX AAW37839 standard; Protein; 241 AA.  
 XX AAW37839;  
 XX 28-JUL-1998 (first entry)  
 XX DE; Amino acid sequence of the human 312C2 T cell protein.

XX Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 KW antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
 KW autoimmune disorders.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FT CDS 1..726  
 FT /\*tag= a  
 FT /product= "human 312C2 protein"  
 XX  
 PN WO9806842-A1.  
 XX 19-FEB-1998.  
 PD  
 XX 14-AUG-1997; 97WO-US13931.  
 PF  
 XX 07-OCT-1996; 96US-0027901.  
 PR 16-AUG-1996; 96US-0689943.  
 PR  
 XX (SCHE ) SCHERING CORP.  
 PA  
 XX Gorman DM, Randall TD, Zlotnik A;  
 PI  
 XX WPI; 1998-159534/14.  
 DR N-PSDB; AAV19153.  
 DR  
 XX Isolated 312C2 T cell gene - used to develop products for treating,  
 PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 PT other T cell disorders  
 XX  
 PS Claim 2; Pages 59-60; 71pp; English.  
 XX  
 CC This is the amino acid sequence encoding the human 312C2 T cell  
 CC protein. The 312C2 proteins are expressed in thymus cells and are  
 CC induced on T cells and spleen cells following activation. Engagement  
 CC of 312C2 stimulates proliferation of T cell clones, antigen-specific  
 CC proliferation and cytokine production by T-cells, and potentiates T  
 CC cell expansion or apoptosis. The products can be used in the  
 CC treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX Sequence 241 AA;  
 SQ  
 Query Match 100.0%; Score 979; DB 19; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 4e-70;  
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAQHGMAGAFRALCGLLCALSLGQRTGPGCGPGRLLLTGTDCRCRVRHTTCCRD 60  
 DB 1 maqhgmgafrafcgllalcalsglrptggpgcgprlllgtgdarccrvhttrccrd 60  
 QY 61 YPGECCSEWDCMVCQPEHFCGDPCTTCRHPCPPGQGVQSGKFSFGQCIDCASGTF 120  
 DB 61 ypgeccsewdcmcvqpefhcgdpcttcrrhpcppgqgvqsgkfsfgqcidcasgtf 120  
 QY 121 SGGHEGCHKPWTDCQFGFLTVFPGNKTHNAVCPVGPSPAPPLG 164  
 DB 121 sgghegchckpwtcdqfgfltvfpgnkthnavcvpsppaepig 164  
 RESULT 4  
 ID AAY06605  
 XX AAY06605 standard; Protein; 241 AA.  
 XX AAY06605;  
 XX AC AAY06605;  
 XX

Db 121 sgghgchckpwtcdctqfgyflvfpnknthnavcvpgspapleplg 164  
 |||

RESULT 7  
 AAY95895  
 ID AAY95895 standard; Protein; 241 AA.

XX AC AAY95895;  
 XX DT 20-NOV-2000 (first entry)  
 XX DE Human tumour necrosis factor receptor-like protein TR11 mutein.

XX KW TR11; human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
 KW dermatological; antiinflammatory; therapy; diagnosis; mutein;  
 KW mutant.

XX OS Homo sapiens.  
 XX PN WO200050459-A1.  
 XX PD 31-AUG-2000.  
 XX PF 23-FEB-2000; 2000WO-US04572.  
 XX PR 24-FEB-1999; 99US-0121648.  
 XX PR 13-MAY-1999; 99US-0134172.  
 XX PR 16-JUL-1999; 99US-0144076.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, NI J;

XX DR WPI; 2000-572072/53.

XX PT Human tumor necrosis factor receptor-like proteins useful for  
 PT diagnosis, prevention and treatment of disease states associated with  
 PT aberrant cell survival such as autoimmune disease and rheumatoid  
 PT arthritis -

XX PS Disclosure; 294-295; 278pp; English.

XX CC The present sequence is that of human tumour necrosis factor  
 CC receptor-like protein TR11 (see also AAY95879), a novel protein  
 CC showing identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The invention provides  
 CC highly conserved TR11, TR11SV1 and TR11SV2 proteins (see AAY95879-81),  
 CC as well as vectors, host cells and recombinant methods for their  
 CC production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an  
 CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IGA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.

XX SQ Sequence 241 AA;

Query Match 100.0%; Score 979; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 4e-70;  
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMGAFAFRALCGIALCALSLGQRPTGGGCGGPRLLLTGTGDARCCRVHTTRCCRD 60  
 |||  
 Db 1 maqhgamafralcgialcalslgqrptggcgpggrllltgtgdarccrvhttrccrd 60  
 QY 61 YPGECCSEWDGCMQVQPFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQCIDCASGTF 120  
 |||  
 Db 61 ypgeccsewdgcmqvqpfhcgdpcccttcrrhpcppgqgvqsgkfsfgqcidcasgtf 120  
 QY 121 SGGHEGHCCKPWTCDCTQFGFLTVFPGNKNTHNAVVCVPGSPAPLEPLG 164  
 |||  
 Db 121 sgghgchckpwtcdctqfgyflvfpnknthnavcvpgspapleplg 164

RESULT 8

AAB24409  
 ID AAB24409 standard; Protein; 241 AA.

XX AC AAB24409;

XX DT 07-NOV-2000 (first entry)

XX DE Human PRO364 protein sequence SEQ ID NO:117.

XX KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
 KW cytostatic; gene therapy; vaccine.

XX OS Homo sapiens.

XX PN WO2000032221-A2.

XX PD 08-JUN-2000.

XX PF 30-NOV-1999; 99WO-US28313.

XX PR 01-DEC-1998; 98WO-US25108.  
 PR 16-DEC-1998; 98US-0112850.  
 PR 12-JAN-1999; 99US-0115554.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 28-APR-1999; 99US-0131445.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-OCT-1999; 99US-0162506.

XX PA (GETH ) GENENTECH INC.

XX PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;  
 PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;  
 PI Watanabe CK, Williams PM, Wood WI;

XX DR WPI; 2000-412154/35.

XX PT N-PSDB; AAA77604.

XX PT Nucleic acids encoding PRO polypeptides useful for preventing,  
 PT diagnosing and treating diagnosing a cardiovascular, endothelial, or  
 PT angiogenic disorders in mammals -

XX PS Claim 72; Fig 44; 315pp; English.

XX CC The present invention describes nucleic acids encoding PRO polypeptides  
 CC useful for preventing, diagnosing and treating diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder in mammals by



CC sequence is one of the proteins of the invention.

SQ Sequence 241 AA;

Query Match 100.0%; Score 979; DB 21; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4e-70;  
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMAGAFRALCGLALLCALSLGQRTGPGCGPGRLLLTGTDCRCRVHTTRCCRD 60  
|||||  
Db 1 maqhgamafralcgallcalslgqrptgpgcgprlllgtgdarcrcrvhttrccrd 60  
QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQVQSQGKFSFGQICDASGTF 120  
|||||  
Db 61 ypgeccsewdcmcvqpefhcgdpcccttrhpcppgqvgsgkfsgfqicdacsgrtf 120  
QY 121 SGGHEGHCCKPWTDCQFGFLTVFPGNKTHNAVCPGSPPAEPLG 164  
|||||  
Db 121 sggheghckpwtcdqfgfltvfpgnkthnavcvpgspppaepig 164

# RESULT 6

AAB33431

ID AAB33431 standard; Protein; 241 AA.

XX AC AAB33431;

XX DT 29-JAN-2001 (first entry)

XX DE Human PRO364 protein UNQ319 SEQ ID NO:92.

XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
KW dermatological; antiarthritic; antiirheumatic; immunosuppressive;  
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;  
KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;  
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
KW autoimmune thrombocytopenia; immune-mediated renal disease;  
KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
KW inflammatory bowel disease; gluten-sensitive enteropathy;  
KW autoimmune disease; immune-mediated skin disease; allergic disease;  
KW immunological disease; transplantation associated disease;  
KW graft rejection; graft-versus-host-disease.

XX OS Homo sapiens.

XX PN WO200053758-A2.

XX PD 14-SEP-2000.

PF 02-MAR-2000; 2000WO-US05841.

XX 08-MAR-1999; 99WO-US05028.  
PR 10-MAR-1999; 99US-0123618.  
PR 12-MAR-1999; 99US-0123957.  
PR 23-MAR-1999; 99US-0125775.  
PR 12-APR-1999; 99US-0128849.  
PR 20-APR-1999; 99WO-US08615.  
PR 28-APR-1999; 99US-0131445.  
PR 04-MAY-1999; 99US-0132371.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 28-JUL-1999; 99US-0146222.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 29-OCT-1999; 99US-0162506.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30999.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
XX  
PA (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;

PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;

PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

XX WPI; 2000-572271/53.

DR N-PSDB; AAC58596.

XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of

PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid

PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -

XX Claim 33; Fig 36; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can  
CC be used in the treatment of immune related diseases. The human PRO  
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
CC treating and diagnosing immune related disorders. The disorders are  
CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central  
CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
CC autoimmune or immune-mediated skin diseases, allergic diseases,  
CC immunological diseases of the lung, and transplantation associated  
CC diseases including graft rejection and graft-versus-host-disease.  
CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.

XX Sequence 241 AA;

Query Match 100.0%; Score 979; DB 21; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4e-70;  
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMAGAFRALCGLALLCALSLGQRTGPGCGPGRLLLTGTDCRCRVHTTRCCRD 60  
|||||

Db 1 maqhgamafralcgallcalslgqrptgpgcgprlllgtgdarcrcrvhttrccrd 60  
|||||

QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQVQSQGKFSFGQICDASGTF 120  
|||||

Db 61 ypgeccsewdcmcvqpefhcgdpcccttrhpcppgqvgsgkfsgfqicdacsgrtf 120  
|||||

QY 121 SGGHEGHCCKPWTDCQFGFLTVFPGNKTHNAVCPGSPPAEPLG 164

XX Human immunostimulant PRO364.  
DE  
XX PRO364; human; immune disease; autoimmune disease;  
KW anticheumatic; antiarthritic; antiinflammatory; antianaemic;  
KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;  
KW hepatotropic; virucide; dermatological; antipsoriatic;  
KW antiasthmatic; antiallergic; immunostimulant.  
XX  
OS Homo sapiens.  
XX  
XX  
XX  
XX Key Location/Qualifiers  
FT Peptide 1..25  
FT Protein /label= Signal\_peptide  
FT Domain /label= Mature\_protein  
FT Modified-site 163..183  
FT Modified-site /note= "transmembrane domain"  
FT Modified-site 5..11  
FT Modified-site /note= "N-myristoylation site"  
FT Modified-site 8..14  
FT Modified-site /note= "N-myristoylation site"  
FT Modified-site 25..31  
FT Modified-site /note= "N-myristoylation site"  
FT Modified-site 30..36  
FT Modified-site /note= "N-myristoylation site"  
FT Modified-site 33..39  
FT Modified-site /note= "N-myristoylation site"  
FT Modified-site 118..124  
FT Modified-site /note= "N-myristoylation site"  
FT Modified-site 122..128  
FT Modified-site /note= "N-myristoylation site"  
FT Modified-site 156..162  
FT Modified-site /note= "N-myristoylation site"  
FT Modified-site 146..150  
FT Modified-site /note= "Asn is N-glycosylated"  
FT Peptide 166..177  
FT Peptide /note= "prokaryotic membrane lipoprotein lipid  
FT Peptide attachment site"  
FT Peptide 171..193  
FT Peptide /note= "leucine zipper pattern"  
XX  
XX W0200105972-A1.  
XX  
XX 25-JAN-2001.  
XX  
XX 15-MAR-2000; 2000WO-US06884.  
XX  
XX 20-JUL-1999; 99US-0144758.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;  
PI Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK;  
PI Wood WI;  
XX  
XX WPI; 2001-103149/11.  
XX  
XX N-PSDB; AAF30057.  
XX  
XX  
XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
PT diagnosing and treating immune-related disorders, such as multiple  
PT sclerosis, rheumatoid arthritis and diabetes -  
XX  
XX Claim 20; Fig 16; 127pp; English.  
XX  
XX The present sequence is that of novel human immunomodulator PRO364  
CC (UNQ319), as deduced from cDNA (see AAF30057) isolated from a  
CC small intestine library. PRO364 (26 kDa, pI 6.34) shows sequence  
CC homology to mouse GTR protein and may be its human counterpart.  
CC The invention provides polynucleotides (see AAF30050-62) encoding  
CC novel human PRO proteins (see AAF20108-20) including PRO364.  
CC Claimed compositions comprising these proteins or their agonists  
CC are useful for increasing infiltration of inflammatory cells into

CC a tissue of a mammal, stimulating or enhancing an immune  
CC response, or increasing the proliferation of T-lymphocytes in a  
CC mammal in response to an antigen. Claimed compositions comprising  
CC a PRO polypeptide or its antagonist have the opposite effect. A  
CC claimed method for treating an immune related disorder, such as a T  
CC cell disorder, involves administering a PRO polypeptide, an agonist  
CC antibody or an antagonist antibody. The disorder is selected from  
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
CC juvenile chronic arthritis, spondyloarthropathy, systemic sclerosis,  
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
CC thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated  
CC renal disease, demyelinated diseases (such as multiple sclerosis),  
CC autoimmune chronic active hepatitis, primary biliary cirrhosis,  
CC granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel  
CC disease (ulcerative colitis and Crohn's disease), gluten-sensitive  
CC enteropathy, Whipple's disease, (auto)immune-mediated skin diseases  
CC (such as bullous skin disease, erythema multiforme and psoriasis),  
CC allergic diseases (such as asthma, allergic rhinitis, atopic  
CC dermatitis, food hypersensitivity and urticaria), immunologic  
CC diseases of the lung and transplantation associated diseases (such  
CC as graft rejection and graft-versus-host disease) (all claimed).  
CC Claimed methods of diagnosing these disorders comprise detecting  
CC the level of expression of the PRO gene. Also claimed are a method  
CC of identifying a compound capable of inhibiting the expression or  
CC activity of the PRO polypeptide, vectors, host cells, antibodies,  
CC and a method of stimulating the proliferation of T lymphocytes  
CC using PRO364.  
XX  
XX Sequence 241 AA;

Query Match 100.0%; Score 979; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4e-70;  
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAQHGMAGAFRALCGLALCALSLGQRTGGPGCGPGRLLLTGTDTARCRVHTTRCD 60  
Db 1 maqhgmagafralcglalcalalqgrptgpgcgprllltgttdarcrvhttrcd 60  
QY 61 YPGECCSPWDCMCVQPEPHCGDPCCTTCRRHPCPGCGVSGGKFSFGQICDASGTF 120  
Db 61 YPGECCSPWDCMCVQPEPHCGDPCCTTCRRHPCPGCGVSGGKFSFGQICDASGTF 120  
QY 121 SGHEGHCCKPWTDCQFGELTVFPGNKTHNAVCPGSPPAEPLG 164  
Db 121 sgheghckpwtcdtqfgeltvfpngkthnavcvgpsppaeplg 164

RESULT 11  
AAB47054  
ID AAB47054 standard; Protein; 241 AA.  
XX  
AC AAB47054;  
XX  
DT 08-MAY-2001 (first entry)  
XX  
DE Human PRO364.  
XX  
KW PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;  
KW hGTR; ligand; hGTRL; PRO175; tumour necrosis factor receptor; TNFR;  
KW human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;  
KW myocardial infarction; PGF.2alpha; trauma; cancer; angiogenesis;  
KW age-related macular degeneration; antibody; periodontal disease;  
KW vascular-related drug targeting; atherosclerosis; hypertension;  
KW inflammatory vasculitides; Reynaud's disease; aneurysm;  
KW arterial restenosis; thrombophlebitis; tumor angiogenesis;  
KW lung; liver; fibrosis; neuropathy; rheumatoid arthritis.  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..26  
FT

CC modulating cell proliferation, angiogenesis and cardiovascularisation,  
CC and for identifying agonists and antagonists of these processes. The  
CC nucleic acids and the proteins they encode may be used in the  
CC prevention, treatment and diagnosis of diseases associated with  
CC inappropriate PRO expression such as cardiovascular, endothelial or  
CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and  
CC cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors  
CC containing them and the PRO polypeptide may be used to treat disorders  
CC associated with decreased PRO expression. AAA77510 to AAA77721 and  
CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in  
CC the exemplification of the present invention.

XX Sequence 241 AA;

Query Match 100.0%; Score 979; DB 21; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4e-70;  
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAQHGMAGFALCGLLALCALSLGQRPTGGCGPGRLLLTGTDTARCCRVHTTRCCRD 60  
Db 1 maqhgamgafalcgllalcalslgqrptggcgpggrlllgtgdarccrvhttrccrd 60  
QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPGQGVQSGKFSFGQCIDCASGTF 120  
Db 61 ypgeccsewdcmcvqpefhcgdpcccttrhhpcpgpgqgvsggkfsfgqcidcasgtf 120  
QY 121 SGGHEGCHKPWTDCQFGFLTVFPNGKTNHNAVCPGSPPAEPLG 164  
Db 121 sggheghckpwtcdctqfgfltvfpngktnhnavcvpgspppaeplg 164

RESULT 9

AA71467  
ID AA71467 standard; Protein; 241 AA.

AC AA71467;

DT 08-NOV-2000 (first entry)

DE Human PRO364 protein.

XX PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;  
KW neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;  
KW breast; prostate; colon; lung; renal; ovarian; central nervous system;  
KW CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue;  
KW tumour necrosis factor receptor; GTR protein homologue.

XX Homo sapiens.

OS Key Location/Qualifiers  
XX Peptide 1..25 /label= Signal\_peptide  
FT Modified-site 5..11 /note= "N-myristoylation site"  
FT Modified-site 8..14 /note= "N-myristoylation site"  
FT Modified-site 25..31 /note= "N-myristoylation site"  
FT Protein 26..241 /label= Mature\_PRO364\_protein  
FT Modified-site 30..36 /note= "N-myristoylation site"  
FT Modified-site 33..39 /note= "N-myristoylation site"  
FT Modified-site 118..124 /note= "N-myristoylation site"  
FT Modified-site 122..128 /note= "N-myristoylation site"  
FT Modified-site 146..150 /note= "N-myristoylation site"  
FT Modified-site 156..162 /note= "N-myristoylation site"  
FT Modified-site 156..162 /note= "N-myristoylation site"

FT Domain 163..183 /label= Transmembrane\_domain  
FT Binding-site 166..177 /note= "Prokaryotic membrane lipoprotein lipid attachment site"  
FT Region 171..193 /note= "Leucine zipper pattern"  
XX WO200032778-A2.  
PN 08-JUN-2000.  
PD 30-NOV-1999; 99WO-US28409.  
PF 01-DEC-1998; 98WO-US25108.  
PR 16-DEC-1998; 98US-0112850.  
PR 22-DEC-1998; 98US-0113296.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
XX (GETH ) GENENTECH INC.  
PA Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;  
PI WPI: 2000-412325/35.  
XX N-PSDB; AAD01240.  
DR New composition useful for inhibiting neoplastic cell growth and for treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or their antagonists  
XX Claim 31; Fig 4; 108pp; English.  
XX The present sequence is the human PRO364 protein, encoded by the cDNA clone, designated as DNA47365-1206. It is isolated from human small intestine tissue cDNA library, identified using probes based on the consensus sequence DNA44825, relative to the incyte expressed sequence tag (EST) 3003460. This EST has homology to tumour necrosis factor receptor (TNFR) family of polypeptides. PRO364 sequence also shows homology to members of the TNFR family and mouse GTR protein.  
CC This clone is assigned the ATCC deposit No: 209436. PRO364 functions as a neoplastic cell growth inhibitor and is used for treating tumours, using an effective amount of PRO655, PRO364 and PRO344. This composition is especially useful for treatment of human cancers such as breast, prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.

XX Sequence 241 AA;

Query Match 100.0%; Score 979; DB 21; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4e-70;  
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAQHGMAGFALCGLLALCALSLGQRPTGGCGPGRLLLTGTDTARCCRVHTTRCCRD 60  
Db 1 maqhgamgafalcgllalcalslgqrptggcgpggrlllgtgdarccrvhttrccrd 60  
QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPGQGVQSGKFSFGQCIDCASGTF 120  
Db 61 ypgeccsewdcmcvqpefhcgdpcccttrhhpcpgpgqgvsggkfsfgqcidcasgtf 120  
QY 121 SGGHEGCHKPWTDCQFGFLTVFPNGKTNHNAVCPGSPPAEPLG 164  
Db 121 sggheghckpwtcdctqfgfltvfpngktnhnavcvpgspppaeplg 164

RESULT 10

AAB20115  
ID AAB20115 standard; Protein; 241 AA.

XX AAB20115;

XX 30-APR-2001 (first entry)

CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
 CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic  
 CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases  
 CC (such as infectious, autoimmune chronic active hepatitis, primary  
 CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
 CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
 CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
 CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
 CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
 CC food hypersensitivity and urticaria), immunological diseases of the  
 CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
 CC and hypersensitivity pneumonitis), transplantation associated diseases  
 CC including graft rejection and graft-versus-host diseases.  
 XX  
 SQ Sequence 241 AA;

Query Match 100.0%; Score 979; DB 22; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 4e-70;  
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMGAFRALCGLALLCALSIGQRTGGPGCGPGRLLLTGTDCRCRVRTTCRRD 60  
 DB 1 maqhgamafralcglallcalslgqrtpggcgpggrlllgtgdarccrvhtrccrd 60  
 QY 61 YPGECCSEWDCMCVQPFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQCIDCASGTF 120  
 DB 61 ypgeccsewdcmcvqpfhcgdpccctcrhhpcppggvgvsgqkfsfgqcidcasgtf 120  
 QY 121 SGGHEGHCKPMWTDCTQFGFLTFVPGNKNTHNAVCPGSPPAEPLG 164  
 DB 121 sggheghckpwtcdtqfgfltfvpgnknthnavcvpgspapleplg 164

RESULT 13  
 AAB50982

ID AAB50982 standard; Protein; 241 AA.

XX

AC AAB50982;

DT 21-MAR-2001 (first entry)

XX Human PRO364 protein.

DE

XX Human; PRO: cardiac; antiangiogenic; antiarteriosclerotic; hypotensive;  
 KW vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;  
 KW vulnary; antianginal; gene therapy; cardiovascular disease;  
 KW endothelial disorder; angiogenic disorder; cancer; periodontal disease;  
 KW wound healing.

XX Homo sapiens.

XX

PN WO200073445-A2.

XX

PD 07-DEC-2000.

XX

PF 17-MAY-2000; 2000WO-US13705.

XX

PR 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 28-JUL-1999; 99US-0146222.

PR 01-SEP-1999; 99WO-US20111.

PR 30-NOV-1999; 99WO-US28313.

PR 30-NOV-1999; 99WO-US28409.

PR 02-DEC-1999; 99WO-US28565.

PR 16-DEC-1999; 99WO-US30095.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.

PR 18-FEB-2000; 2000WO-US04342.

PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen MF;  
 PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;  
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
 XX  
 DR WPI; 2001-025251/03.  
 DR N-PSDB; AAC90566.

XX  
 PT Seventeen nucleic acids encoding PRO polypeptides which are useful in  
 PT diagnosis and treatment of cardiovascular, endothelial or angiogenic  
 PT disorders in a mammal -

PS Claim 71; Fig 8; 182pp; English.

XX

CC The present sequence is one of seventeen novel PRO polypeptides. The PRO  
 CC nucleic acids, polypeptides, agonists and antagonists are useful for  
 CC treating cardiovascular, endothelial or angiogenic disorders in a mammal.  
 CC Examples of these disorders include cardiac hypertrophy, trauma, cancer,  
 CC age-related macular degeneration, atherosclerosis, hypertension, arterial  
 CC restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial  
 CC infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and  
 CC antagonists are also used to prevent tumour angiogenesis and for treating  
 CC periodontal diseases. They are also used to stimulate wound healing and  
 CC tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO  
 CC antibodies are useful for diagnosing a cardiovascular, endothelial or  
 CC angiogenic disorder.  
 XX

SQ Sequence 241 AA;

Query Match 100.0%; Score 979; DB 22; Length 241;

Best Local Similarity 100.0%; Pred. No. 4e-70;

Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMGAFRALCGLALLCALSIGQRTGGPGCGPGRLLLTGTDCRCRVRTTCRRD 60  
 DB 1 maqhgamafralcglallcalslgqrtpggcgpggrlllgtgdarccrvhtrccrd 60

QY 61 YPGECCSEWDCMCVQPFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQCIDCASGTF 120  
 DB 61 ypgeccsewdcmcvqpfhcgdpccctcrhhpcppggvgvsgqkfsfgqcidcasgtf 120

QY 121 SGGHEGHCKPMWTDCTQFGFLTFVPGNKNTHNAVCPGSPPAEPLG 164

DB 121 sggheghckpwtcdtqfgfltfvpgnknthnavcvpgspapleplg 164

RESULT 14

AAB53090

ID AAB53090 standard; Protein; 241 AA.

XX

AC AAB53090;

XX

DT 28-FEB-2001 (first entry)

XX

DE Human angiogenesis-associated protein PRO364, SEQ ID NO:142.

XX Human; angiogenesis-associated protein; PRO: endothelial cell growth;  
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
 KW gene therapy; transgenic animal.

XX

FT Modified-site /note= "Potential signal peptide"  
 FT /note= "N-glycosylated"  
 FT Domain 162..180  
 FT /note= "Potential transmembrane domain"  
 XX  
 XX WO200103720-A2.  
 PN  
 XX  
 PD 18-JAN-2001.  
 XX  
 XX 11-JUL-2000; 2000WO-US18867.  
 XX  
 XX 12-JUL-1999; 99US-0143304.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Williams PM, Gerritsen ME;  
 PI  
 XX WPI: 2001-138257/14.  
 DR N-PSDB; AAC85433.

Composition for diagnosing and treating cardiovascular, endothelial and angiogenic disorders, comprises a PRO364 or PRO175 polypeptide -

Claim 1; Fig 1; 76pp; English.

This sequence represents PRO364 polypeptide, which is a human glucocorticoid-induced tumor necrosis factor receptor (hGTR). The corresponding ligand (hGTR), PRO175, is given in AAB47056. PRO364 and PRO175 may be used in a mixture with a cardiovascular, endothelial, angiogenic or angiotensin agent for the treatment of a cardiovascular, endothelial, angiogenic or angiotensin disorder. The PRO364 cDNA sequence was isolated from an expressed sequence tag (EST) database as having homology to members of the tumour necrosis factor receptor (TNFR) family of polypeptides. The PRO175 cDNA sequence was isolated from a library of cDNA fragments derived from human umbilical vein endothelial cells (HUVBC). Administering an effective amount of PRO364 or PRO175 or their antagonists is useful for treating cardiac hypertrophy (which is initiated by myocardial infarction and characterized by the presence of an elevated level of PGF<sub>2</sub>alpha), trauma, a cancer, or age-related macular degeneration in a human. Administering a therapeutically effective amount of an antibody that binds PRO364 or PRO175 is useful for inhibiting angiogenesis induced by PRO364 or PRO175 in a human suffering from a tumor or a retinal disorder. PRO364 or PRO175, or their antagonists, are useful for vascular-related drug targeting or as therapeutic targets for the treatment or prevention of atherosclerosis, hypertension, inflammatory vasculitides, Reynaud's disease, aneurysms, arterial restenosis, thrombophlebitis, tumor angiogenesis, gut protection or regeneration and treatment of lung or liver fibrosis, periodontal diseases, attraction of bone-forming cells, central and peripheral nervous system disease and neuropathies and rheumatoid arthritis.

Sequence 241 AA;

Query Match 100.0%; Score 979; DB 22; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 4e-70; Indels 0; Gaps 0;  
 Matches 164; Conservative 0; Mismatches 0;

QY 1 MAQHGMAGAFRALCGLALCALSLGQRTGGCGPGRLLLTGTCDARCCRVHTTCRCD 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 maqhgmgafRALCGLALCALSLGRTGGCGPGRLLLTGTCDARCCRVHTTCRCD 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 61 YPGEECCSEWDCMVCQPEFHCGPCCCTTCRHHPCPGQGVQSGKFSFGQCIDCASGTF 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 YPGEECCSEWDCMVCQPEFHCGPCCCTTCRHHPCPGQGVQSGKFSFGQCIDCASGTF 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 121 SGHEGHCXPDWTDCTQFGILTVPFGKNTNNAVCPGSPPAEPLG 164  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 sgghgchxpdwtdctqfgiltvfpgnktnnavcvpgspppaep1g 164  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 12  
 AAB50910  
 ID AAB50910 standard; Protein; 241 AA.  
 XX  
 AC AAB50910;  
 XX  
 DT 21-MAR-2001 (first entry).  
 XX  
 XX Human PRO364 protein.  
 XX  
 KW Human; PRO; antiinflammatory; dermatological; antiarthritic;  
 KW antirheumatic; cardiac; antianemic; immunosuppressive; antithyroid;  
 KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;  
 KW antiallergic; antiasthmatic; immune related disorder;  
 KW hepatobiliary disease; autoimmune disease; allergy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200073452-A2.  
 XX  
 PD 07-DEC-2000.  
 XX  
 XX 02-JUN-2000; 2000WO-US15264.  
 XX  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 20-JUL-1999; 99US-0144732.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 XX  
 XX (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;  
 PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tamas D, Watanabe CK;  
 PI Wood WI;

WPI: 2001-025253/03.  
 N-PSDB; AAC91469.

Thirty three nucleic acids encoding PRO polypeptides which are useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus -

Claim 58; Fig 18; 218pp; English.

The present sequence is one of thirty three novel PRO polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic

Query Match 96.7%; Score 947; DB 19; Length 228;  
Best Local Similarity 100.0%; Pred. No. 1.3e-67;  
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	7	MGAFRALGGLALLCALSLGQRPTGGPGCGPGRLLLGTTGDARCCRVHTTRCCRDYPGEEC	66
Db	1	mgafralcglallcalslgrptgpgcgpgrrlllgttdarccrvhttrccrdypgeec	60
Qy	67	CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGQVQSQKFSFGQCIDCASGTFSGGHEG	126
Db	61	csewdcmcvqpefhcgdpccctcrhhpcppggvgvsgqkfsfgqcidcasgtfsggheg	120
Qy	127	HCKPWTDTQTQGFLLTVFPGNKTHNAVCPGSPPAEPLG	164
Db	121	hckpwtddtqfgfltvfpgnkthnavcvpgspppaeplg	158

Search completed: September 4, 2001, 15:56:25  
Job time: 342 sec

OS Homo sapiens.  
XX WO200053753-A2.  
XX 14-SEP-2000.  
XX 05-JAN-2000; 2000WO-US000219.  
XX 08-MAR-1999; 99WO-US050528.  
XX 12-MAR-1999; 99US-0123957.  
XX 14-MAY-1999; 99US-0134287.  
XX 02-JUN-1999; 99WO-US12252.  
XX 23-JUN-1999; 99US-0141037.  
XX 20-JUL-1999; 99US-0144758.  
XX 26-JUL-1999; 99US-0145698.  
XX 01-SEP-1999; 99WO-US20111.  
XX 08-SEP-1999; 99WO-US20594.  
XX 15-SEP-1999; 99WO-US21090.  
XX 15-SEP-1999; 99WO-US21347.  
XX 05-OCT-1999; 99WO-US23089.  
XX 30-NOV-1999; 99WO-US28313.  
XX 30-NOV-1999; 99WO-US28409.  
XX 02-DEC-1999; 99WO-US28564.  
XX 02-DEC-1999; 99WO-US28565.  
XX (GETH ) GENENTECH INC.  
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
PI Godowski PU, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
XX WPI: 2001-090793/10.  
XX N-PSDB; AAC9479.  
XX New isolated nucleic acid for producing a PRO polypeptide, analyzing  
PT genetic disorders and treating cardiovascular, endothelial or  
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
XX Claim 69; Fig 54; 293pp; English.  
XX The invention relates to novel human angiogenesis-associated proteins  
CC designated PRO proteins (AA853064-B53097), and to nucleic acids encoding  
CC PRO proteins. The invention also relates to vectors and host cells  
CC comprising a PRO nucleic acid, the recombinant production of a PRO  
CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
CC compounds which inhibit the expression of a PRO gene. The invention  
CC additionally encompasses methods of identifying modulators of PRO  
CC expression or activity; diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
CC mutations in a PRO gene, or the expression level of a PRO gene within a  
CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
CC administration of a PRO protein, or an agonist or antagonist thereof.  
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
CC agonists and PRO antagonists may be used as therapeutic agents to treat  
CC cardiovascular, endothelial or angiogenic disorders, such as  
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
CC disease, or stroke. PRO nucleic acids are additionally useful in the  
CC recombinant production of PRO proteins, as hybridisation probes to  
CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
CC animals useful for the development and screening of potential  
CC therapeutic agents. The present sequence represents a PRO protein of the  
XX invention.  
XX Sequence 241 AA;

Query Match 100.0%; Score 979; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 4e-70;  
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAQHGAMGAFRALCGIALCALSLGQRTGGPGCGRLLLTGTGTARCCRVHTTRCCRD 60  
Db 1 maqhgamgafraleglallcalslgqrptggpgcggrlllgtgtardccrvhttrccrd 60  
Qy 61 YPGECCSEWDCMCVQPEFHGCDPCTTCRHHPCCPPGGVQSGQKFSFGFCIDCASGTF 120  
Db 61 ypgeccsewdcmcvqpefhgcpcttcrhpcppggvgqskfsfgfcidcasgtf 120  
Qy 121 SGGHEGHCKPMWTDCTQFGFLTVFPGNKTNAVCPGSPAPPLG 164  
Db 121 sggheghckpwtcdctqfgfltvfpgnkthnavcvpgspapaelg 164  
RESULT 15  
AAW37840  
ID AAW37840 standard; Protein; 228 AA.  
XX AAW37840;  
XX 28-JUL-1998 (first entry)  
XX Truncated human 312C2 protein from clone\_A8 amino acid sequence.  
DE Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
KW antigen-specific T cell proliferation; cytokine production by T-cell;  
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
KW autoimmune disorders.  
XX Homo sapiens.  
XX WO9806842-A1.  
XX 19-FEB-1998.  
XX 14-AUG-1997; 97WO-US13931.  
XX 07-OCT-1996; 96US-0027901.  
XX 16-AUG-1996; 96US-0689943.  
XX (SCHE ) SCHERING CORP.  
XX Gorman DM, Randall TD, Zlotnik A;  
XX WPI: 1998-159534/14.  
XX N-PSDB; AAV19154.  
XX Isolated 312C2 T cell gene - used to develop products for treating,  
PT e.g. cancers, auto-immune disorders, transplantation rejection and  
PT other T cell disorders  
XX Disclosure; Pages 61-62; 71pp; English.  
XX This is the amino acid sequence of the truncated human 312C2 T cell  
CC protein from clone\_A8. The 312C2 proteins are expressed in thymus  
CC cells and are induced on T cells and spleen cells following activation.  
CC Engagement of 312C2 stimulates proliferation of T cell clones,  
CC antigen-specific proliferation and cytokine production by T-cells, and  
CC potentiates T cell expansion or apoptosis. The products can be used  
CC in the treatment of conditions associated with abnormal physiology or  
CC development, including abnormal proliferation, e.g. cancerous  
CC conditions or degenerative conditions. They can be used in the  
CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
CC which affect immunological responses, e.g. autoimmune disorders.  
XX Sequence 228 AA;

|||||  
Db 26 qrtggpgcpgrrlllgttdarccrvhttrccrdypgeccsewdcmcvqpefhcgdp 85  
QY 61 CTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGCKPWTDCQTQGF 114  
Db 86 cttcrhhpcpppgvgvgqgkfsfgfcidcasgtfsggheghckpwtcdctqfgf 139  
  
RESULT 15  
AAB50982  
ID AAB50982 standard; Protein; 241 AA.  
XX  
AC AAB50982;  
XX  
DT 21-MAR-2001 (first entry)  
XX  
DE Human PRO364 protein.  
XX  
KW Human; PRO: cardiant; antiangiogenic; antiarteriosclerotic; hypotensive;  
KW vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;  
KW vulnery; antianginal; gene therapy; cardiovascular disease;  
KW endothelial disorder; angiogenic disorder; cancer; periodontal disease;  
KW wound healing.  
XX  
OS Homo sapiens.  
XX  
PN WO200073445-A2.  
XX  
PD 07-DEC-2000.  
XX  
PF 17-MAY-2000; 2000WO-US13705.  
XX  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 28-JUL-1999; 99US-0146222.  
PR 01-SEP-1999; 99WO-US20111.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;  
PI Paoni NF, Pitti RM, Watanabe CK, Williams PW, Wood WI;  
XX  
DR WPI; 2001-025251/03.  
DR N-PSDB; AAC90566.  
XX  
PT Seventeen nucleic acids encoding PRO polypeptides which are useful in  
PT diagnosis and treatment of cardiovascular, endothelial or angiogenic  
PT disorders in a mammal -  
XX  
PS Claim 71; Fig 8; 182pp; English.  
XX  
CC The present sequence is one of seventeen novel PRO polypeptides. The PRO  
CC nucleic acids, polypeptides, agonists and antagonists are useful for  
CC treating cardiovascular, endothelial or angiogenic disorders in a mammal.  
CC Examples of these disorders include cardiac hypertrophy, trauma, cancer,  
CC age-related macular degeneration, atherosclerosis, hypertension, arterial  
CC restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial

CC infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and  
CC antagonists are also used to prevent tumour angiogenesis and for treating  
CC periodontal diseases. They are also used to stimulate wound healing and  
CC tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO  
CC antibodies are useful for diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder.  
XX  
SQ Sequence 241 AA;  
  
Query Match 100.0%; Score 711; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2.9e-50;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 QRPTGGPGCGPGRLLLTGTDTDARCCRVHTTRCCRDYGECCSEWDCMCVQPEFHCGDPC 60  
Db 26 qrtggpgcpgrrlllgttdarccrvhttrccrdypgeccsewdcmcvqpefhcgdp 85  
  
QY 61 CTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTFSGGHEGCKPWTDCQTQGF 114  
Db 86 cttcrhhpcpppgvgvgqgkfsfgfcidcasgtfsggheghckpwtcdctqfgf 139  
  
Search completed: September 4, 2001, 15:56:23  
Job time: 340 sec



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XX Composition for diagnosing and treating cardiovascular, endothelial and  
 PT angiogenic disorders, comprises a PRO364 or PRO175 polypeptide -  
 PS Claim 1; Fig 1; 76pp; English.  
 XX This sequence represents PRO364 polypeptide, which is a human gluco-  
 CC corticoid-induced tumor necrosis factor receptor (hGTR). The  
 CC corresponding ligand (hGTRL), PRO175, is given in ABA47056.  
 CC PRO364 and PRO175 may be used in a mixture with a cardiovascular,  
 CC endothelial, angiogenic or angiostatic agent for the treatment of a  
 CC cardiovascular, endothelial, angiogenic or angiostatic disorder. The  
 CC PRO364 cDNA sequence was isolated from an expressed sequence tag (EST)  
 CC database as having homology to members of the tumour necrosis factor  
 CC receptor (TNFR) family of polypeptides. The PRO175 cDNA sequence was  
 CC isolated from a library of cDNA fragments derived from human umbilical  
 CC vein endothelial cells (HUEVC). Administering an effective amount of  
 CC PRO364 or PRO175 or their antagonists is useful for treating cardiac  
 CC hypertrophy (which is initiated by myocardial infarction and  
 CC characterized by the presence of an elevated level of PGF<sub>2</sub>alpha),  
 CC trauma, a cancer, or age-related macular degeneration in a human.  
 CC Administering a therapeutically effective amount of an antibody that  
 CC binds PRO364 or PRO175 is useful for inhibiting angiogenesis induced  
 CC by PRO364 or PRO175 in a human suffering from a tumor or a retinal  
 CC disorder. PRO364 or PRO175, or their antagonists, are useful for  
 CC vascular-related drug targeting or as therapeutic targets for the  
 CC treatment or prevention of atherosclerosis, hypertension, inflammatory  
 CC vasculitides, Reynaud's disease, aneurysms, arterial restenosis,  
 CC thrombophlebitis, tumor angiogenesis, gut protection or regeneration  
 CC and treatment of lung or liver fibrosis, periodontal diseases,  
 CC attraction of bone-forming cells, central and peripheral nervous  
 CC system disease and neuropathies and rheumatoid arthritis.  
 XX Sequence 241 AA;

Query Match 100.0%; Score 711; DB 22; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-50;  
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QRPTEGGCGPGRLLLTGTDCRCRVRTTCRDYPGEECCSEWDCMCVQPEFHGCDPC 60  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 26 qrpTEGGCGPGRLLLTGTDCRCRVRTTCRDYPGEECCSEWDCMCVQPEFHGCDPC 85  
 Oy 61 CTCRHPCPPGGQSQGKFSFGQICDASGTFSGHEGCKPWTCTQFG 114  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 86 cttcrhpcppggvsgqgkfsfgqicdasgTfsgghegckpwtctqfg 139

RESULT 14  
 AAB50910  
 ID AAB50910 standard; Protein; 241 AA.

XX AC AAB50910;  
 XX DT 21-MAR-2001 (first entry)  
 XX DE Human PRO364 protein.  
 XX KW Human; PRO; antiinflammatory; dermatological; antiarthritic;  
 KW antiinflammatory; cardiac; antianaemic; immunosuppressive; antithyroid;  
 KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;  
 KW antiallergic; antiasthmatic; immune related disorder;  
 KW hepatobiliary disease; autoimmune disease; allergy.

OS Homo sapiens.

XX WO200073452-A2.

XX PD 07-DEC-2000.

XX PF 02-JUN-2000; 2000WO-US15264.

XX

PR 02-JUN-1999; 99WO-US12252.  
 PR 20-JUL-1999; 99US-0144732.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.

(GETH ) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;  
 PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;  
 PI Wood WI;

DR WPI; 2001-025253/03.  
 DR N-PSDB; AAC91469.

XX Thirty three nucleic acids encoding PRO polypeptides which are useful  
 PT in the diagnosis and treatment of immune related disorders, e.g.  
 PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 PT thyroiditis and diabetes mellitus -

XX Claim 58; Fig 18; 218pp; English.

XX The present sequence is one of thirty three novel PRO polypeptides.  
 CC The PRO polypeptides, anti-PRO antibodies, agonists and  
 CC antagonists are useful for treating and diagnosing immune related  
 CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
 CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic  
 CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases  
 CC (such as infectious, autoimmune chronic active hepatitis, primary  
 CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
 CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
 CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
 CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
 CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
 CC food hypersensitivity and urticaria), immunological diseases of the  
 CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
 CC and hypersensitivity pneumonitis), transplantation associated diseases  
 CC including graft rejection and graft-versus-host diseases.

XX Sequence 241 AA;

Query Match 100.0%; Score 711; DB 22; Length 241;

Best Local Similarity 100.0%; Pred. No. 2.9e-50;  
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRPTEGGCGPGRLLLTGTDCRCRVRTTCRDYPGEECCSEWDCMCVQPEFHGCDPC 60



CC associated with decreased PRO expression. AAA77510 to AAA77721 and  
 CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in  
 CC the exemplification of the present invention.

XX Sequence 241 AA;

Query Match 100.0%; Score 711; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-50; Indels 0; Gaps 0;  
 Matches 114; Conservative 0; Mismatches 0;

Qy 1 QRP TGCGCGRLLLGTGTARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60  
 |||||  
 Db 26 qrp tggpgcgprlllgttdarccrvhttrccrdypgeccsewdcmcvqpefhcgdp 85  
 |||||  
 Qy 61 CTTCRHPCPPGGVQSGQKFSFGFCIDCASGTFSGGHEGHCKPWTDCQTQGF 114  
 |||||  
 Db 86 ctterhhpcppggvgqgkfsfgfcidcasgtfsggheghckpwtcdtqfgf 139  
 |||||

RESULT 11

AA71467  
 ID AA71467 standard; Protein; 241 AA.

XX AC AA71467;

XX DT 08-NOV-2000 (first entry)

XX DE Human PRO364 protein.

XX KW PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;  
 KW neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;  
 KW breast; prostate; colon; lung; renal; ovarian; central nervous system;  
 KW CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue;  
 KW tumour necrosis factor receptor; GTR protein homologue.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..25 /label= Signal\_peptide  
 FT Modified-site 5..11 /note= "N-myristoylation site"  
 FT Modified-site 8..14 /note= "N-myristoylation site"  
 FT Modified-site 25..31 /note= "N-myristoylation site"  
 FT Protein 26..241 /label= Mature\_PRO364\_protein  
 FT Modified-site 30..36 /note= "N-myristoylation site"  
 FT Modified-site 33..39 /note= "N-myristoylation site"  
 FT Modified-site 118..124 /note= "N-myristoylation site"  
 FT Modified-site 122..128 /note= "N-myristoylation site"  
 FT Modified-site 146..150 /note= "Asn is N-glycosylated"  
 FT Modified-site 156..162 /note= "N-myristoylation site"  
 FT Domain 163..183 /label= Transmembrane\_domain  
 FT Binding-site 166..177 /note= "Prokaryotic membrane lipoprotein lipid attachment site"  
 FT Region 171..193 /note= "Leucine zipper pattern"

XX WO200032778-A2.

XX PD 08-JUN-2000.

XX

PF 30-NOV-1999; 99WO-US28409.  
 XX  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 16-DEC-1998; 98US-0112850.  
 PR 22-DEC-1998; 98US-0113296.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;  
 XX  
 DR WPI: 2000-412325/35.  
 XX  
 DR N-PSDB; AAD01240.  
 XX

PT New composition useful for inhibiting neoplastic cell growth and for  
 PT treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or  
 PT their antagonists

XX Claim 31; Fig 4; 108pp; English.

XX The present sequence is the human PRO364 protein, encoded by the cDNA  
 CC clone, designated as DNA47365-1206. It is isolated from human small  
 CC intestine tissue cDNA library, identified using probes based on the  
 CC consensus sequence DNA44825, relative to the Incyte expressed sequence  
 CC tag (EST) 3003460. This EST has homology to tumour necrosis factor  
 CC receptor (TNFR) family of polypeptides. PRO364 sequence also shows  
 CC homology to members of the TNFR family and mouse GTR protein.  
 CC This clone is assigned the ATCC deposit No: 209436. PRO364 functions as  
 CC a neoplastic cell growth inhibitor and is used for treating tumours,  
 CC using an effective amount of PRO655, PRO364 and PRO344. This composition  
 CC is especially useful for treatment of human cancers such as breast,  
 CC prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.

XX Sequence 241 AA;

Query Match 100.0%; Score 711; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-50;  
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRP TGCGCGRLLLGTGTARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60  
 |||||  
 Db 26 qrp tggpgcgprlllgttdarccrvhttrccrdypgeccsewdcmcvqpefhcgdp 85  
 |||||  
 Qy 61 CTTCRHPCPPGGVQSGQKFSFGFCIDCASGTFSGGHEGHCKPWTDCQTQGF 114  
 |||||  
 Db 86 ctterhhpcppggvgqgkfsfgfcidcasgtfsggheghckpwtcdtqfgf 139  
 |||||

RESULT 12

AAB20115  
 ID AAB20115 standard; Protein; 241 AA.

XX AC AAB20115;

XX DT 30-APR-2001 (first entry)

XX DE Human immunostimulant PRO364.

XX KW PRO364; UNQ319; human; immune disease; autoimmune disease;  
 KW antirheumatic; antiarthritic; antiinflammatory; antianemic;  
 KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;  
 KW hepatotropic; virucide; dermatological; antipsoriatic;  
 KW antiasthmatic; antiallergic; immunostimulant.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..25 /label= Signal\_peptide  
 FT Protein 26..241 /label= Mature\_protein



CC PRO840, PRO877, PRO878, PRO879, PRO882, PRO885 or PRO887. These  
 CC proteins were identified by isolating cDNA clones encoding secreted  
 CC proteins. The proteins of the invention may be used to diagnose and  
 CC treat cardiovascular, endothelial or angiogenic disorders. The present  
 CC sequence is one of the proteins of the invention.  
 XX  
 SQ Sequence 241 AA;

Query Match 100.0%; Score 711; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-50;  
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGPGCGPGLLLGTGTDAACRCRVHTTRCCRDYPGECCESEWDCMCVQPEFHCGDPC 60  
 |||||||  
 Db 26 grptggpgcgprlllgtgtardccrvhttrccrdypggeccsewdcmcvqpefhcgdp 85  
 |||||||  
 QY 61 CTTCRHHPCPGGVGSQGRKFSFGFCIDCASGTFSGHGHCKPWTDCQTFGF 114  
 |||||||  
 Db 86 cttcrhnpccpggvgvsgqkfsfgfcidcasgtfsgghghckpwtcdctqgfg 139  
 |||||||

## RESULT 8

AAB33431

ID AAB33431 standard; Protein; 241 AA.

XX AAB33431;

XX 29-JAN-2001 (first entry)

DE Human PRO364 protein UNQ319 SEQ ID NO:92.

XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
 KW dermatological; antiarthritic; antirheumatic; immunosuppressive;  
 KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;  
 KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;  
 KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
 KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;  
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
 KW autoimmune thrombocytopaenia; immune-mediated renal disease;  
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
 KW inflammatory bowel disease; gluten-sensitive enteropathy;  
 KW autoimmune disease; immune-mediated skin disease; allergic disease;  
 KW immunological disease; transplantation associated disease;  
 KW graft rejection; graft-versus-host-disease.  
 XX Homo sapiens.

OS

PN WO200053758-A2.

PD 14-SEP-2000.

XX 02-MAR-2000; 2000WO-US05841.

XX 08-MAR-1999; 99WO-US05028.

PR 10-MAR-1999; 99US-0123618.

PR 12-MAR-1999; 99US-0123957.

PR 23-MAR-1999; 99US-0125775.

PR 12-APR-1999; 99US-0128849.

PR 20-APR-1999; 99WO-US08615.

PR 28-APR-1999; 99US-0131445.

PR 04-MAY-1999; 99US-0132371.

PR 14-MAY-1999; 99US-0134287.

PR 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 28-JUL-1999; 99US-0146222.

PR 01-SEP-1999; 99WO-US20111.

PR 08-SEP-1999; 99WO-US20594.

PR 13-SEP-1999; 99WO-US20944.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 30-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30939.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 11-FEB-2000; 2000WO-US00376.  
 PR 18-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 XX  
 PA (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;  
 XX  
 XX WPI: 2000-572271/53.

DR N-PSDB; AAC58596.  
 DR  
 XX

XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
 XX  
 XX Claim 33; Fig 36; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are  
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthritis,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
 CC autoimmune or immune-mediated skin diseases, allergic diseases,  
 CC immunological diseases of the lung, and transplantation associated  
 CC diseases including graft rejection and graft-versus-host-disease.  
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.  
 XX  
 SQ Sequence 241 AA;

Query Match 100.0%; Score 711; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-50;  
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGPGCGPGLLLGTGTDAACRCRVHTTRCCRDYPGECCESEWDCMCVQPEFHCGDPC 60  
 |||||||  
 Db 26 grptggpgcgprlllgtgtardccrvhttrccrdypggeccsewdcmcvqpefhcgdp 85  
 |||||||  
 QY 61 CTTCRHHPCPGGVGSQGRKFSFGFCIDCASGTFSGHGHCKPWTDCQTFGF 114  
 |||||||  
 Db 86 cttcrhnpccpggvgvsgqkfsfgfcidcasgtfsgghghckpwtcdctqgfg 139  
 |||||||

This is the amino acid sequence of the human tumour necrosis factor receptor-like protein (Trll receptor). The invention relates to Trll and two splice variants TrllSV1 and TrllSV2. The nucleotide sequences were determined by sequencing cloned cDNAs AAZ37765-2 and 377766. The Trll receptor and its splice variants show homology to the murine glucocorticoid induced tumour necrosis factor receptor family-related gene (GTR). Trll, TrllSV1 and TrllSV2 polypeptides may be involved in the regulation of cell-type specific receptor-mediated cell growth, differentiation, and ultimately, cell death. They can be used for screening for agonists/antagonists. The polypeptides, agonists or antagonists can be used for treating a disease state associated with aberrant cell survival. They can be used for treating immune deficiency disorders, Digeorge syndrome, HIV infection, severe combined immunodeficiency (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood platelet disorders or wounds resulting from trauma or surgery. They can also be used to treat heart attacks, strokes, Addison's disease, haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome, systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis, hypersensitivity to an antigenic molecule, organ rejection or graft versus host disease, inflammatory conditions, ischaemia-reperfusion injury, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, hyperproliferative disorders, or infections. They can also be used to repair, replace, or protect tissue damaged by congenital defects, trauma, age, disease, surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, peripheral nerve injuries, neuropathies, and central nervous system disease (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome). The products can also be used for detection, diagnosis and prognosis.



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 FT /label= signature\_sequence  
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 FT 122..129  
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 FT Modified-site /note= "Potential phosphorylation site"  
 FT 82  
 FT Modified-site /note= "Potential phosphorylation site"  
 FT 205  
 FT Modified-site /note= "Potential phosphorylation site"  
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 FT Modified-site /note= "N-glycosylated"  
 FT XX  
 PN WO20005374-A2.  
 XX  
 XX 03-FEB-2000.  
 XX  
 XX 21-JUL-1999; 99WO-US16637.  
 XX  
 PR 22-JUL-1998; 98US-0093827.  
 XX  
 XX (INCY-) INCYTE PHARM INC.  
 PA  
 XX Tang YT, Lal P, Hillman JL, Corley NC, Patterson C, Baughn MR;  
 PI  
 XX WPI; 2000-182699/16.  
 DR  
 DR N-PSDB; AAZ49948.  
 XX  
 XX Polypeptides and polynucleotides useful for treating and detecting cell  
 PT proliferation disorders e.g. actinic keratosis, and immune disorders  
 PT e.g. Crohn's disease  
 XX  
 PS Claim 1; Pages 64-65; 67pp; English.  
 XX  
 CC The present sequence is a molecule associated with cell  
 CC proliferation, MACP-5 from Incyte clone 2809903 isolated from TLYMNOT06  
 CC CDNA library. This sequence is expressed in cardiovascular and  
 CC haematopoietic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV,  
 CC hepatotropic, antiinflammatory, antipsoriatic, cytostatic, antiasthmatic,  
 CC dermatological, antidiabetic, nephrotropic, antithyroid, thyromimetic,  
 CC immunosuppressive, osteopathic, antiarthritic, uropathic, antiulcer,  
 CC and ophthalmological activities. The present sequence is useful in the  
 CC diagnosis, treatment and prevention of cell proliferative disorders e.g.  
 CC actinic keratosis, arteriosclerosis, atherosclerosis, bursitis and  
 CC hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and  
 CC anaemia.  
 XX  
 XX Sequence 235 AA;

Query Match 100.0%; Score 711; DB 21; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-50;  
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGPGCGPGRLLLTGTARCCRVHTRCCRDYPGECCSEWDCMCVQPEFHCGDPC 60  
 |||||  
 Db 20 qrtgpgcgprlllgttdarccrvhtrccrdypgeccsewdcmcvqpefhcgdp 79  
 |||||  
 QY 61 CTTCTRHHPCPGGQVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTDCQFGF 114  
 |||||

Db 80 cttcrhhpcppgqvgqskfsfgfcidcasgtfsgghegchekpwtcdctqfgf 133

RESULT 5  
 AAW37839  
 ID AAW37839 standard; Protein; 241 AA.  
 XX  
 AC AAW37839;  
 XX 28-JUL-1998 (first entry)  
 XX  
 DE Amino acid sequence of the human 312C2 T cell protein.  
 XX  
 KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 KW antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
 KW autoimmune disorders.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..726  
 FT /\*tag= a  
 FT /product= "human 312C2 protein"  
 FT XX  
 PN WO9806842-A1.  
 XX  
 XX 19-FEB-1998.  
 XX  
 XX 14-AUG-1997; 97WO-US13931.  
 XX  
 PR 07-OCT-1996; 96US-0027901.  
 PR 16-AUG-1996; 96US-0689943.  
 XX  
 XX (SCHE ) SCHERING CORP.  
 XX  
 XX Gorman DM, Randall TD, Zlotnik A;  
 PI  
 XX WPI; 1998-159534/14.  
 DR  
 DR N-PSDB; AAV19153.  
 XX  
 PT Isolated 312C2 T cell gene - used to develop products for treating,  
 PT e.g. cancers, autoimmune disorders, transplantation rejection and  
 PT other T cell disorders  
 XX  
 PS Claim 2; Pages 59-60; 71pp; English.  
 XX  
 CC This is the amino acid sequence encoding the human 312C2 T cell  
 CC protein. The 312C2 proteins are expressed in thymus cells and are  
 CC induced on T cells and spleen cells following activation. Engagement  
 CC of 312C2 stimulates proliferation of T cell clones, antigen-specific  
 CC proliferation and cytokine production by T-cells, and potentiates T  
 CC cell expansion or apoptosis. The products can be used in the  
 CC treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.  
 XX  
 XX Sequence 241 AA;

Query Match 100.0%; Score 711; DB 19; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-50;  
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGPGCGPGRLLLTGTARCCRVHTRCCRDYPGECCSEWDCMCVQPEFHCGDPC 60  
 |||||  
 Db 26 qrtgpgcgprlllgttdarccrvhtrccrdypgeccsewdcmcvqpefhcgdp 85  
 |||||  
 QY 61 CTTCTRHHPCPGGQVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTDCQFGF 114  
 |||||  
 Db 86 cttcrhhpcppgqvgqskfsfgfcidcasgtfsgghegchekpwtcdctqfgf 139

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:56:22 ; Search time 136.12 Seconds  
(without alignments)  
54.798 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_26\_139

Perfect score: 711

Sequence: 1 QRTGPGCGCPGRLLLTGT.....FSGHGCHCKPWTDTQFGF 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	711	100.0	228	19 AAW37840	Truncated human 31
2	711	100.0	234	21 AAY95879	Human tumour necro
3	711	100.0	234	21 AAY52158	Tumour necrosis fa
4	711	100.0	235	21 AAY44825	Human molecule ass
5	711	100.0	241	19 AAW37839	Amino acid sequenc
6	711	100.0	241	20 AAY06605	Human TNF receptor
7	711	100.0	241	21 AAB27651	Human protein PRO3
8	711	100.0	241	21 AAB33431	Human PRO364 prote
9	711	100.0	241	21 AAY95895	Human tumour necro
10	711	100.0	241	21 AAB24409	Human PRO364 prote
11	711	100.0	241	21 AAY71467	Human PRO364 prote

12	711	100.0	241	22 AAB20115	Human immunostimul
13	711	100.0	241	22 AAB47054	Human PRO364. Hom
14	711	100.0	241	22 AAB50910	Human PRO364. prote
15	711	100.0	241	22 AAB50982	Human PRO364. prote
16	711	100.0	241	22 AAB53090	Human anglogenesis
17	711	100.0	311	19 AAW37842	Human 312C2 protei
18	711	100.0	316	22 AAB47055	Polyptide encode
19	711	100.0	317	21 AAY06645	PRO364-related EST
20	695	97.7	240	21 AAY95881	Human tumour necro
21	695	97.7	240	21 AAY52160	TRILSV2 amino acid
22	509	71.6	232	19 AAW37841	Human 312C2 protei
23	502	70.6	241	21 AAY95880	Human tumour necro
24	502	70.6	241	21 AAY52159	TRILSV1 amino acid
25	373.5	52.5	222	19 AAW49018	Mouse glucocortico
26	373.5	52.5	228	19 AAW49016	Mouse glucocortico
27	373.5	52.5	228	19 AAW37838	Amino acid sequenc
28	373.5	52.5	294	19 AAW49017	Mouse glucocortico
29	219.5	30.9	89	21 AAY76013	Murine TNF-alpha f
30	219.5	30.9	89	22 AAB55952	Skin cell protein,
31	147.5	20.7	206	16 AAR81881	Mouse type-II memb
32	147.5	20.7	206	19 AAW48977	Mouse OX40 extrac
33	147.5	20.7	438	16 AAR81882	Plasmid pDC406/OX4
34	147.5	20.7	438	19 AAW48976	OX40/Fc protein. C
35	141	19.8	205	22 AAB66985	41bb protein. Uni
36	140	19.7	191	22 AAB66986	41bb protein. Uni
37	140	19.7	256	16 AAR70978	4-1BB receptor pro
38	140	19.7	256	16 AAR64199	Murine 4-1BB poly
39	140	19.7	256	17 AAW04173	Mouse receptor 4-1
40	140	19.7	256	18 AAW26659	Mouse 4-1BB recept
41	140	19.7	256	20 AAY33215	Murine CD137 prote
42	140	19.7	256	20 AAY28687	Mouse Receptor 4-1
43	135.5	19.1	255	16 AAR70977	H4-1BB receptor pr
44	135.5	19.1	255	16 AAR64197	Human 4-1BB polype
45	135.5	19.1	255	18 AAW26658	Human 4-1BB recept

#### ALIGNMENTS

RESULT 1

AAW37840  
ID AAW37840 standard; Protein; 228 AA.

AC AAW37840;

DT 28-JUL-1998 (first entry)

DE Truncated human 312C2 protein from clone\_A8 amino acid sequence.

DE Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
KW antigen-specific T cell proliferation; cytokine production by T-cell;  
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;  
KW autoimmune disorders.

OS Homo sapiens.

PN WO9806842-A1.

PD 19-FEB-1998.

PF 14-AUG-1997; 97WO-US13931.

PR 07-OCT-1996; 96US-0027901.

PR 16-AUG-1996; 96US-0689943.

PA (SCHE ) SCHERING CORP.

PI Gorman DM, Randall TD, Zlotnik A;

XX WPI; 1998-159534/14.

DR N-PSDB; AAV19154.

XX Isolated 312C2 T cell gene - used to develop products for treating,

PT e.g. cancers, auto-immune disorders, transplantation rejection and  
PT other T cell disorders  
PS Disclosure; Pages 61-62; 71pp; English.  
XX  
CC This is the amino acid sequence of the truncated human 312C2 T cell  
CC protein from clone A8. The 312C2 proteins are expressed in thymus  
CC cells and are induced on T cells and spleen cells following activation.  
CC Engagement of 312C2 stimulates proliferation of T cell clones,  
CC antigen-specific proliferation and cytokine production by T-cells, and  
CC potentiates T cell expansion or apoptosis. The products can be used  
CC in the treatment of conditions associated with abnormal physiology or  
CC development, including abnormal proliferation, e.g. cancerous  
CC conditions or degenerative conditions. They can be used in the  
CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
CC which affect immunological responses, e.g. autoimmune disorders.  
XX  
SQ Sequence 228 AA;

Query Match 100.0%; Score 711; DB 19; Length 228;  
Best Local Similarity 100.0%; Pred. NO. 2.8e-50;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGPGCGPGRLLIGTGDARCRVHTTRCCRDYPCGECSEWDCMVCOPFHCgDPC 60  
Db 20 qrtgpgcgpgrrlllgtdarccrvhttrccrdypgeccsewdcmcvqpfhcgdp 79

QY 61 CTTCTRHHPGPPGQGVQSGQKFSFGFCIDCASGTFSGHEGHCkPWTDCQTQGF 114  
Db 80 cttcrhhpcppgqgvqsgqkfsfgfcidcasgtfsgghegchekpwtctqfg 133

RESULT 2  
AAY95879  
ID AAY95879 standard; Protein; 234 AA.  
AC AAY95879;  
XX  
DT 20-NOV-2000 (first entry)  
XX  
DE Human tumour necrosis factor receptor-like protein TR11.  
XX  
KW TR11; human; tumour necrosis factor receptor-like protein;  
KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
KW dermatological; antiinflammatory; therapy; diagnosis.  
XX  
OS Homo sapiens.  
XX

Key Location/Qualifiers  
FH Peptide 1..25  
FT /label= Signal\_peptide  
FT Protein 26..234  
FT /label= Mature\_protein  
FT Domain 26..162  
FT /label= Extracellular\_domain  
FT Domain 163..179  
FT /label= Transmembrane\_domain  
FT Domain 180..234  
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FT Modified-site 146  
FT /note= "N-glycosylated"  
FT Domain 72..81  
FT /note= "conserved domain CD-II"  
FT Domain 84..93  
FT /note= "conserved domain CD-III"  
FT Domain 107..113  
FT /note= "conserved domain CD-IV"  
FT Domain 128..134  
FT /note= "conserved domain CD-V"  
FT Domain 153..160  
FT /note= "conserved domain CD-VI"

FT Domain 176..186  
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FT Domain 224..233  
FT /note= "conserved domain CD-X"  
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FT Region 59..67  
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FT Region 66..71  
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FT Region 156..164  
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FT Region 203..211  
FT /note= "epitope-bearing region"  
FT Region 222..230  
FT /note= "epitope-bearing region"  
XX WO200050459-A1.  
XX 31-AUG-2000.  
XX  
XX 23-FEB-2000; 2000WO-US04572.  
XX  
XX 24-FEB-1999; 99US-0121648.  
XX 13-MAY-1999; 99US-0134172.  
XX 16-JUL-1999; 99US-0144076.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Ruben SM, NI J;  
XX  
XX WPI; 2000-572072/53.  
XX N-PSDB; AAA50304.  
XX  
XX Human tumor necrosis factor receptor-like proteins useful for  
XX diagnosis, prevention and treatment of disease states associated with  
XX aberrant cell survival such as autoimmune disease and rheumatoid  
XX arthritis  
XX  
XX Claim 14(c); Fig 1A-B; 278pp; English.  
XX  
XX The present sequence is that of human tumour necrosis factor  
XX receptor-like protein TR11, a novel 25 kDa protein which shows  
XX 58.6% identity to murine glucocorticoid induced tumour necrosis  
XX factor receptor family-related gene. The sequence was deduced from  
XX a cDNA clone (see AAA50304) discovered in a T-helper cell library.  
XX TR11 activated NF-kappaB through a TRAF2-mediated mechanism.  
XX Expression is activation-inducible. The TR11 ligand is constitutively  
XX expressed in an endothelial cell line. This suggests that TR11 and  
XX its ligand may be involved in activated T-cell trafficking.  
XX The invention provides TR11, TR11SV1 and TR11SV2 nucleic acids  
XX (see AAA50304-06) and highly conserved encoded proteins (see  
XX AAY95879-81), as well as vectors, host cells and recombinant methods for  
XX their production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful  
XX for treating, preventing, prognosis and/or diagnosis of an  
XX immunodeficiency, especially common variable immunodeficiency,  
XX X-linked agammaglobulinemia, severe combined immunodeficiency  
XX (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
XX deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
XX antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
XX and/or diagnose an autoimmune disease, especially rheumatoid





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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:56:22 ; Search time 126.12 Seconds  
(without alignments)  
65.854 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_26\_162

Perfect score: 841

Sequence: 1 QPRTGPGCGPGRLLGTCT.....FPGKTNHAVCVPGSPPAEP 137

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries.

#### Database :

A\_Geneseq\_0601:\*

- 1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT:\*
- 2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT:\*
- 3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT:\*
- 4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT:\*
- 5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT:\*
- 6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT:\*
- 7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT:\*
- 8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT:\*
- 9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT:\*
- 10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT:\*
- 11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT:\*
- 12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT:\*
- 13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT:\*
- 14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT:\*
- 15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT:\*
- 16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT:\*
- 17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT:\*
- 18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT:\*
- 19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT:\*
- 20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT:\*
- 21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT:\*
- 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	841	100.0	228	19 AAW37840	Truncated human 31
2	841	100.0	234	21 AAY95879	Human tumour necro
3	841	100.0	234	21 AAY52158	Tumour necrosis fa
4	841	100.0	235	21 AAY44825	Human molecule ass
5	841	100.0	241	19 AAW37839	Amino acid sequenc
6	841	100.0	241	20 AAY06605	Human TNF receptor
7	841	100.0	241	21 AAB27651	Human protein PRO3
8	841	100.0	241	21 AAB33431	Human PRO364 prote
9	841	100.0	241	21 AAY95895	Human tumour necro
10	841	100.0	241	21 AAB24409	Human PRO364 prote
11	841	100.0	241	21 AAY71467	Human PRO364 prote

12	841	100.0	241	22 AAB20115	Human immunostimul
13	841	100.0	241	22 AAB47054	Human PRO364. Hom
14	841	100.0	241	22 AAB50910	Human PRO364 prote
15	841	100.0	241	22 AAB50982	Human PRO364 prote
16	841	100.0	241	22 AAB53090	Human angiogenesis
17	841	100.0	311	19 AAW37842	Human 312C2 protei
18	825	98.1	240	21 AAY95881	Human tumour necro
19	825	98.1	240	21 AAY52160	Human 312C2 protei
20	746.5	88.8	316	22 AAB47055	Mouse glucocortico
21	746.5	88.8	317	20 AAV06645	Polypeptide encode
22	632	75.1	241	20 AAY95880	PRO364-related EST
23	632	75.1	241	21 AAY52159	Human tumour necro
24	509	60.5	232	19 AAW37841	TRILSV1 amino acid
25	465.5	55.4	222	19 AAW49016	Human 312C2 protei
26	465.5	55.4	228	19 AAW49016	Mouse glucocortico
27	465.5	55.4	228	19 AAW37838	Mouse glucocortico
28	465.5	55.4	294	19 AAW49017	Amino acid sequenc
29	219.5	26.1	89	21 AAY76013	Mouse glucocortico
30	219.5	26.1	89	22 AAB55952	Murine TNF-alpha f
31	166.5	19.8	206	16 AAR81881	Skin cell protein,
32	166.5	19.8	206	19 AAW48977	Mouse type-II memb
33	166.5	19.8	438	16 AAR81882	Mouse OX40 extrace
34	166.5	19.8	438	19 AAW48976	Plasmid pDC406/OX4
35	162.5	19.3	277	16 AAR76996	Deduced sequence e
36	160.5	19.1	255	16 AAR70977	H4-1BB receptor pr
37	160.5	19.1	255	16 AAR64197	Human 4-1BB polype
38	160.5	19.1	255	18 AAW26658	Human 4-1BB recept
39	160.5	19.1	255	20 AAY32214	Human CD137 protei
40	160.5	19.1	255	20 AAY28688	Human receptor pro
41	160.5	19.1	255	22 AAB50521	Human tumour necro
42	158.5	18.8	219	18 AAW31759	A novel human h4-1
43	158.5	18.8	219	20 AAW92523	Human h4-1BBSV rec
44	158.5	18.8	277	16 AAR74737	ACT-4 cell surface
45	158.5	18.8	277	16 AAR79904	ACT-4-h-1 receptor

#### ALIGNMENTS

RESULT 1

AAW37840

ID AAW37840 standard; Protein; 228 AA.

AC AAW37840;

XX

XX 28-JUL-1998 (first entry)

DT

XX Truncated human 312C2 protein from clone\_A8 amino acid sequence.

DE

XX Human 312C2 T cell protein; thymus cell; spleen cell; T cell;

KW antigen-specific T cell proliferation; cytokine production by T-cell;

KW apoptosis; cancer; haematopoietic cells; lymphoid cell;

KW autoimmune disorders.

OS Homo sapiens.

XX

XX WO9806842-A1.

PN

XX 19-FEB-1998.

PD

XX

XX 14-AUG-1997; 97WO-US13931.

PF

XX 07-OCT-1996; 96US-0027901.

PR 16-AUG-1996; 96US-0689943.

XX

PA (SCHE ) SCHERING CORP.

XX

PI Gorman DM, Randall TD, Zlotnik A;

XX

XX WPI; 1998-159534/14.

DR N-PSDB; AAV19154.

XX

PT Isolated 312C2 T cell gene - used to develop products for treating,

PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 XX other T cell disorders

PS Disclosure; Pages 61-62; 71pp; English.

XX This is the amino acid sequence of the truncated human 312C2 T cell  
 CC protein from clone A8. The 312C2 proteins are expressed in thymus  
 CC cells and are induced on T cells and spleen cells following activation.  
 CC Engagement of 312C2 stimulates proliferation of T cell clones,  
 CC antigen-specific proliferation and cytokine production by T-cells, and  
 CC potentiates T cell expansion or apoptosis. The products can be used  
 CC in the treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous  
 CC conditions or degenerative conditions. They can be used in the  
 CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
 CC which affect immunological responses, e.g. autoimmune disorders.

XX Sequence 228 AA;

Query Match 100.0%; Score 841; DB 19; Length 228;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-60;  
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGPGCGPGLLLGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPERHCGDPC 60  
 Db 20 qrtgpgcgpggrrlllgtgdarccrvhttrccrdypgeccsewcmcvqperhcgdp 79  
 QY 61 CTTCRHHPGPPGQGVQSGQSFQFCIDCASGTFSGGEGHCKPWTDCQFGFLTVPFG 120  
 Db 80 cttcrhhpcpggvgvsgqkfsgfqcldcasgtsfsggheghckpwtcdctqfgfltp 139  
 QY 121 NKTHNAVCPGSPPAEP 137  
 Db 140 nkthnavcpgspap 156

# RESULT 2

AA95879  
 ID AAY95879 standard; Protein; 234 AA.

AC AAY95879;

XX 20-NOV-2000 (first entry)

XX Human tumour necrosis factor receptor-like protein TR11.

XX TR11: human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
 KW dermatological; antiinflammatory; therapy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH Peptide 1..25  
 FT /label= Signal\_peptide  
 FT Protein 26..234  
 FT Domain /label= Mature\_protein  
 FT Domain 26..162  
 FT Domain /label= Extracellular\_domain  
 FT Domain 163..179  
 FT Domain /label= Transmembrane\_domain  
 FT Domain 180..234  
 FT Domain /label= Intracellular\_domain

FT Modified-site 146

FT /note= "N-glycosylated"

FT Domain 72..81

FT /note= "conserved domain CD-II"

FT Domain 84..93

FT /note= "conserved domain CD-III"

FT Domain 107..113

FT /note= "conserved domain CD-IV"

FT Domain 128..134  
 FT /note= "conserved domain CD-V"  
 FT Domain 153..160  
 FT /note= "conserved domain CD-VI"  
 FT Domain 176..186  
 FT /note= "conserved domain CD-VII"  
 FT Domain 204..209  
 FT /note= "conserved domain CD-IX"  
 FT Domain 224..233  
 FT /note= "conserved domain CD-X"  
 FT Region 27..36  
 FT /note= "epitope-bearing region"  
 FT Region 43..51  
 FT /note= "epitope-bearing region"  
 FT Region 59..67  
 FT /note= "epitope-bearing region"  
 FT Region 56..64  
 FT /note= "epitope-bearing region"  
 FT Region 66..71  
 FT /note= "epitope-bearing region"  
 FT Region 99..107  
 FT /note= "epitope-bearing region"  
 FT Region 125..133  
 FT /note= "epitope-bearing region"  
 FT Region 143..151  
 FT /note= "epitope-bearing region"  
 FT Region 156..164  
 FT /note= "epitope-bearing region"  
 FT Region 203..211  
 FT /note= "epitope-bearing region"  
 FT Region 222..230  
 FT /note= "epitope-bearing region"

XX WO200050459-A1.

XX 31-AUG-2000.

XX 23-FEB-2000; 2000WO-US04572.

XX 24-FEB-1999; 99US-0121648.

XX 13-MAY-1999; 99US-0134172.

XX 16-JUL-1999; 99US-0144076.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Ni J;

XX WPI: 2000-572072/53.

XX N-PSDB: AAA50304.

XX Human tumor necrosis factor receptor-like proteins useful for

XX diagnosis, prevention and treatment of disease states associated with

XX aberrant cell survival such as autoimmune disease and rheumatoid

XX arthritis -

XX Claim 14(c): Fig 1A-B; 278pp; English.

XX The present sequence is that of human tumour necrosis factor

XX receptor-like protein TR11, a novel 25 kDa protein which shows

XX 58.6% identity to murine glucocorticoid induced tumour necrosis

XX factor receptor family-related gene. The sequence was deduced from

XX a cDNA clone (see AAA50304) discovered in a T-helper cell library.

XX TR11 activated NF-kappaB through a TRAF2-mediated mechanism.

XX Expression is activation-inducible. The TR11 ligand is constitutively

XX expressed in an endothelial cell line. This suggests that TR11 and

XX its ligand may be involved in activated T-cell trafficking.

XX The invention provides TR11, TR11SV1 and TR11SV2 nucleic acids

XX (see AAA50304-06) and highly conserved encoded proteins (see

XX AAY95879-81), as well as vectors, host cells and recombinant methods for

XX their production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful

XX for treating, preventing, prognosis and/or diagnosis of an

XX immunodeficiency, especially common variable immunodeficiency,

XX X-linked agammaglobulinemia, severe combined immunodeficiency

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PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
XX (GETH ) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;
PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;
PI Wood WI;
XX WPI: 2001-025253/03.
DR N-PSDB; AAC91469.
XX
XX Thirty three nucleic acids encoding PRO polypeptides which are useful
PT in the diagnosis and treatment of immune related disorders, e.g.
PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
PT thyroiditis and diabetes mellitus -
XX
PS Claim 58; Fig 18; 218pp; English.
XX
XX The present sequence is one of thirty three novel PRO polypeptides.
CC The PRO polypeptides, anti-PRO antibodies, agonists and
CC antagonists are useful for treating and diagnosing immune related
CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic
CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases
CC (such as infectious, autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
CC disease, autoimmune or immune-mediated skin diseases (such as bullous
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
CC food hypersensitivity and urticaria), immunological diseases of the
CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis
CC and hypersensitivity pneumonitis), transplantation associated diseases
CC including graft rejection and graft-versus-host diseases.
XX
SQ Sequence 241 AA;

Query Match 100.0%; Score 841; DB 22; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.9e-60;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGPGGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGECCECCSWDCMVOPEFHCGDPC 60
Db 26 qrptgpgcgpggrlllgtgdarccrvhttrccrdypgeccceccsewdcmvqpfhcgdp 85

QY 61 CTTCRHPCPPGCGVQSQGFSFGQICDASGTFSGGHEGHCCKPWTDCNQGFALTVPFG 120
Db 86 cttcrhhpcppggvgvsgqkfsfgqicdcsqtfsggheghckpwtcdtqgfaltvfp 145

QY 121 NKTHNAVCPGSPPAEP 137
Db 146 nkthnavcpgpsppaep 162

RESULT 15
AAB50982
ID AAB50982 standard; Protein; 241 AA.
XX
XX AAB50982;
XX
XX 21-MAR-2001 (first entry)
XX
XX Human PRO364 protein.

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XX Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive;
XX vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;
XX KW vulnary; antianginal; gene therapy; cardiovascular disease;
XX KW endothelial disorder; angiogenic disorder; cancer; periodontal disease;
XX wound healing.
XX
XX Homo sapiens.
OS
XX WO200073445-A2.
PN
XX 07-DEC-2000.
PD
XX
XX 17-MAY-2000; 2000WO-US13705.
XX
XX 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 01-SEP-1999; 99WO-US20111.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
XX
XX WPI: 2001-025251/03.
DR N-PSDB; AAC90566.
XX
XX Seventeen nucleic acids encoding PRO polypeptides which are useful in
PT diagnosis and treatment of cardiovascular, endothelial or angiogenic
PT disorders in a mammal -
XX
XX Claim 71; Fig 8; 182pp; English.
XX
XX The present sequence is one of seventeen novel PRO polypeptides. The PRO
XX nucleic acids, polypeptides, agonists and antagonists are useful for
XX treating cardiovascular, endothelial or angiogenic disorders in a mammal.
XX Examples of these disorders include cardiac hypertrophy, trauma, cancer,
XX age-related macular degeneration, atherosclerosis, hypertension, arterial
XX restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial
XX infarction, thrombophlebitis and lymphangitis. The PRO polypeptides and
XX antagonists are also used to prevent tumour angiogenesis and for treating
XX periodontal diseases. They are also used to stimulate wound healing and
XX tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO
XX antibodies are useful for diagnosing a cardiovascular, endothelial or
XX angiogenic disorder.
XX
XX Sequence 241 AA;

Query Match 100.0%; Score 841; DB 22; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.9e-60;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGPGGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGECCECCSWDCMVOPEFHCGDPC 60
Db 26 qrptgpgcgpggrlllgtgdarccrvhttrccrdypgeccceccsewdcmvqpfhcgdp 85

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Search completed: September 4, 2001, 15:56:22  
Job time: 339 sec

XX	Sequence	241 AA;
SQ	Query Match	100.0%; Score 841; DB 21; Length 241;
	Best Local Similarity	100.0%; Pred. No. 1.9e-60;
	Matches 137; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 QRPTEGPGCGRGLLGGTDARCCRVHTTRCCRDYPGECCSEWDCMCVQPEFHCGDPC	60
Db	26 qrpTgpgcgprlllgtgdarccrvhttrccrdypgeccsewdmcvqpefhcgpdc	85
Qy	61 CTTCRHHPCPGQGVSQKGSFPGQCIDCASGTPSGSGHGCHKPWTCTOGFTLVFPFG	120
Db	86 cttcrhhpcpgqvgvsqgkfsfgfcidcasgtfsgghchckpwtctogftlvfpfg	145
Qy	121 NKTHNAVCPGSPPAEP	137
Db	146 nkthnavcvpgsppaep	162
RESULT	12	
AAB20115	ID AAB20115 standard; Protein; 241 AA.	
XX	AC AAB20115;	
XX	DT 30-APR-2001 (first entry)	
XX	DE Human immunostimulant PRO364.	
XX	KW PRO364; UNQ319; human; immune disease; autoimmune disease;	
KW	antirheumatic; antiarthritic; antiinflammatory; antianaemic;	
KW	immunosuppressive; antithyroid; antidiabetic; neuroprotective;	
KW	hepatotropic; virucide; dermatological; antipsoriatic;	
KW	antiasthmatic; antiallergic; immunostimulant.	
XX	Homo sapiens.	
OS		
XX	FH Location/Qualifiers	
FT	Peptide	1..25 Signal_peptide
FT	Protein	/label=Signal_peptide 26..241
FT	Domain	/label=Mature_protein 163..183
FT	Modified-site	/note="transmembrane domain" 5..11
FT	Modified-site	/note="N-myristoylation site" 8..14
FT	Modified-site	/note="N-myristoylation site" 25..31
FT	Modified-site	/note="N-myristoylation site" 30..36
FT	Modified-site	/note="N-myristoylation site" 33..39
FT	Modified-site	/note="N-myristoylation site" 118..124
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FT	Modified-site	/note="N-myristoylation site" 156..162
FT	Modified-site	/note="N-myristoylation site" 146..150
FT	Peptide	/note="Asn is N-glycosylated" 166..177
FT	Peptide	/note="prokaryotic membrane lipoprotein lipid attachment site" 171..193
XX	WO200105972-A1.	
PN	25-JAN-2001.	
XX		
PD		

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DB 146 nkthnavcvpgspap 162
|||||
RESULT 13
AAB47054
ID AAB47054 standard; Protein; 241 AA.
XX
XX AAB47054;
XX
XX 08-MAY-2001 (first entry)
XX
XX Human PRO364.
XX
KW PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;
KW hGTR; ligand; hGTRL; PRO175; tumour necrosis factor receptor; TNFR;
KW human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;
KW myocardial infarction; PGF_2alpha; trauma; cancer; angiogenesis;
KW age-related macular degeneration; antibody; periodontal disease;
KW vascular-related drug targeting; atherosclerosis; hypertension;
KW inflammatory vasculitides; Reynaud's disease; aneurysm;
KW arterial restenosis; thrombophlebitis; tumor angiogenesis;
KW lung; liver; fibrosis; neuropathy; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Peptide 1..26 "Potential signal peptide"
FT Modified-site 146 /note= "N-glycosylated"
FT Domain 162..180 /note= "Potential transmembrane domain"
XX
XX WO200103720-A2.
PN
XX
XX 18-JAN-2001.
XX
XX 11-JUL-2000; 2000WO-US18867.
XX
XX 12-JUL-1999; 99US-0143304.
XX
XX (GETH ) GENENTECH INC.
XX
XX Williams PM, Gerritsen ME;
XX
XX WPI; 2001-138257/14.
XX
XX N-PSDB; AAC85433.
XX
XX Composition for diagnosing and treating cardiovascular, endothelial and
XX angiogenic disorders, comprises a PRO364 or PRO175 polypeptide -
XX
XX Claim 1; Fig 1; 76pp; English.
XX
XX This sequence represents PRO364 polypeptide, which is a human gluco-
XX corticoid-induced tumor necrosis factor receptor (hGTR). The
XX corresponding ligand (hGTRL), PRO175, is given in AAB47056.
XX PRO364 and PRO175 may be used in a mixture with a cardiovascular,
XX endothelial, angiogenic or angiostatic agent for the treatment of a
XX cardiovascular, endothelial, angiogenic or angiostatic disorder. The
XX PRO364 cDNA sequence was isolated from an expressed sequence tag (EST)
XX database as having homology to members of the tumour necrosis factor
XX receptor (TNFR) family of polypeptides. The PRO175 cDNA sequence was
XX isolated from a library of cDNA fragments derived from human umbilical
XX vein endothelial cells (HUVEC). Administering an effective amount of
XX PRO364 or PRO175 or their antagonists is useful for treating cardiac
XX hypertrophy (which is initiated by myocardial infarction and
XX characterized by the presence of an elevated level of PGF_2alpha),
XX trauma, a cancer, or age-related macular degeneration in a human.
XX Administering a therapeutically effective amount of an antibody that
XX binds PRO364 or PRO175 is useful for inhibiting angiogenesis induced
XX by PRO364 or PRO175 in a human suffering from a tumor or a retinal
XX disorder. PRO364 or PRO175, or their antagonists, are useful for

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CC vascular-related drug targeting or as therapeutic targets for the
CC treatment or prevention of atherosclerosis, hypertension, inflammatory
CC vasculitides, Reynaud's disease, aneurysms, arterial restenosis,
CC thrombophlebitis, tumor angiogenesis, gut protection or regeneration
CC and treatment of lung or liver fibrosis, periodontal diseases,
CC attraction of bone-forming cells, central and peripheral nervous
CC system disease and neuropathies and rheumatoid arthritis.
XX
XX Sequence 241 AA;
XX
XX Query Match 100.0%; Score 841; DB 22; Length 241;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-60;
XX Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ORPTGGPGCGPRLILGTGTDAACCRVHTTRCCRDYPCGECSEWDCMCVQPEFHCGDPC 60
DB |||||||
DB 26 grtpgpgcgprlllgtgtardccrvhttrccrdypgeccsewdcmcvqpefhcgopc 85
QY 61 CTTCTRHHPCCPGQGVQSGKFSFGFCIDCASGTFSGGHEGHCKPWTCTQFGFLTVPFG 120
DB |||||||
DB 86 cttcrhpcpgpgvgvsgqkfsfgfcidcasgtfsggheghckpwtctqfgfltvpfg 145
QY 121 NKTHNAVCPGSPAP 137
DB |||||||
DB 146 nkthnavcvpgspap 162
XX
XX RESULT 14
XX AAB50910
XX ID AAB50910 standard; Protein; 241 AA.
XX
XX AC AAB50910;
XX
XX DT 21-MAR-2001 (first entry)
XX
XX DE Human PRO364 protein.
XX
XX KW Human; PRO; antiinflammatory; dermatological; antiarthritic;
XX anti rheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;
XX antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;
XX antiallergic; antiasthmatic; immune related disorder;
XX hepatobiliary disease; autoimmune disease; allergy.
XX
XX OS Homo sapiens.
XX
XX PN WO200073452-A2.
XX
XX XX 07-DEC-2000.
XX
XX PF 02-JUN-2000; 2000WO-US15264.
XX
XX PS 02-JUN-1999; 99WO-US12252.
XX 20-JUL-1999; 99US-0144732.
XX 20-JUL-1999; 99US-0144758.
XX 28-JUL-1999; 99US-0146222.
XX 01-SEP-1999; 99WO-US20111.
XX 15-SEP-1999; 99WO-US21090.
XX 25-SEP-1999; 99WO-US21547.
XX 29-OCT-1999; 99US-0162506.
XX 30-NOV-1999; 99WO-US28313.
XX 01-DEC-1999; 99WO-US28634.
XX 09-DEC-1999; 99US-0170262.
XX 20-DEC-1999; 99WO-US30911.
XX 05-JAN-2000; 2000WO-US00219.
XX 06-JAN-2000; 2000WO-US00376.
XX 11-FEB-2000; 2000WO-US03565.
XX 18-FEB-2000; 2000WO-US04341.
XX 22-FEB-2000; 2000WO-US04342.
XX 24-FEB-2000; 2000WO-US04414.
XX 25-FEB-2000; 2000WO-US04914.
XX 15-MAR-2000; 2000WO-US06884.
XX 20-MAR-2000; 2000WO-US07377.
XX

```

CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
 CC autoimmune or immune-mediated skin diseases, allergic diseases,  
 CC immunological diseases of the lung, and transplantation associated  
 CC diseases including graft rejection and graft-versus-host-disease.  
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.  
 XX  
 XX Sequence 241 AA;

Query Match 100.0%; Score 841; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-60;  
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYFGECSSWDGMCVQPEFHCGDPC 60  
 |||||||  
 Db 26 qrtgpgpgcgprlllgtgdarcrcrvhttrccrdypgeccsewdcmcvqpefhcgdp 85  
 61 CTTCTRHHPGPPGGVQSGQKFSFGFCIDCASGTFSGGHEGCHKPWTDTCTQFGFLTVPFG 120  
 |||||||  
 Db 86 cttcrhhpcppggvgqgkfsfgfcidcasgtfsgghegchkpwtddctqfgfltvfp 145  
 QY 121 NKTHNAVCPGSPPAEP 137  
 |||||||  
 Db 146 nkthnavcvpgspap 162

RESULT 9  
 AAY95895  
 ID AAY95895 standard; Protein; 241 AA.  
 AC AAY95895;  
 XX  
 XX 20-NOV-2000 (first entry)  
 XX Human tumour necrosis factor receptor-like protein TR11 mutein.

XX TR11; human; tumour necrosis factor receptor-like protein;  
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
 KW dermatological; antiinflammatory; therapy; diagnosis; mutein;  
 KW mutant.  
 XX Homo sapiens.  
 OS  
 XX WO200050459-A1.  
 XX  
 XX 31-AUG-2000.  
 PD  
 XX 23-FEB-2000; 2000WO-US04572.  
 PF  
 XX 24-FEB-1999; 99US-0121648.  
 PR  
 PR 13-MAY-1999; 99US-0134172.  
 PR  
 XX 16-JUL-1999; 99US-0144076.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Ruben SM, Ni J;  
 PI  
 XX WPI; 2000-572072/53.  
 DR  
 XX Human tumor necrosis factor receptor-like proteins useful for  
 PT diagnosis, prevention and treatment of disease states associated with  
 PT aberrant cell survival such as autoimmune disease and rheumatoid  
 PT arthritis -  
 PT  
 XX Disclosure; 294-295; 278pp; English.  
 PS  
 XX

CC The present sequence is that of human tumour necrosis factor  
 CC receptor-like protein TR11 (see also AAY95879), a novel protein  
 CC showing identity to murine glucocorticoid induced tumour necrosis  
 CC factor receptor family-related gene. The invention provides  
 CC highly conserved TR11, TR11SV1 and TR11SV2 proteins (see AAY95879-81),  
 CC as well as vectors, host cells and recombinant methods for their  
 CC production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful  
 CC for treating, preventing, prognosis and/or diagnosis of an  
 CC immunodeficiency, especially common variable immunodeficiency,  
 CC X-linked agammaglobulinemia, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
 CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
 CC and/or diagnose an autoimmune disease, especially rheumatoid  
 CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
 CC or IGA nephropathy. The polypeptides, polynucleotides and/or  
 CC antibodies can be administered to cells in vitro, ex vivo or in  
 CC vivo or to a multicellular organism. Soluble forms of the  
 CC polypeptides may also be used. Methods for screening for  
 CC agonist/antagonist compounds are also provided.  
 XX  
 XX Sequence 241 AA;

Query Match 100.0%; Score 841; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-60;  
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYFGECSSWDGMCVQPEFHCGDPC 60  
 |||||||  
 Db 26 qrtgpgpgcgprlllgtgdarcrcrvhttrccrdypgeccsewdcmcvqpefhcgdp 85  
 61 CTTCTRHHPGPPGGVQSGQKFSFGFCIDCASGTFSGGHEGCHKPWTDTCTQFGFLTVPFG 120  
 |||||||  
 Db 86 cttcrhhpcppggvgqgkfsfgfcidcasgtfsgghegchkpwtddctqfgfltvfp 145  
 QY 121 NKTHNAVCPGSPPAEP 137  
 |||||||  
 Db 146 nkthnavcvpgspap 162

RESULT 10  
 AAB24409  
 ID AAB24409 standard; Protein; 241 AA.  
 AC AAB24409;  
 XX  
 XX 07-NOV-2000 (first entry)  
 XX Human PRO364 protein sequence SEQ ID NO:117.  
 XX  
 XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
 KW cytostatic; gene therapy; vaccine.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200032221-A2.  
 PN  
 XX 08-JUN-2000.  
 PD  
 XX 30-NOV-1999; 99WO-US28313.  
 PF  
 XX 01-DEC-1998; 98WO-US25108.  
 PR  
 PR 16-DEC-1998; 98US-0112850.  
 PR  
 PR 12-JAN-1999; 99US-0115554.  
 PR  
 PR 08-MAR-1999; 99WO-US05028.  
 PR  
 PR 12-MAR-1999; 99US-0123957.  
 PR  
 PR 28-APR-1999; 99US-0131445.  
 PR  
 PR 04-MAY-1999; 99US-0134287.  
 PR  
 PR 02-JUN-1999; 99WO-US12252.  
 PR  
 PR 23-JUN-1999; 99US-0141037.

```
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-OCT-1999; 99US-0162506.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;
PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;
PI Watanabe CK, Williams PM, Wood WI;
XX
XX WPI; 2000-412154/35.
DR N-PSDB; AAA77604.
XX
XX Nucleic acids encoding PRO polypeptides useful for preventing,
PT diagnosing and treating disorders in mammals -
PT angiogenic disorders in mammals -
XX
XX Claim 72; Fig 44; 315pp; English.
XX
XX The present invention describes nucleic acids encoding PRO polypeptides
CC useful for preventing, diagnosing and treating disorders in mammals
CC cardiovascular, endothelial or angiogenic disorder in mammals by
CC modulating cell proliferation, angiogenesis and cardiovascularisation,
CC and for identifying agonists and antagonists of these processes. The
CC nucleic acids and the proteins they encode may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PRO expression such as cardiovascular, endothelial or
CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
CC cardiac hypertrophy). For example, the nucleic acids (NCS) and vectors
CC containing them and the PRO polypeptide may be used to treat disorders
CC associated with decreased PRO expression. AAA77510 to AAA77721 and
CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in
CC the exemplification of the present invention.
XX
XX Sequence 241 AA;
SQ
Query Match 100.0%; Score 841; DB 21; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.9e-60;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QRPTGGPGCGRLLLGTGTARCCRVHTRCRDYPGEECCSEWDCMCVQPEFHCgDPC 60
Db 26 qrptgpgcgprlllgtgtarccrvhttrccrdypgeecscsewdcmcvqpefhcgdp 85
Qy 61 CTTCRHPCPPGQVQSGKFSFGQCIDCASGTFSGHGHCPEWTDCTQFGTLTVFPG 120
Db 86 cttcrhpcppgqvgqgkfsfgqicdcasgtfsghgchekpwtcdctqfgtltvfpg 145
Qy 121 NKTHNAVCPGSPPAEP 137
Db 146 nkthnavcvpsppaep 162
RESULT 11
AAAY71467
ID AA71467 standard; Protein; 241 AA.
XX
XX AAAY71467;
AC
XX 08-NOV-2000 (first entry)
DT
XX Human PRO364 protein.
DE
XX
XX PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;
KW neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;
KW breast; prostate; colon; lung; renal; ovarian; central nervous system;
```

```
KW CNS: leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue;
KW tumour necrosis factor receptor; G1FR protein homologue.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide /label= Signal_peptide
XX Modified-site /note= "N-myristoylation site"
XX Modified-site /note= "N-myristoylation site"
XX Modified-site /note= "N-myristoylation site"
XX Protein /label= Mature_PRO364_protein
XX Modified-site /note= "N-myristoylation site"
XX Modified-site /note= "N-myristoylation site"
XX Modified-site /note= "N-myristoylation site"
XX Modified-site /note= "N-myristoylation site"
XX Modified-site /note= "N-myristoylation site"
XX Modified-site /note= "N-myristoylation site"
XX Modified-site /note= "Asn is N-glycosylated"
XX Domain /label= Transmembrane_domain
XX Binding-site /note= "Prokaryotic membrane lipoprotein lipid
XX attachment site"
XX Region /note= "Leucine zipper pattern"
XX
XX WO200032778-A2.
XX
XX 08-JUN-2000.
XX
XX 30-NOV-1999; 99WO-US28409.
XX
XX 01-DEC-1998; 98WO-US25108.
XX 16-DEC-1998; 98US-0112850.
XX 22-DEC-1998; 98US-0113296.
XX 20-JUL-1999; 99US-0144758.
XX 26-JUL-1999; 99US-0145698.
XX
XX (GETH ) GENENTECH INC.
XX
XX Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;
PI WPI; 2000-412325/35.
DR N-PSDB; AAD01240.
XX
XX New composition useful for inhibiting neoplastic cell growth and for
PT treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or
PT their antagonists -
XX
XX Claim 31; Fig 4; 108pp; English.
XX
XX The present sequence is the human PRO364 protein, encoded by the cDNA
CC clone, designated as DNA47365-1206. It is isolated from human small
CC intestine tissue cDNA library, identified using probes based on the
CC consensus sequence DNA44825, relative to the Incyte expressed sequence
CC tag (EST) 3003460. This EST has homology to tumour necrosis factor
CC receptor (TNFR) family of polypeptides. PRO364 sequence also shows
CC homology to members of the TNFR family and mouse G1FR protein.
CC This clone is assigned the ATCC deposit No: 209436. PRO364 functions as
CC a neoplastic cell growth inhibitor and is used for treating tumours,
CC using an effective amount of PRO655, PRO364 and PRO344. This composition
CC is especially useful for treatment of human cancers such as breast,
CC prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.
CC
```

CC which affect immunological responses, e.g. autoimmune disorders.  
 XX  
 SQ Sequence 241 AA;

Query Match 100.0%; Score 841; DB 19; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-60;  
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRPTEGPGCGPGRLLLTGTDAACRCRVHTTRCCRDYFGEECCSEWDCMCVQPEPHCGDPC 60  
 Db 26 qrpTEGPGCGPGRlllgtgdarcrcrvhttrccrdypgeccsewdcmcvqpefhcgdp 85

QY 61 CTTCTRRHPCPPGGVQSGQKFSFGFCIDCASGTFSGHGHCKPWTDCQFGFLTVPFG 120  
 Db 86 ctctcrhhpcppggvgqsgkfsgfcldcasgtfsgghghckpwtcdctqfgfltvfp 145

QY 121 NKTHNAVCPGSPPAEP 137  
 Db 146 nkthnavcvpgsppaep 162

RESULT 6  
 AAY06605  
 ID AAY06605 standard; Protein; 241 AA.  
 XX  
 AC AAY06605;  
 XX  
 DT 26-OCT-1999 (first entry)  
 XX  
 DE Human TNF receptor homologue PRO364.  
 XX  
 KW PRO364; tumour necrosis factor receptor; human; apoptosis;  
 KW inflammation; antiinflammatory; NF-KB activation;  
 KW autoimmune disease; therapy.  
 XX  
 OS Homo sapiens.  
 XX

Key Location/Qualifiers  
 FT Peptide 1..25  
 FT /note= "signal peptide"  
 FT Protein 26..241  
 FT /note= "mature protein"  
 FT Modified-site 146  
 FT /note= "N-glycosylated"  
 FT Domain 162..180  
 FT /note= "transmembrane domain"  
 XX  
 PN W09940196-A1.  
 XX  
 XX 12-AUG-1999.  
 XX  
 XX 09-FEB-1999; 99WO-US02642.  
 XX  
 XX 09-FEB-1998; 98US-0024087.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;  
 PI Pitti RM, Wood WI;  
 XX  
 XX WPI: 1999-494296/41.  
 DR  
 DR N-PSDB; AAX87670.  
 XX  
 XX Tumour necrosis factor receptor homologue - useful for, e.g.  
 PT modulating apoptosis and NF-KB activation and proinflammatory or  
 PT autoimmune responses  
 XX  
 PS Claim 17; Fig 2A; 104pp; English.  
 XX  
 CC The present sequence represents human PRO364, a novel member of the  
 CC tumour necrosis factor receptor family. The sequence was deduced  
 CC from a bone marrow cDNA clone (see AAX87670). Methods for the

CC recombinant production of PRO364 polypeptides, e.g. in CHO,  
 CC Escherichia coli or yeast host cells, are provided. Claimed  
 CC polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the  
 CC mature protein) and 26-X of the present sequence, where X is any  
 CC one of amino acid residues 157-167 of PRO364. PRO364 polypeptides  
 CC are useful for modulating apoptosis, NF-KB activation and  
 CC proinflammatory or autoimmune responses in mammalian cells  
 CC (claimed). Chimeric molecules comprising a PRO364 polypeptide  
 CC fused to a heterologous sequence such as epitope tag or  
 CC immunoglobulin Fc region are also claimed. PRO364 can be used in  
 CC assays to identify other proteins or molecules involved in binding  
 CC interactions. This is useful for identifying inhibitors or  
 CC agonists of receptor/ligand binding. The PRO364 polypeptides may  
 CC also be combined with an agent that is cytotoxic, chemotherapeutic  
 CC or a growth inhibitor. PRO364 antibodies are useful in diagnostic  
 CC methods, purification methods and also in therapy, e.g. as  
 CC inhibitors.  
 XX  
 SQ Sequence 241 AA;

Query Match 100.0%; Score 841; DB 20; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-60;  
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRPTEGPGCGPGRLLLTGTDAACRCRVHTTRCCRDYFGEECCSEWDCMCVQPEPHCGDPC 60  
 Db 26 qrpTEGPGCGPGRlllgtgdarcrcrvhttrccrdypgeccsewdcmcvqpefhcgdp 85

QY 61 CTTCTRRHPCPPGGVQSGQKFSFGFCIDCASGTFSGHGHCKPWTDCQFGFLTVPFG 120  
 Db 86 ctctcrhhpcppggvgqsgkfsgfcldcasgtfsgghghckpwtcdctqfgfltvfp 145

QY 121 NKTHNAVCPGSPPAEP 137  
 Db 146 nkthnavcvpgsppaep 162

RESULT 7  
 AAB27651  
 ID AAB27651 standard; Protein; 241 AA.  
 XX  
 AC AAB27651;  
 XX  
 DT 26-JAN-2001 (first entry)  
 XX  
 DE Human protein PRO364.  
 XX  
 KW Cardiovascular; endothelial; angiogenic disorder; PRO179;  
 KW PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333;  
 KW PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;  
 KW gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT /label= "signal peptide"  
 FT  
 XX  
 XX WO200053757-A2.  
 XX  
 XX 14-SEP-2000.  
 XX  
 XX 24-FEB-2000; 2000WO-US05004.  
 XX  
 XX 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 30-NOV-1999; 99WO-US28313.



OS Homo sapiens.

PN WO200053753-A2.

XX 14-SEP-2000.

XX 05-JAN-2000; 2000WO-US00219.

XX 08-MAR-1999; 99WO-US05028.

XX 12-MAR-1999; 99US-0123957.

XX 14-MAY-1999; 99US-0134287.

XX 20-JUN-1999; 99WO-US12252.

XX 23-JUN-1999; 99US-0141037.

XX 20-JUL-1999; 99US-0144758.

XX 26-JUL-1999; 99US-0145698.

XX 01-SEP-1999; 99WO-US20111.

XX 08-SEP-1999; 99WO-US20594.

XX 15-SEP-1999; 99WO-US21090.

XX 15-SEP-1999; 99WO-US21547.

XX 05-OCT-1999; 99WO-US23089.

XX 30-NOV-1999; 99WO-US28313.

XX 30-NOV-1999; 99WO-US28409.

XX 02-DEC-1999; 99WO-US28564.

XX 02-DEC-1999; 99WO-US28565.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;

XX Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;

XX Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;

XX WPI; 2001-090793/10.

XX N-PSDB; AAC97479.

XX New isolated nucleic acid for producing a PRO polypeptide, analyzing

XX genetic disorders and treating cardiovascular, endothelial or

XX angiogenic disorders, such as atherosclerosis, wounds or cancer -

XX Claim 69; Fig 54; 293pp; English.

XX The invention relates to novel human angiogenesis-associated proteins  
XX designated PRO proteins (AA053064-B53097), and to nucleic acids encoding  
XX PRO proteins. The invention also relates to vectors and host cells  
XX comprising a PRO nucleic acid, the recombinant production of a PRO  
XX protein, PRO antibodies specific for a PRO protein, fusion proteins  
XX comprising a PRO protein, agonists or antagonists of a PRO protein, and  
XX compounds which inhibit the expression of a PRO gene. The invention  
XX additionally encompasses methods of identifying modulators of PRO  
XX expression or activity; diagnosing a cardiovascular, endothelial or  
XX angiogenic disorder, or a susceptibility to such a disorder by detecting  
XX mutations in a PRO gene, or the expression level of a PRO gene within a  
XX particular tissue; treating a cardiovascular, endothelial or angiogenic  
XX disorder via the administration of a PRO protein, PRO nucleic acid, or  
XX PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
XX PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
XX cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
XX administration of a PRO protein, or an agonist or antagonist thereof.  
XX PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
XX agonists and PRO antagonists may be used as therapeutic agents to treat  
XX cardiovascular, endothelial or angiogenic disorders, such as  
XX atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
XX diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
XX endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
XX disease, or stroke. PRO nucleic acids are additionally useful in the  
XX recombinant production of PRO proteins, as hybridisation probes to  
XX screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
XX to map genes encoding PRO proteins, to analyse genetic disorders, and in  
XX gene therapy. PRO nucleic acids can also be used to produce transgenic  
XX animals useful for the development and screening of potential  
XX therapeutic agents. The present sequence represents a PRO protein of the  
XX invention.

XX Sequence 241 AA;

Query Match 100.0%; Score 969; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred No. 1.3e-69;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMGAFRALCGLALLCALSLGQRPTGGPGCGRLLLTGTGDARCCRVHTTRCCRD 60

Db 1 maghgamafralcgallcalslgqrptggpgcggrllltgtgdarccrvhttrccrd 60

QY 61 YPGECCSEWDCMCVQPFHCGPCCTTCRHHPCPPGGVQSGKFSFGQCIDCASGTF 120

Db 61 ypgeccsewdcmcvqpfhcgpccttcrrhhpcppggvgsgkfsfgqicdcaasgtf 120

QY 121 SGGHEGCKPWTDCQTQFGFTLVFPGNKTHNAVCPVGPSPPAEP 162

Db 121 sggheghckpwtcdtqfgftlvfpgnktthnavcvpgspppaep 162

RESULT 15

AAW37840

ID AAW37840 standard; Protein; 228 AA.

XX AC AAW37840;

XX DT 28-JUL-1998 (first entry)

XX DE Truncated human 312C2 protein from clone\_A8 amino acid sequence.

XX KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;

XX KW antigen-specific T cell proliferation; cytokine production by T-cell;

XX KW apoptosis; cancer; haematopoietic cells; lymphoid cell;

XX KW auto-immune disorders.

XX OS Homo sapiens.

XX PN WO9806842-A1.

XX PD 19-FEB-1998.

XX PF 14-AUG-1997; 97WO-US13931.

XX PR 07-OCT-1996; 96US-0027901.

XX PR 16-AUG-1996; 96US-0689943.

XX PA (SCHE ) SCHERING CORP.

XX PI Gorman DM, Randall TD, Zlotnik A;

XX DR N-PSDB; AA19154.

XX PT Isolated 312C2 T cell gene - used to develop products for treating,

XX PT e.g. cancers, auto-immune disorders, transplantation rejection and

XX PT other T cell disorders

XX PS Disclosure; Pages 61-62; 71pp; English.

XX This is the amino acid sequence of the truncated human 312C2 T cell  
XX protein from clone\_A8. The 312C2 proteins are expressed in thymus  
XX cells and are induced on T cells and spleen cells following activation.  
XX Engagement of 312C2 stimulates proliferation of T cell clones.  
XX Antigen-specific proliferation and cytokine production by T-cells, and  
XX potentiates T cell expansion or apoptosis. The products can be used  
XX in the treatment of conditions associated with abnormal physiology or  
XX development, including abnormal proliferation, e.g. cancerous  
XX conditions or degenerative conditions. They can be used in the  
XX regulation or development of haematopoietic cells, e.g. lymphoid cells  
XX which affect immunological responses, e.g. autoimmune disorders.

XX Sequence 228 AA;



```
Query Match      96.78; Score 937; DB 19; Length 228;
Best Local Similarity 100.0%; Pred. NO. 4.3e-67;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLILGTGTARCCRVHTTRCCRDYPGEEC 66
    |||
Db 1 mgafralcglallcalslgqrptggpgcgprlllgtgtardccrvhttrccrdypgeec 60
    |||

QY 67 CSEWDCMCVQPEFHCGDPCCCTTCRHHPCPPCGQVQSOGKFSFGQCIDCASGTFSGGHEG 126
    |||
Db 61 csewdcmcvqpefhcgdpcccttcrrhpcppcgvgvgqgkfsfgqcidcasgtfsggheg 120
    |||

QY 127 HCRPWTDTQFGFLTVPFGNKTNNAVCVGSPSPAEP 162
    |||
Db 121 hckpwtddtdqfgfltvfpngkthnavcvpgsppaep 156
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Job time: 339 sec

FT Modified-site /note= "Potential signal peptide"  
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 FT /note= "N-glycosylated"  
 FT 162..180  
 FT Domain /note= "Potential transmembrane domain"  
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 XX  
 PN WO200103720-A2.  
 XX  
 XX 18-JAN-2001.  
 XX  
 XX 11-JUL-2000; 2000WO-US18867.  
 XX  
 XX 12-JUL-1999; 99US-0143304.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Williams PM, Gerritsen ME;  
 XX  
 XX WPI; 2001-138257/14.  
 DR N-PSDB; AAC85433.  
 XX  
 XX Composition for diagnosing and treating cardiovascular, endothelial and  
 PT angiogenic disorders, comprises a PRO364 or PRO175 polypeptide -  
 XX  
 XX Claim 1; Fig 1; 76pp; English.  
 PS  
 XX This sequence represents PRO364 polypeptide, which is a human gluco-  
 CC corticoid-induced tumor necrosis factor receptor (hGIR). The  
 CC corresponding ligand (hGIRL), PRO175, is given in AAB47056.  
 CC PRO364 and PRO175 may be used in a mixture with a cardiovascular,  
 CC endothelial, angiogenic or angiostatic agent for the treatment of a  
 CC cardiovascular, endothelial, angiogenic or angiostatic disorder. The  
 CC PRO364 cDNA sequence was isolated from an expressed sequence tag (EST)  
 CC database as having homology to members of the tumour necrosis factor  
 CC receptor (TNFR) family of polypeptides. The PRO175 cDNA sequence was  
 CC isolated from a library of cDNA fragments derived from human umbilical  
 CC vein endothelial cells (HUVEC). Administering an effective amount of  
 CC PRO364 or PRO175 or their antagonists is useful for treating cardiac  
 CC hypertrophy (which is initiated by myocardial infarction and  
 CC characterized by the presence of an elevated level of PGF<sub>2</sub>alpha),  
 CC trauma, a cancer, or age-related macular degeneration in a human.  
 CC Administering a therapeutically effective amount of an antibody that  
 CC binds PRO364 or PRO175 is useful for inhibiting angiogenesis induced  
 CC by PRO364 or PRO175 in a human suffering from a tumor or a retinal  
 CC disorder. PRO364 or PRO175, or their antagonists, are useful for  
 CC vascular-related drug targeting or as therapeutic targets for the  
 CC treatment or prevention of atherosclerosis, hypertension, inflammatory  
 CC vasculitides, Reynaud's disease, aneurysms, arterial restenosis,  
 CC thrombophlebitis, tumor angiogenesis, gut protection or regeneration  
 CC and treatment of lung or liver fibrosis, periodontal diseases,  
 CC attraction of bone-forming cells, central and peripheral nervous  
 CC system disease and neuropathies and rheumatoid arthritis.  
 XX  
 SQ Sequence 241 AA;

Query Match 100.0%; Score 969; DB 22; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-69;  
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMAGAFRALCGIALCALSLGQRPTGGCGGRLLLTGTGDARCCRVHTTRCCRD 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 maqhgmagafralcglialcalslgrptggcggrlllgtgdarcrcrvhttrccrd 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 YPGEECCSEWDCMCVPEFHCGDPCTTCRHHPCPPGQVQSQKTFSGFQCIDCASGTF 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 ypgEECCSEWDCMCVPEFHCGDPCTTCRHHPCPPGQVQSQKTFSGFQCIDCASGTF 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 SGHEGHCXFPWTDQFGFLTFVPGKNTNNAVCPGSPAP 162  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 sggheghckpwtcdtqfgfltfvpgnkntnnavcpvgsppap 162  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 12  
 AAB50910  
 ID AAB50910 standard; Protein; 241 AA.  
 XX  
 AC AAB50910;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Human PRO364 protein.  
 XX  
 KW Human; PRO; antiinflammatory; dermatological; antiarthritic;  
 KW antirheumatic; cardiant; antianemic; immunosuppressive; antithyroid;  
 KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;  
 KW antiallergic; antiasthmatic; immune related disorder;  
 KW hepatobiliary disease; autoimmune disease; allergy.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200073452-A2.  
 PN  
 XX  
 PD 07-DEC-2000.  
 XX  
 PF 02-JUN-2000; 2000WO-US15264.  
 XX  
 XX 02-JUN-1999; 99WO-US12252.  
 PR 20-JUL-1999; 99US-0144732.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;  
 PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;  
 PI Wood WI;  
 XX  
 DR WPI; 2001-025253/03.  
 DR N-PSDB; AAC91469.  
 XX  
 PT Thirty three nucleic acids encoding PRO polypeptides which are useful  
 PT in the diagnosis and treatment of immune related disorders, e.g.  
 PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 PT thyroiditis and diabetes mellitus -  
 XX  
 XX Claim 58; Fig 18; 218pp; English.  
 XX  
 CC The present sequence is one of thirty three novel PRO polypeptides.  
 CC The PRO polypeptides, anti-PRO antibodies, agonists and  
 CC antagonists are useful for treating and diagnosing immune related  
 CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic

CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central  
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic  
CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases  
CC (such as infectious, autoimmune chronic active hepatitis, primary  
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
CC food hypersensitivity and urticaria), immunological diseases of the  
CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
CC and hypersensitivity pneumonitis), idiopathic pulmonary fibrosis  
CC including graft rejection and graft-versus-host diseases.  
XX  
SQ Sequence 241 AA;

Query Match 100.0%; Score 969; DB 22; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1.3e-69;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAMGAFRALCGLALCALSLGQRTGPGCGPGRLLILCTGTDARCCRVHTTRCCRD 60  
DB 1 maqhgamafralcglalcalcslgqrptgpgcgprllilgtgdarccrvhttrccrd 60  
QY 61 YPGEECCSEWDCMCVQPFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
DB 61 ypgeecscwdcmcvqpfhcgdpccctcrhhpcppgqgvsgkfsfgfcidcasgtf 120  
QY 121 SGGHEGCHKPWTCTQFGFLTFVPGNKTHNAVCPGSPPAEP 162  
DB 121 sgghgchckpwtctqfgfltfvpgnknthnavcvpgsppaep 162

## RESULT 13

AAB50982  
ID AAB50982 standard; Protein; 241 AA.

XX AAB50982;

DT 21-MAR-2001 (first entry)

XX Human PRO364 protein.

XX Human; PRO; cardiac; antiangiogenic; antiarteriosclerotic; hypotensive;  
KW vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;  
KW vulnerable; antianginal; gene therapy; cardiovascular disease;  
KW endothelial disorder; angiogenic disorder; cancer; periodontal disease;  
KW wound healing.

XX Homo sapiens.

XX WO200073445-A2.

XX 07-DEC-2000.

XX 17-MAY-2000; 2000WO-US13705.

XX 02-JUN-1999; 99WO-US12252.

XX 23-JUN-1999; 99US-0141037.

XX 20-JUL-1999; 99US-0144758.

XX 26-JUL-1999; 99US-0145698.

XX 28-JUL-1999; 99US-0146222.

XX 01-SEP-1999; 99WO-US20111.

XX 30-NOV-1999; 99WO-US28313.

XX 30-NOV-1999; 99WO-US28409.

XX 02-DEC-1999; 99WO-US28565.

XX 16-DEC-1999; 99WO-US30095.

XX 11-FEB-2000; 2000WO-US03565.

XX 18-FEB-2000; 2000WO-US04341.

XX 18-FEB-2000; 2000WO-US04342.

PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;

PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;

PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;

XX WPI; 2001-025251/03.

DR N-PSDB; AAC90366.

XX Seventeen nucleic acids encoding PRO polypeptides which are useful in  
PT diagnosis and treatment of cardiovascular, endothelial or angiogenic  
PT disorders in a mammal -

XX Claim 71; Fig 8; 182pp; English.

PS The present sequence is one of seventeen novel PRO polypeptides. The PRO  
CC nucleic acids, polypeptides, agonists and antagonists are useful for  
CC treating cardiovascular, endothelial or angiogenic disorders in a mammal.  
CC Examples of these disorders include cardiac hypertrophy, trauma, cancer,  
CC age-related macular degeneration, atherosclerosis, hypertension, arterial  
CC restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial  
CC infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and  
CC antagonists are also used to prevent tumour angiogenesis and for treating  
CC periodontal diseases. They are also used to stimulate wound healing and  
CC tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO  
CC antibodies are useful for diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder.

XX Sequence 241 AA;

Query Match 100.0%; Score 969; DB 22; Length 241;

Best Local Similarity 100.0%; Pred. No. 1.3e-69;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAMGAFRALCGLALCALSLGQRTGPGCGPGRLLILCTGTDARCCRVHTTRCCRD 60

DB 1 maqhgamafralcglalcalcslgqrptgpgcgprllilgtgdarccrvhttrccrd 60

QY 61 YPGEECCSEWDCMCVQPFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTF 120

DB 61 ypgeecscwdcmcvqpfhcgdpccctcrhhpcppgqgvsgkfsfgfcidcasgtf 120

QY 121 SGGHEGCHKPWTCTQFGFLTFVPGNKTHNAVCPGSPPAEP 162

DB 121 sgghgchckpwtctqfgfltfvpgnknthnavcvpgsppaep 162

## RESULT 14

AAB53090

ID AAB53090 standard; Protein; 241 AA.

XX AAB53090;

XX 28-FEB-2001 (first entry)

XX Human angiogenesis-associated protein PRO364, SEQ ID NO:142.

XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
KW gene therapy; transgenic animal.

XX





CC sequence is one of the proteins of the invention.

XX Sequence 241 AA;

Query Match 100.0%; Score 969; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-69;  
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAHQGAMGAFRALCGLLALCALSLGQRTGGPCGGRLLLTGTGDARCRVHTTRCCRD 60  
 |||||||  
 DB 1 maqhgamafralcgllalcalslgqrpgcgprlllgtgdarcrvhttrccrd 60  
 |||||||  
 QY 61 YPGECCSEWDCMCVQPEFHCGDPCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
 |||||||  
 DB 61 ypgeccsewdcmvcvqpefhcgdpcttcrhhpcppgqgvqsgkfsgfqcldcasgtf 120  
 |||||||  
 QY 121 SGGHEGHCKPWTDCTQFGFLTVPFGKNTNACVCPGSPPAEP 162  
 |||||||  
 DB 121 sgghegchckpwtcdctqfgfltvpgnkthnavcvpgspap 162  
 |||||||

# RESULT 6

AAB33431

ID AAB33431 standard; Protein; 241 AA.

XX AAB33431;

DT 29-JAN-2001 (first entry)

XX Human PRO364 protein UNQ319 SEQ ID NO:92.

XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
 KW dermatological; antiarthritic; antiarthritis; antiarthritis; immunosuppressive;  
 KW haemostatic; antithyroid; antidiabetic; antipruritic; neuroprotective;  
 KW antianemic; hepatotropic; viricide; antipruritic; antiallergic;  
 KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
 KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;  
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
 KW systemic vasculitis; autoimmune hemolytic anaemia; diabetes mellitus;  
 KW autoimmune thrombocytopenia; immune-mediated renal disease;  
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
 KW inflammatory bowel disease; gluten-sensitive enteropathy;  
 KW autoimmune disease; immune-mediated skin disease; allergic disease;  
 KW immunological disease; transplantation associated disease;  
 KW graft rejection; graft-versus-host-disease.

XX Homo sapiens.

OS WO200053758-A2.

XX 14-SEP-2000.

PD 02-MAR-2000; 2000WO-US05841.

PF 08-MAR-1999; 99WO-US05028.

XX 10-MAR-1999; 99US-0123618.

PR 12-MAR-1999; 99US-0123957.

PR 23-MAR-1999; 99US-0125775.

PR 12-APR-1999; 99US-0128849.

PR 20-APR-1999; 99WO-US08615.

PR 28-APR-1999; 99US-0131445.

PR 04-MAY-1999; 99US-0132371.

PR 14-MAY-1999; 99US-0134287.

PR 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 28-JUL-1999; 99US-0146222.

PR 01-SEP-1999; 99WO-US20111.

PR 08-SEP-1999; 99WO-US20594.

PR 13-SEP-1999; 99WO-US20944.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 XX

(GETH ) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;

PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;

PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

XX WPI; 2000-572271/53.

DR N-PSDB; AAC58596.

XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
 XX Claim 33; Fig 36; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are  
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthritis,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
 CC autoimmune or immune-mediated skin diseases, allergic diseases,  
 CC immunological diseases of the lung, and transplantation associated  
 CC diseases including graft rejection and graft-versus-host-disease.  
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.

XX Sequence 241 AA;

Query Match 100.0%; Score 969; DB 21; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-69;  
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAHQGAMGAFRALCGLLALCALSLGQRTGGPCGGRLLLTGTGDARCRVHTTRCCRD 60  
 |||||||

DB 1 maqhgamafralcgllalcalslgqrpgcgprlllgtgdarcrvhttrccrd 60  
 |||||||

QY 61 YPGECCSEWDCMCVQPEFHCGDPCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
 |||||||

DB 61 ypgeccsewdcmvcvqpefhcgdpcttcrhhpcppgqgvqsgkfsgfqcldcasgtf 120  
 |||||||

QY 121 SGGHEGHCKPWTDCTQFGFLTVPFGKNTNACVCPGSPPAEP 162

Db 121 sgghegckpwtcdtqfglvtvfgnknthnavcvpgspap 162  
|||||

## RESULT 7

AA95895  
ID AAY95895 standard; Protein; 241 AA.

XX AAY95895;

XX 20-NOV-2000 (first entry)

XX Human tumour necrosis factor receptor-like protein TR11 mutein.

XX TR11; human; tumour necrosis factor receptor-like protein;  
KW immunodeficiency; autoimmune disease; rheumatoid arthritis;  
KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;  
KW dermatological; antiinflammatory; therapy; diagnosis; mutein;  
KW mutant.

XX Homo sapiens.

XX WO200050459-A1.

XX 31-AUG-2000.

XX 23-FEB-2000; 2000WO-US04572.

XX 24-FEB-1999; 99US-0121648.

XX 13-MAY-1999; 99US-0134172.

XX 16-JUL-1999; 99US-0144076.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Ni J;

XX WPI; 2000-572072/53.

XX Human tumor necrosis factor receptor-like proteins useful for  
PT diagnosis, prevention and treatment of disease states associated with  
PT aberrant cell survival such as autoimmune disease and rheumatoid  
PT arthritis

XX Disclosure; 294-295; 278pp; English.

XX The present sequence is that of human tumour necrosis factor  
CC receptor-like protein TR11 (see also AAY95879), a novel protein  
CC showing identity to murine glucocorticoid induced tumour necrosis  
CC factor receptor family-related gene. The invention provides  
CC highly conserved TR11, TR11SV1 and TR11SV2 proteins (see AAY95879-81),  
CC as well as vectors, host cells and recombinant methods for their  
CC production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful  
CC for treating, preventing, prognosis and/or diagnosis of an  
CC immunodeficiency, especially common variable immunodeficiency,  
CC X-linked agammaglobulinemia, severe combined immunodeficiency  
CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
CC and/or diagnose an autoimmune disease, especially rheumatoid  
CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
CC antibodies can be administered to cells in vitro, ex vivo or in  
CC vivo or to a multicellular organism. Soluble forms of the  
CC polypeptides may also be used. Methods for screening for  
CC agonist/antagonist compounds are also provided.

XX Sequence 241 AA;

XX Query Match 100.0%; Score 969; DB 21; Length 241;

XX Best Local Similarity 100.0%; Pred. No. 1.3e-69;

XX Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAMGAFRALCGIALCALSLGCRPTGGCGGPRLLLTGTGDARCRVHTTRCCRD 60  
Db |||||||  
1 maqhgamgafRALCGIALCALSLGCRPTGGCGGPRLLLTGTGDARCRVHTTRCCRD 60  
QY 61 YPGECCSEWDCMCVQPEPHCGDPCCTTCRHHPCPGGVQSGKFSFGFCIDCASGTF 120  
Db |||||||  
61 ypgeccsewDCMCVQPEPHCGDPCCTTCRHHPCPGGVQSGKFSFGFCIDCASGTF 120  
QY 121 SGGHEGCKPWTCDTQFGFLTVFPGNKNTHNAVCVFSGSPAP 162  
Db |||||||  
121 sgghegckpwtcdtqfglvtvfgnknthnavcvfsgspap 162

## RESULT 8

AA24409

ID AAB24409 standard; Protein; 241 AA.

AC AAB24409;

XX 07-NOV-2000 (first entry)

XX Human PRO364 protein sequence SEQ ID NO:117.

XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
KW angiogenic; proliferative; cardiac; cardiovascular; antiatherosclerotic;  
KW cytostatic; gene therapy; vaccine.

XX Homo sapiens.

XX WO200032221-A2.

XX 08-JUN-2000.

XX 30-NOV-1999; 99WO-US28313.

XX 01-DEC-1998; 98WO-US25108.

XX 16-DEC-1998; 98US-0112850.

XX 12-JAN-1999; 99US-0115554.

XX 08-MAR-1999; 99WO-US05028.

XX 12-MAR-1999; 99US-0123957.

XX 28-APR-1999; 99US-0131445.

XX 14-MAY-1999; 99US-0134287.

XX 02-JUN-1999; 99WO-US12252.

XX 23-JUN-1999; 99US-0141037.

XX 26-JUL-1999; 99US-0144758.

XX 01-SEP-1999; 99WO-US20111.

XX 08-SEP-1999; 99WO-US20594.

XX 13-SEP-1999; 99WO-US20944.

XX 15-SEP-1999; 99WO-US21090.

XX 05-SEP-1999; 99WO-US21547.

XX 05-OCT-1999; 99WO-US23089.

XX 29-OCT-1999; 99US-0162506.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;  
PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;  
PI Watanabe CK, Williams PM, Wood WI;  
XX WPI; 2000-412154/35.  
DR N-PSDB; AAA77604.

XX Nucleic acids encoding PRO polypeptides useful for preventing,  
PT diagnosing and treating diagnosing a cardiovascular, endothelial or  
PT angiogenic disorders in mammals -  
XX Claim 72; Fig 44; 315pp; English.

XX The present invention describes nucleic acids encoding PRO polypeptides  
CC useful for preventing, diagnosing and treating diagnosing a  
CC cardiovascular, endothelial or angiogenic disorder in mammals by





DT XX 26-OCT-1999 (first entry)

DE XX Human TNF receptor homologue PRO364.

KW PRO364; tumour necrosis factor receptor; human; apoptosis;  
 inflammation; antiinflammatory; NF-KB activation;  
 autoimmune disease; therapy.

KW KX Homo sapiens.

OS XX

XX Key Location/Qualifiers

FT Peptide 1..25

FT Protein /note= "signal peptide"

FT Protein 26..241

FT Modified-site /note= "mature protein"

FT 146

FT /note= "N-glycosylated"

FT 162..180

FT Domain /note= "transmembrane domain"

XX

XX WO9940196-A1.

XX

XX 12-AUG-1999.

XX

XX 09-FEB-1999; 99WO-US02642.

XX

XX 09-FEB-1999; 98US-0024087.

XX

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;  
 Pitti RM, Wood WI;

XX WPI; 1999-494296/41.

XX N-PSDB; AAX87670.

XX

XX Tumour necrosis factor receptor homologue - useful for, e.g.  
 modulating apoptosis and NF-KB activation and proinflammatory or  
 autoimmune responses

XX

XX Claim 17; Fig 2A; 104pp; English.

XX

XX The present sequence represents human PRO364, a novel member of the  
 tumour necrosis factor receptor family. The sequence was deduced  
 from a bone marrow cDNA clone (see AAX87670). Methods for the  
 recombinant production of PRO364 polypeptides, e.g. in CHO,  
 Escherichia coli or yeast host cells, are provided. Claimed  
 polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the  
 mature protein) and 26-X of the present sequence, where X is any  
 one of amino acid residues 157-167 of PRO364. PRO364 polypeptides  
 are useful for modulating apoptosis, NF-KB activation and  
 proinflammatory or autoimmune responses in mammalian cells  
 (claimed). Chimeric molecules comprising a PRO364 polypeptide  
 fused to a heterologous sequence such as epitope tag or  
 immunoglobulin Fc region are also claimed. PRO364 can be used in  
 assays to identify other proteins or molecules involved in binding  
 interactions. This is useful for identifying inhibitors or  
 agonists of receptor/ligand binding. The PRO364 polypeptides may  
 also be combined with an agent that is cytotoxic, chemotherapeutic  
 or a growth inhibitor. PRO364 antibodies are useful in diagnostic  
 methods, purification methods and also in therapy, e.g. as  
 inhibitors.

XX

XX Sequence 241 AA;

XX

Query Match 100.0%; Score 969; DB 20; Length 241;  
 Best Local Similarity 100.0%; Pred. NO. 1.3e-69;  
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMGAFRALCGALLCALSLGQRPTGPGCGPGLLLGTGTDCRCRVHTRCCRD 60  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 maqhgmgafralcgallcalslgqrptgpgcgpglllgtgtddrcrcrvhtrccrd 60

QY 61 YPGECCSEWDCMCVQPFHCGDPCTTCRRHPGQVQSGKFSFGQIDCASGTF 120  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 ypgeccsewdcmcvqpfhcgdpcttcrrhpcpggvgqgkfsfgqldcasgtf 120

QY 121 SGGHGHGCKPMTDCTQFGFLTVFPGNKTNAVCVPGSPPAEP 162  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 sggheghckpmtctqfgfltvfpgnktnavcvpgspap 162

RESULT 5

AAB27651

ID AAB27651 standard; Protein; 241 AA.

XX

AC AAB27651;

XX

DT 26-JAN-2001 (first entry)

XX

DE Human protein PRO364.

XX

KW Cardiovascular; endothelial; angiogenic disorder; PRO179;  
 PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333;  
 PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;  
 gene therapy.

KW

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FT Peptide 1..25

FT /label= "Signal peptide"

XX

PN WO200053757-A2.

XX

XX 14-SEP-2000.

XX

XX 24-FEB-2000; 2000WO-US05004.

XX

XX 08-MAR-1999; 99WO-US05028.

PR 12-MAR-1999; 99US-0123957.

PR 02-JUN-1999; 99WO-US12252.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 01-SEP-1999; 99WO-US20111.

PR 15-SEP-1999; 99WO-US21090.

PR 30-NOV-1999; 99WO-US28313.

PR 30-NOV-1999; 99WO-US28409.

PR 02-DEC-1999; 99WO-US28565.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.

XX

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
 Goddard A, Gurney AL, Hillan KJ, Marsters SA, Paoni NF, Pitti RM;  
 Watanabe CK, Williams PM, Wood WI;

PI WPI; 2000-611444/58.

DR N-PSDB; AAA99903.

XX

XX Novel PRO polypeptides and agonists and antagonists of them, used to  
 diagnose and treat cardiovascular, endothelial and angiogenic disorders

PT

XX

XX Claim 71; Fig 6; 181pp; English.

XX

XX The present invention relates to methods for stimulating or inhibiting  
 angiogenesis and cardiovascularization. The methods involve the use of  
 pharmaceutical compositions based on the following proteins, PRO179,  
 PRO238, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333,  
 PRO840, PRO877, PRO878, PRO879, PRO882, PRO885 or PRO887. These  
 proteins were identified by isolating cDNA clones encoding secreted  
 proteins. The proteins of the invention may be used to diagnose and  
 treat cardiovascular, endothelial or angiogenic disorders. The present

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OK protein - protein search, using sw model

Run on: September 4, 2001, 15:56:21 ; Search time 126.12 Seconds  
(without alignments)  
77.871 Million cell updates/sec

Title: US-09-512-363-2-copy\_1\_162

Perfect score: 969

Sequence: 1 MACHGAMGAFRALCGLALIC.....FPGNKTHNAVCPGSPPAEP 162

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_0601.\*

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22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	969	100.0	234	21 AAY95879	Human tumour necro
2	969	100.0	234	21 AAY52158	Tumour necrosis fa
3	969	100.0	241	19 AAW37839	Amino acid sequenc
4	969	100.0	241	20 AAY06505	Human TNF receptor
5	969	100.0	241	21 AAB27651	Human protein PRO3
6	969	100.0	241	21 AAB33431	Human PRO364 prote
7	969	100.0	241	21 AAY95895	Human tumour necro
8	969	100.0	241	21 AAB24409	Human PRO364 prote
9	969	100.0	241	21 AAY71467	Human PRO364 prote
10	969	100.0	241	22 AAB20115	Human immunostimul
11	969	100.0	241	22 AAB47054	Human PRO364. Hom

12	969	100.0	241	22 AAB50910	Human PRO364 prote
13	969	100.0	241	22 AAB50982	Human PRO364 prote
14	969	100.0	241	22 AAB53090	Human angiogenesis
15	937	96.7	228	19 AAW37840	Truncated human 31
16	937	96.7	235	21 AAY44825	Human molecule ass
17	937	96.7	311	19 AAW37842	Human 312C2 protei
18	921	95.0	240	21 AAY95881	Human tumour necro
19	921	95.0	240	21 AAY52160	TRILSV2 amino acid
20	842.5	86.9	317	20 AAY06645	PRO364-related EST
21	837.5	86.4	316	22 ABA47055	Polypeptide encode
22	639	65.9	241	21 AAY95880	Human tumour necro
23	639	65.9	241	21 AAY52159	TRILSV1 amino acid
24	605	62.4	232	19 AAW37841	Human 312C2 protei
25	506	52.2	228	19 AAW49018	Mouse glucocorticoid
26	506	52.2	228	19 AAW49016	Mouse glucocorticoid
27	506	52.2	228	19 AAW37838	Amino acid sequenc
28	506	52.2	294	19 AAW49017	Mouse glucocorticoid
29	255	26.3	89	21 AAY76013	Murine TNF-alpha f
30	255	26.3	89	22 AAB55952	Skin cell protein,
31	166.5	17.2	206	16 AAR81881	Mouse type-II memb
32	166.5	17.2	206	19 AAW48977	Mouse OX40 extrace
33	166.5	17.2	438	16 AAR81882	Plasmid pDC406/OX4
34	166.5	17.2	438	19 AAW48976	Deduced sequence e
35	166	17.1	277	16 AAR76996	ACT-4 cell surface
36	162	16.7	277	16 AAR74737	ACT-4-h-1 receptor
37	162	16.7	277	16 AAR79904	Human OX40 protein
38	162	16.7	277	22 AAB35329	Human tumour necro
39	162	16.7	277	22 AAB50522	H4-1BB receptor pr
40	160.5	16.6	255	16 AAR70977	Human 4-1BB polype
41	160.5	16.6	255	16 AAR64197	Human 4-1BB recept
42	160.5	16.6	255	18 AAW26658	Human CD137 protei
43	160.5	16.6	255	20 AAY33214	Human receptor pro
44	160.5	16.6	255	20 AAY28688	Human tumour necro
45	160.5	16.6	255	22 AAB50521	

#### ALIGNMENTS

```
RESULT 1
AAY95879
ID AAY95879 standard; Protein; 234 AA.
XX
AC AAY95879;
XX
DT 20-NOV-2000 (first entry)
XX
DE Human tumour necrosis factor receptor-like protein TR11.
XX
KW TR11; human; tumour necrosis factor receptor-like protein;
KW immunodeficiency; autoimmune disease; rheumatoid arthritis;
KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;
KW dermatological; antiinflammatory; therapy; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..25 /label= Signal_peptide
FT Protein 26..234 /label= Mature_protein
FT FT /label= Extracellular_domain
FT Domain 26..162 /label= Transmembrane_domain
FT Domain 163..179 /label= Transmembrane_domain
FT Domain 180..234 /label= Intracellular_domain
FT FT /note= "N-glycosylated"
FT Modified-site 146
FT Domain 72..81 /note= "conserved domain CD-II"
FT Domain 84..93 /note= "conserved domain CD-III"
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FT Domain 107..113 /note= "conserved domain CD-IV"

FT Domain 128..134 /note= "conserved domain CD-V"

FT Domain 153..160 /note= "conserved domain CD-VI"

FT Domain 176..186 /note= "conserved domain CD-VII"

FT Domain 204..209 /note= "conserved domain CD-IX"

FT Domain 224..233 /note= "conserved domain CD-X"

FT Region 27..36 /note= "epitope-bearing region"

FT Region 43..51 /note= "epitope-bearing region"

FT Region 59..67 /note= "epitope-bearing region"

FT Region 56..64 /note= "epitope-bearing region"

FT Region 66..71 /note= "epitope-bearing region"

FT Region 99..107 /note= "epitope-bearing region"

FT Region 125..133 /note= "epitope-bearing region"

FT Region 143..151 /note= "epitope-bearing region"

FT Region 156..164 /note= "epitope-bearing region"

FT Region 203..211 /note= "epitope-bearing region"

FT Region 222..230 /note= "epitope-bearing region"

FT Region 222..230 /note= "epitope-bearing region"

XX WO200050459-A1.

XX 31-AUG-2000.

XX 23-FEB-2000; 2000WO-US04572.

XX 24-FEB-1999; 99US-0121648.

XX 13-MAY-1999; 99US-0134172.

XX 16-JUL-1999; 99US-0144076.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Ni J;

XX WPI; 2000-572072/53.

XX N-PSDB; AAA50304.

XX Human tumor necrosis factor receptor-like proteins useful for

PT diagnosis, prevention and treatment of disease states associated with

PT aberrant cell survival such as autoimmune disease and rheumatoid

PT arthritis

XX Claim 14(c); Fig 1A-B; 278pp; English.

XX The present sequence is that of human tumour necrosis factor

CC receptor-like protein TR11, a novel 25 kDa protein which shows

CC 58.6% identity to murine glucocorticoid induced tumour necrosis

CC factor receptor family-related gene. The sequence was deduced from

CC a cDNA clone (see AAA50304) discovered in a T-helper cell library.

CC TR11 activated NF-kappaB through a TRAF2-mediated mechanism.

CC Expression is activation-inducible. The TR11 ligand is constitutively

CC expressed in an endothelial cell line. This suggests that TR11 and

CC its ligand may be involved in activated T-cell trafficking.

CC The invention provides TR11, TR11SV1 and TR11SV2 nucleic acids

CC (see AAA50304-06) and highly conserved encoded proteins (see

CC AAY95879-81), as well as vectors, host cells and recombinant methods for

CC their production. TR11, TR11SV1 and/or TR11SV2 polypeptides are useful

CC for treating, preventing, prognosis and/or diagnosis of an

CC immunodeficiency, especially common variable immunodeficiency,

CC X-linked agammaglobulinemia, severe combined immunodeficiency,

CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin

CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2

CC antagonists (e.g. antibodies) are used to treat, prevent, prognose

CC and/or diagnose an autoimmune disease, especially rheumatoid

CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura

CC or IgA nephropathy. The polypeptides, polynucleotides and/or

CC antibodies can be administered to cells in vitro, ex vivo or in

CC vivo or to a multicellular organism. Soluble forms of the

CC polypeptides may also be used. Methods for screening for

CC agonist/antagonist compounds are also provided.

XX Sequence 234 AA;

SQ

Query Match 100.0%; Score 969; DB 21; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.3e-69;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQHGAAGAFALCALSLGQRTGGPGCGRLLLTGTDAACRVRHTTRCCRD 60

Db 1 maqhgaagafalcalslgqrtggpgcgrrlllgtgtdarccrvhttrccrd 60

Qy 61 YPEEECCSEWDCMCVQPEFHCGDPCTTCRHHPCPPGGVQSGKFSFGQICDASGTF 120

Db 61 ypgeecscsewdcmcvqpefhcgdpcttcrrhhpcppggvgvsgkfsgfgqicdasgtf 120

Qy 121 SGGHEGHCKPMWTDCTQFGFLTVFPNGKTHNAVCPGSPPAEP 162

Db 121 sggheghckpmtwtdctqfgfltvfpngkthnavcvpgspapaep 162

RESULT 2

AAAY52158

ID AAY52158 standard; Protein; 234 AA.

XX AC AAY52158;

XX DT 01-FEB-2000 (first entry)

XX Tumour necrosis factor receptor-like protein (TR11) amino acid sequence.

XX Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2;

XX G1TR; growth; differentiation; cell death; immune deficiency disorder;

XX DiGeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia;

XX Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes;

XX Alzheimer's disease; Parkinson's disease; Huntington's disease;

XX inflammatory condition.

XX Homo sapiens.

XX Key Location/Qualifiers

PH Peptide 1..25 /label= Signal\_peptide

FT Protein 26..234 /label= TR11

FT Domain 26..162 /note= "Extracellular domain"

FT Domain 163..179 /note= "Transmembrane domain"

FT Domain 180..234 /note= "Intracellular domain"

XX WO9920758-A1.

XX 29-APR-1999.

XX 21-OCT-1998; 98WO-US22085.

XX 21-OCT-1997; 97US-0063212.

XX (HUMA-) HUMAN GENOME SCI INC.

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	Matches 162;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	MAOHGACAFRALCGLALLCALSIGQRTGPGCGGPRLLLGTTGDARCCRVHTRCCRD	60			
Db	1	MAOHGAGAFRALCGLALLCALSIGQRTGPGCGGPRLLLGTTGDARCCRVHTRCCRD	60			
Qy	61	YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPGPGGVQSQGFSGFCIDCASGTF	120			
Db	61	YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPGPGGVQSQGFSGFCIDCASGTF	120			
Qy	121	SGGHEGCKPWTDTQRGFLTVPFGNKTNNAVCPGSPPAEP	162			
Db	121	SGGHEGCKPWTDTQRGFLTVPFGNKTNNAVCPGSPPAEP	162			

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RESULT 2
US-08-911-423-6
; Sequence 6, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911.423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: '07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-911-423-6

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Best Local Similarity 100.0%; Pred. No. 3e-74;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGAFRALCGLALLCALSIGQRPTGPGCGPRLLLGTGTDARCCRVHTTRCDYVPGREC 60
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[illegible]

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US-08-911-423-8
: Sequence 8, Application US/08911423
: Patent No. 6111090
: GENERAL INFORMATION:
: APPLICANT: Gorman, Daniel M.
: APPLICANT: Randall, Troy D.
: APPLICANT: Zlotnik, Albert
: TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
: TITLE OF INVENTION: REAGENTS
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DNAX Research Institute
: STREET: 901 California Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/911,423
: FILING DATE: 14-AUG-1997
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/023,419
: FILING DATE: 16-AUG-1996
: APPLICATION DATA:
: APPLICATION NUMBER: US 60/027,901
: FILING DATE: 07-OCT-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Ching, Edwin P.
: REGISTRATION NUMBER: 34,090
: REFERENCE/DOCKET NUMBER: DX0612K
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-852-9196
: TELEFAX: 650-496-1200
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 311 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-911-423-8

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		RCCNDYPGEEC	
Qy	67	CSEWDCMCVQPEFHCGDPCCCTCRHHPCPPQGVQSGKSF	136
		FGQCIDCASGTSFGGHEG	
Db	61	CSEWDCMCVQPEFHCGDPCCCTCRHHPCPPQGVQSGKSF	130
		FGQCIDCASGTSFGGHEG	
Qy	127	HCKPTWTDCTCGFLTVPFGNKTTHNAVCPVGSPPAEP	162

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:57:34 ; Search time 65.86 Seconds  
(without alignments)  
50.647 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_1\_162

Perfect score: 969

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2\_6/ptodata/2/1aa/6A-COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/1aa/6B-COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/1aa/PCTUS-COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	937	96.7	311	3	US-08-911-423-8
4	605	62.4	232	3	US-08-911-423-7
5	506	52.2	228	3	US-08-911-423-2
6	255	26.3	89	4	US-09-188-930-191
7	166.5	17.2	206	1	US-08-097-827-7
8	166.5	17.2	206	1	US-08-494-574-7
9	166.5	17.2	438	1	US-08-097-827-11
10	166.5	17.2	438	1	US-08-494-574-11
11	162	16.7	277	2	US-08-147-784-2
12	162	16.7	277	4	US-08-195-967-2
13	160.5	16.6	255	1	US-08-236-918A-8
14	160.5	16.6	255	2	US-08-816-605-9
15	160.5	16.6	255	5	PCT-US96-03965-8
16	158.5	16.4	219	2	US-08-816-605-2
17	153	15.8	191	3	US-08-974-022-52
18	153	15.8	256	1	US-08-236-918A-6
19	153	15.8	256	5	PCT-US96-03965-2
20	153	15.8	300	2	US-08-794-796-2
21	151	15.6	205	3	US-08-974-022-51
22	149	15.4	140	4	US-08-477-347-17
23	141.5	14.6	401	3	US-08-974-022-2
24	139.5	14.4	139	2	US-08-219-237B-8
25	139.5	14.4	401	3	US-08-974-022-4
26	139.5	14.4	401	4	US-09-042-785A-13
27	138.5	14.3	451	3	US-08-996-139-4

Query Match 100.0%; Score 969; DB 3; Length 241;

28	138.5	14.3	451	4	US-08-995-659-4	Sequence 4, Appli
29	138.5	14.3	616	3	US-08-996-139-6	Sequence 6, Appli
30	138.5	14.3	616	4	US-08-995-659-6	Sequence 6, Appli
31	135.5	14.0	197	3	US-08-974-022-49	Sequence 49, Appl
32	135.5	14.0	289	4	US-05-042-785A-11	Sequence 11, Appl
33	133	13.7	401	3	US-08-974-022-6	Sequence 6, Appli
34	133	13.7	401	4	US-09-042-785A-12	Sequence 12, Appl
35	131	13.5	591	3	US-08-996-139-2	Sequence 2, Appli
36	131	13.5	591	4	US-08-995-659-2	Sequence 2, Appli
37	129.5	13.4	253	4	US-09-042-785A-4	Sequence 4, Appli
38	129.5	13.4	605	4	US-09-042-785A-23	Sequence 23, Appl
39	129.5	13.4	655	3	US-08-959-382-2	Sequence 2, Appli
40	123	12.7	625	3	US-08-996-139-15	Sequence 15, Appl
41	123	12.5	625	4	US-08-995-659-15	Sequence 15, Appl
42	121	12.5	227	3	US-08-974-022-48	Sequence 48, Appl
43	121	12.5	461	4	US-09-042-785A-7	Sequence 7, Appli
44	119	12.3	461	1	US-08-385-229-2	Sequence 2, Appli
45	119	12.3	461	6	5395760-2	Patent No. 5395760

ALIGNMENTS

RESULT 1  
US-08-911-423-4  
; Sequence 4, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911.423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Chiang, Egwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-4

APPLICANT: Murison, James Greg  
TITLE OF INVENTION: Compositions Isolated From Skin Cells  
FILE REFERENCE: 11000.1011c1  
CURRENT APPLICATION NUMBER: US/09/188.930A  
CURRENT FILING DATE: 1998-11-09  
NUMBER OF SEQ ID NOS: 348  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 191  
LENGTH: 89  
TYPE: PRT  
ORGANISM: mouse  
US-09-188-930-191

Query Match 26.3%; Score 255; DB 4; Length 89;  
Best Local Similarity 46.3%; Pred. No. 1.2e-15;  
Matches 44; Conservative 17; Mismatches 26; Indels 8; Gaps 2;  
QY 8 GATFALCGLALLCALSIGQ-RPTGGCGGGRLLLTGTGDARCCRVHTTRCCRDYPGGEC 66  
DB 1 GAWAMLYGVSMCLVDLDGQSVVEEPGCGKVGQSGNNTCCSLYA-----PGKED 53  
QY 67 CSEWDCVCQPEFHCGDPCCTTCRHHPCCPPGQGVQ 101  
DB 54 CPKERCICVTPYHCGDPQCKICKHYCPQGPQGRVE 88

RESULT 7  
US-08-097-827-7  
Sequence 7, Application US/08097827  
Patent No. 5457035  
GENERAL INFORMATION:  
APPLICANT: Baum, Peter  
APPLICANT: Goodwin, Ray  
APPLICANT: Fanslow, William  
APPLICANT: Gayle, Richard  
TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/097,827  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2806  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0730  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 206 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-097-827-7

Query Match 17.2%; Score 166.5; DB 1; Length 206;  
Best Local Similarity 28.7%; Pred. No. 1.2e-07;

Matches 50; Conservative 12; Mismatches 51; Indels 61; Gaps 9;  
QY 26 QRPTGGCGGGRLLLG--TGTDA--CCRVHT---TRCCRD-YPG-----ECCSEWDC 72  
DB 6 QOPT-----ALLLLGLTGVTTARRLNCVKHTYPSGHKCCRECQPGHGMVNRCDHTRDT 58  
QY 73 MCVPQPEFHCGDPC-----CTTCRHHP-----CPPGQG 99  
DB 59 LC-----HPCETGFYNEAVNYDTCKOCTCNHRSGSELKQNCPTQDTVCRCPGTQ 110  
QY 100 VOSQKSFSGFQCIDCASCTFSGGHGHCKPWTDCQTFQGLTVFGNKTHNAVC 153  
DB 111 PRQSGYKLGVDVCPGPHFSPGNQACKPWTNCTLSGKQTRHFPASDSDAVC 164  
RESULT 8  
US-08-494-574-7  
Sequence 7, Application US/08494574  
Patent No. 5783665  
GENERAL INFORMATION:  
APPLICANT: Baum, Peter  
APPLICANT: Goodwin, Ray  
APPLICANT: Fanslow, William  
APPLICANT: Gayle, Richard  
TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand for  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/494,574  
FILING DATE: 22-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/097,827  
FILING DATE: 23-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2806  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0730  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 206 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-494-574-7

Query Match 17.2%; Score 166.5; DB 1; Length 206;  
Best Local Similarity 28.7%; Pred. No. 1.2e-07;  
Matches 50; Conservative 12; Mismatches 51; Indels 61; Gaps 9;  
QY 26 QRPTGGCGGGRLLLG--TGTDA--CCRVHT---TRCCRD-YPG-----ECCSEWDC 72  
DB 6 QOPT-----ALLLLGLTGVTTARRLNCVKHTYPSGHKCCRECQPGHGMVNRCDHTRDT 58  
QY 73 MCVPQPEFHCGDPC-----CTTCRHHP-----CPPGQG 99  
DB 59 LC-----HPCETGFYNEAVNYDTCKOCTCNHRSGSELKQNCPTQDTVCRCPGTQ 110

Db 121 HCKPWTDCQFGFLVFPNGKTHNAVCPGSPPAEP 156  
|||||

RESULT 4  
US-08-911-423-7  
; Sequence 7, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 232 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-7

Query Match 62.4%; Score 605; DB 3; Length 232;  
Best Local Similarity 78.1%; Pred. No. 1.6e-45;  
Matches 107; Conservative 5; Mismatches 17; Indels 8; Gaps 3;

Qy 7 MGAFRALCGLALLCALSLGQRTGGPGGGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 66  
Db 1 MGAFRALCGLALLCALSLGQRTGGPGGGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 60  
Qy 67 CSEWDCMCVQPEFHGCDPCTTCRHHPCPPGQGVQSGKFSFGFQCI-----DCASGTFSG 122  
Db 61 CSEWDCMCVQPEFHGCDPCTTCRHHPCPPGQGVQSGKFSFGFQCI-----SWRCLWESTQARGSTRAR 117  
Qy 123 GH-EGHCKPWTDCQFG 138  
Db 118 GRARGHRCPARTCGWVG 134

RESULT 5  
US-08-911-423-2

; Sequence 2, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-2

Query Match 52.2%; Score 506; DB 3; Length 228;  
Best Local Similarity 54.5%; Pred. No. 5.7e-37;  
Matches 85; Conservative 25; Mismatches 38; Indels 8; Gaps 2;

Qy 7 MGAFRALCGLALLCALSLGQ-RPTGGPGGGRLLLTGTGDARCCRVHTTRCCRDYPGEE 65  
Db 1 MGAWAMLYGVSMCLVLDLQGFVVEEFGCGKGVQSGNNTRCCSLYA-----PKGE 53  
Qy 66 CCSEWDCMCVQPEFHGCDPCTTCRHHPCPPGQGVQSGKFSFGFQCIDCASGTFSGSGHE 125  
Db 54 DCPKERCICVTYTHCGDPCKICKHYPCQPGQGVQSGDIVFGRCVACAMGTFISAGRD 113  
Qy 126 GHCKPWTDCQFGFLVFPNGKTHNAVCPGSPPAE 161  
Db 114 GHCLWNCVSQFGFLVFPNGKTHNAVCIPEPLPTE 149

RESULT 6  
US-09-188-930-191  
; Sequence 191, Application US/09188930A  
; Patent No. 6150502  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,784
; FILING DATE: 03-NOV-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 05490A-220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-147-784-2

Query Match 16.7%; Score 162; DB 2; Length 277;
Best Local Similarity 29.7%; Pred. No. 3.9e-07;
Matches 51; Conservative 11; Mismatches 92; Indels 18; Gaps 5;

QY 5 GAMGAFRALCGLALLCALSGLG-----QRTGGPGCGPGRLLLTGTGDARCCRVHT 54
   || || || || || || || || || || || || || || || || || || || ||
Db 4 GARRLGRGPCAALLLLGLGLSTVTGLHCVGDTYPSNDRCCHECR--PGNGMVSRCSRQN 61
   || || || || || || || || || || || || || || || || || || || ||
QY 55 TRCCRDYFG--EECCSEWDCM-CVQPEFHCGD---PCCTTCRHHPCPPGQGVQSGKFSF 108
   || || || || || || || || || || || || || || || || || || || ||
Db 62 TVCRPCGPGFYNDVVSRRKPKCTWCNLRSGSERKQLCTATQDTCRCRAGTQPLDSYKP 121
   || || || || || || || || || || || || || || || || || || || ||
QY 109 GFQCIDCASGTFSGHGCHCKPWTCTQFGFLTVPFGNKTNAVCPGSPPA 160
   || || || || || || || || || || || || || || || || || || || ||
Db 122 GVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLOPASNSSDAICEDRDPPA 173
   || || || || || || || || || || || || || || || || || || || ||

RESULT 12
US-08-195-967-2
; Sequence 2, Application US/08195967
; Patent No. 6242566
; GENERAL INFORMATION:
; APPLICANT: Godfrey, Wayne
; APPLICANT: Engleman, Edgar G.
; TITLE OF INVENTION: LIGAND (ACT-4-L) TO A RECEPTOR ON THE SURFACE OF ACTIVATED
; TITLE OF INVENTION: CD4+ T-CELLS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourle and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,967
; FILING DATE: 10-FEB-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 05490A-230
; TELECOMMUNICATION INFORMATION:
```

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;
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-195-967-2

Query Match 16.7%; Score 162; DB 4; Length 277;
Best Local Similarity 29.7%; Pred. No. 3.9e-07;
Matches 51; Conservative 11; Mismatches 92; Indels 18; Gaps 5;

QY 5 GAMGAFRALCGLALLCALSGLG-----QRTGGPGCGPGRLLLTGTGDARCCRVHT 54
   || || || || || || || || || || || || || || || || || || || ||
Db 4 GARRLGRGPCAALLLLGLGLSTVTGLHCVGDTYPSNDRCCHECR--PGNGMVSRCSRQN 61
   || || || || || || || || || || || || || || || || || || || ||
QY 55 TRCCRDYFG--EECCSEWDCM-CVQPEFHCGD---PCCTTCRHHPCPPGQGVQSGKFSF 108
   || || || || || || || || || || || || || || || || || || || ||
Db 62 TVCRPCGPGFYNDVVSRRKPKCTWCNLRSGSERKQLCTATQDTCRCRAGTQPLDSYKP 121
   || || || || || || || || || || || || || || || || || || || ||
QY 109 GFQCIDCASGTFSGHGCHCKPWTCTQFGFLTVPFGNKTNAVCPGSPPA 160
   || || || || || || || || || || || || || || || || || || || ||
Db 122 GVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLOPASNSSDAICEDRDPPA 173
   || || || || || || || || || || || || || || || || || || || ||

RESULT 13
US-08-236-918A-8
; Sequence 8, Application US/08236918A
; Patent No. 5674704
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple 7.5.3
; SOFTWARE: Microsoft Word, Version #6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,918A
; FILING DATE: 06-May-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,843
; FILING DATE: 07-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2801-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-236-918A-8
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US-08-494-574-11  
; Sequence 11, Application US/08494574  
; Patent No. 5783665  
; GENERAL INFORMATION:  
; APPLICANT: Baum, Peter  
; APPLICANT: Goodwin, Ray  
; APPLICANT: Fanslow, William

COUNTRY: U  
ZTP: 94301

ZIP: 94301

Search completed: September 4, 2001, 15:57:34  
Job time: 376 sec

0

Query Match 16.6%; Score 160.5; DB 1; Length 255;  
Best Local Similarity 30.9%; Pred. No. 4.9e-07;  
Matches 47; Conservative 12; Mismatches 52; Indels 41; Gaps 9;

QY 34 CGPGRLLLTGTADRCRVTTRCCRDYPG-----ECCS-----EWDGCMVQPFHCGDP 84  
DB 48 CPPNSFSSAGG--QRTCDI-----CRQCKGVFTRKESSTSNACDC---TPGFHCLGA 97

QY 85 CCTTCRHHPCPPGQVQSGKSFQFCIDCASGTFSGHGHGCKPWTCTQFGFLTVFP 144  
DB 98 GCSMC-EQDCKQGQELTKKG-----CKDCCFGTFNDQKRGICRPTWNCSLDGKSVLVN 149

QY 145 GNKTHNAVCPG-----SPPA---EP 162  
DB 150 GTKERDVVCGPSPADLSPGASSVTPPAPAREP 181

RESULT 14  
US-08-816-605-9  
; Sequence 9, Application US/08816605  
; Patent No. 5874240  
; GENERAL INFORMATION:  
; APPLICANT: NI, Jian  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Gentz, Reiner  
; TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/816,605  
; FILING DATE: 13-MAR-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF254  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8512  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 255 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-816-605-9

Query Match 16.6%; Score 160.5; DB 2; Length 255;  
Best Local Similarity 30.9%; Pred. No. 4.9e-07;  
Matches 47; Conservative 12; Mismatches 52; Indels 41; Gaps 9;

QY 34 CGPGRLLLTGTADRCRVTTRCCRDYPG-----ECCS-----EWDGCMVQPFHCGDP 84  
DB 48 CPPNSFSSAGG--QRTCDI-----CRQCKGVFTRKESSTSNACDC---TPGFHCLGA 97

QY 85 CCTTCRHHPCPPGQVQSGKSFQFCIDCASGTFSGHGHGCKPWTCTQFGFLTVFP 144  
DB 98 GCSMC-EQDCKQGQELTKKG-----CKDCCFGTFNDQKRGICRPTWNCSLDGKSVLVN 149

QY 145 GNKTHNAVCPG-----SPPA---EP 162  
DB 150 GTKERDVVCGPSPADLSPGASSVTPPAPAREP 181

RESULT 15  
PCT-US96-03965-8  
; Sequence 8, Application PC/TUS9603965  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung Se  
; APPLICANT: Kang, Chang-Yuil  
; TITLE OF INVENTION: Monoclonal antibody against human  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Barnard, Brown & Michaels  
; STREET: 306 East State Street, Suite 220  
; CITY: Ithaca  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 14850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/03965  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/122,796  
; FILING DATE: 16-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/012,269  
; FILING DATE: 01-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/922,996  
; FILING DATE: 30-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/267,577  
; FILING DATE: 07-NOV-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michaels, Christopher A  
; REGISTRATION NUMBER: 34,390  
; REFERENCE/DOCKET NUMBER: KW05  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 607-273-1711  
; TELEFAX: 607-273-2609  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 255 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US96-03965-8

Query Match 16.6%; Score 160.5; DB 5; Length 255;  
Best Local Similarity 30.9%; Pred. No. 4.9e-07;  
Matches 47; Conservative 12; Mismatches 52; Indels 41; Gaps 9;

QY 34 CGPGRLLLTGTADRCRVTTRCCRDYPG-----ECCS-----EWDGCMVQPFHCGDP 84  
DB 48 CPPNSFSSAGG--QRTCDI-----CRQCKGVFTRKESSTSNACDC---TPGFHCLGA 97

QY 85 CCTTCRHHPCPPGQVQSGKSFQFCIDCASGTFSGHGHGCKPWTCTQFGFLTVFP 144  
DB 98 GCSMC-EQDCKQGQELTKKG-----CKDCCFGTFNDQKRGICRPTWNCSLDGKSVLVN 149

QY 145 GNKTHNAVCPG-----SPPA---EP 162  
DB 150 GTKERDVVCGPSPADLSPGASSVTPPAPAREP 181

SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-03965-8

Query Match 19.1%; Score 160.5; DB 5; Length 255;  
Best Local Similarity 30.9%; Pred. No. 3.8e-07;  
Matches 47; Conservative 12; Mismatches 52; Indels 41; Gaps 9;  
Qy 9 CGPGRLLGTGDARCRVHTTRCCRDYPG-----ECCS-----EWDKMCVQPEFHCGDP 59  
Db 48 CPNNSFSAGG--QRTCDI-----CRQCKGVTRKESSTSNACDC---TPGFHCLGA 97  
Qy 60 CTTTCRHHPCPPGQGVQSGKFSFGQICDCASGTFSGGHEGHCRTWTCTQFGFLTVP 119  
Db 98 GCSMC-EQDCKQGGELTKKG-----CKDCFGTFNDQKRGICRPWTNCSLDGKSVLYN 149  
Qy 120 GNKTHNAVCPG-----SPPA-----EP 137  
Db 150 GTKERDVVCGSPADLSPGASSVTPAPAREP 181

RESULT 14  
US-08-816-605-2  
Sequence 2, Application US/08816605  
Patent No. 5874240  
GENERAL INFORMATION:  
APPLICANT: NI, Jian  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Gentz, Reiner  
TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/816.605  
FILING DATE: 13-MAR-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF254  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8512  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 219 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-816-605-2

Query Match 18.8%; Score 158.5; DB 2; Length 219;  
Best Local Similarity 33.0%; Pred. No. 5e-07;  
Matches 38; Conservative 11; Mismatches 45; Indels 21; Gaps 5;  
Qy 33 CRDYPG-----EECS-----EWDKMCVQPEFHCGDPCCCTCRHHPCPPGQGVQSGKFS 82

Db 28 CSNCPAGVFRTRKESSTSNACDC---TPGFHCLGAGCSMC-EQDCKQGGELTKKG--- 80  
Qy 83 FGFQCIDCASGTFSGGHEGHCRTWTCTQFGFLTVPFGNKTTHNAVCPVPGSPAP 137  
Db 81 ---CKDCFGTFNDQKRGICRPWTNCSLDGKSVLYNCTKERDVVCGPSSADLSP 131  
RESULT 15  
US-08-147-784-2  
Sequence 2, Application US/08147784  
Patent No. 5821332  
GENERAL INFORMATION:  
APPLICANT: Godfrey, Wayne  
APPLICANT: Buck, David  
APPLICANT: Engleman, Edgar G.  
TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/147,784  
FILING DATE: 03-NOV-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 05490A-220  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 277 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-147-784-2

Query Match 18.8%; Score 158.5; DB 2; Length 277;  
Best Local Similarity 31.6%; Pred. No. 6.2e-07;  
Matches 42; Conservative 10; Mismatches 70; Indels 11; Gaps 4;  
Qy 9 CGPGRLLGTGDARCRVHTTRCCRDYPG--ECCSSEWDCM-CVQPEFHCGD---PCT 62  
Db 46 CRP-----GNGMVSRCRSRSONTVCRPCGPGFYNDVSSKPKCKPCTWCNLSGSRKQLCT 100  
Qy 63 TCRHFPCCPGQGVQSGKFSFGQICDCASGTFSGGHEGHCRTWTCTQFGFLTVPFGNK 122  
Db 101 ATQDTCRCRAGTQPLDSYKPGVDCAPCPGHFSPGDNQACKPWTNCTLAGKHTLPASN 160  
Qy 123 THNAVCPGSPPA 135  
Db 161 SSDAICEDRDPPA 173

Search completed: September 4, 2001, 15:57:34  
Job time: 376 sec



```

RESULT 9
US-08-097-827-11
; Sequence 11, Application US/08097827
; Patent No. 5457035
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for
; TITLE OF INVENTION: OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-097-827-11

Query Match 19.8%; Score 166.5; DB 1; Length 438;
Best Local Similarity 28.7%; Pred. No. 1.9e-07;
Matches 50; Conservative 12; Mismatches 51; Indels 61; Gaps 9;

Qy 1 QRTGGPGCGPGRLLG--TGTDA--CCRVHT---TRCCRD-YPG-----EECCSEWDC 47
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 6 QOPT-----ALLLLGLTGLVTARRLNCVKHTYPSGHKCCRECPQGHGMVNRCDHTRDT 58
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Qy 48 MCVOPEFHCGDPC-----CTTCRHHP-----CPPGQG 74
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 59 LC-----HPCETGFYNEAVNYDTCKQCTCNHRSGSELKQNCPTQDTCRCRPGTQ 110
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Qy 75 VOSQKRFSGFCIDCASGTFSGGHEGHCKPWTDCQFGFLTVPGNKTHNAV 128
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 111 PRQDSGYKLGVDVCPGPPGHFSPGNQACKPWTNCTLSGKQTRHPASDSLDAVC 164
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 10
US-08-494-574-11
; Sequence 11, Application US/08494574
; Patent No. 5783665
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand for
; TITLE OF INVENTION: OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple 7.5.3
; SOFTWARE: Microsoft Word, Version #6.0.1
```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,574
; FILING DATE: 22-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE: 23-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-494-574-11

Query Match 19.8%; Score 166.5; DB 1; Length 438;
Best Local Similarity 28.7%; Pred. No. 1.9e-07;
Matches 50; Conservative 12; Mismatches 51; Indels 61; Gaps 9;

Qy 1 QRTGGPGCGPGRLLG--TGTDA--CCRVHT---TRCCRD-YPG-----EECCSEWDC 47
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 6 QOPT-----ALLLLGLTGLVTARRLNCVKHTYPSGHKCCRECPQGHGMVNRCDHTRDT 58
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Qy 48 MCVOPEFHCGDPC-----CTTCRHHP-----CPPGQG 74
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 59 LC-----HPCETGFYNEAVNYDTCKQCTCNHRSGSELKQNCPTQDTCRCRPGTQ 110
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Qy 75 VOSQKRFSGFCIDCASGTFSGGHEGHCKPWTDCQFGFLTVPGNKTHNAV 128
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 111 PRQDSGYKLGVDVCPGPPGHFSPGNQACKPWTNCTLSGKQTRHPASDSLDAVC 164
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 11
US-08-236-918A-8
; Sequence 8, Application US/08236918A
; Patent No. 5674704
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple 7.5.3
; SOFTWARE: Microsoft Word, Version #6.0.1
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RESULT 13  
PCT-US96-03965-8  
Sequence 8, Application PC/TUS9603965  
GENERAL INFORMATION:  
APPLICANT: KWON, Byoung Se  
APPLICANT: Kang, Chang-Yuul  
TITLE OF INVENTION: Monoclonal antibody against human  
TITLE OF INVENTION: receptor 4-1BB  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Barnard, Brown & Michaels  
STREET: 306 East State Street, Suite 220  
CITY: Ithaca  
STATE: NY  
COUNTRY: USA  
ZIP: 14850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: PCT/US96/03965  
APPLICATION FILING DATE:  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/122,796  
FILING DATE: 16-SEP-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/012,269  
FILING DATE: 01-FEB-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/922,996  
FILING DATE: 30-JUL-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/267,577  
FILING DATE: 07-NOV-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Michaels, Christopher A  
REGISTRATION NUMBER: 34,390  
REFERENCE/DOCKET NUMBER: KW05  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 607-273-1711  
TELEFAX: 607-273-2609  
INFORMATION FOR SEQ ID NO: 8:

Db 140 NKTHNAVCPGSPAP 156  
|||||

## RESULT 4

US-08-911-423-7

; Sequence 7, Application US/08911423

; Patent No. 611090

; GENERAL INFORMATION:

; APPLICANT: Gorman, Daniel M.

; APPLICANT: Randall, Troy D.

; APPLICANT: Zlotnik, Albert

; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED

; TITLE OF INVENTION: REAGENTS

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DNAX Research Institute

; STREET: 901 California Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/911,423

; FILING DATE: 14-AUG-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/023,419

; FILING DATE: 16-AUG-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/027,901

; FILING DATE: 07-OCT-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: DX0612K

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-496-1200

; TELEFAX: 650-496-1200

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 232 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-911-423-7

Query Match 60.5%; Score 509; DB 3; Length 232;

Best Local Similarity 74.6%; Pred No. 2.1e-37;

Matches 88; Conservative 5; Mismatches 17; Indels 8; Gaps 3;

Qy 1 QRTGPGCGPGRLLLTGTARCCRVHTTRCCRDYPGECCSEWDCMCVQPEFHGCDPC 60

Db 20 QRTGPGCGPGRLLLTGTARCCRVHTTRCCRDYPGECCSEWDCMCVQPEFHGCDPC 79

Qy 61 CTTCHRHCPGQGVQSGKSFQFCI-----DCASGTFSGGH-EGHCKPWTDCQFG 113

Db 80 CTTCHRHCPGQGVQSGKSFQFCI-----DCASGTFSGGH-EGHCKPWTDCQFG 134

## RESULT 5

US-08-911-423-2

; Sequence 2, Application US/08911423

; Patent No. 611090

; GENERAL INFORMATION:

; APPLICANT: Gorman, Daniel M.

; APPLICANT: Randall, Troy D.

; APPLICANT: Zlotnik, Albert

; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED

; TITLE OF INVENTION: REAGENTS

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DNAX Research Institute

; STREET: 901 California Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/911,423

; FILING DATE: 14-AUG-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/023,419

; FILING DATE: 16-AUG-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/027,901

; FILING DATE: 07-OCT-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: DX0612K

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-852-9196

; TELEFAX: 650-496-1200

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 228 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-911-423-2

Query Match

55.4%; Score 465.5; DB 3; Length 228;

Best Local Similarity 56.9%; Pred. No. 1.2e-33;

Matches 74; Conservative 21; Mismatches 28; Indels 7; Gaps 1;

Qy 7 PGCGPGRLLLTGTARCCRVHTTRCCRDYPGECCSEWDCMCVQPEFHGCDPCCTTCH-66

Db 27 PGCGPGRLLLTGTARCCRVHTTRCCRDYPGECCSEWDCMCVQPEFHGCDPCCTTCH-66

Qy 67 HPCPPGQGVQSGKSFQFCI-----DCASGTFSGGHGCKPWTDCQFGFLVFPNGKTHNA 126

Db 80 YPCQGRVQSGDIVFGFRCVACAMGTFSGAGRDGHCRLWTNCSQFGLTFMFGKTHNA 139

Qy 127 VCVPGSPPAE 136

Db 140 VCIPEPLTE 149

## RESULT 6

US-09-188-930-191

; Sequence 191, Application US/09188930A

; Patent No. 6150502

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Strachan, Lorna

; APPLICANT: Sleeman, Matthew

; APPLICANT: Onrust, Rene

; APPLICANT: Murison, James Greg

; TITLE OF INVENTION: Compositions Isolated From Skin Cells

; TITLE OF INVENTION: and Methods For Their Use

; FILE REFERENCE: 11000.1011c1



```

; CURRENT APPLICATION NUMBER: US/09/188, 930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 191
; LENGTH: 89
; TYPE: PRT
; ORGANISM: mouse
US-09-188-930-191

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```

Query Match      26.1%; Score 219.5; DB 4; Length 89;
Best Local Similarity 48.6%; Pred. No. 1.1e-12;
Matches 34; Conservative 13; Mismatches 16; Indels 7; Gaps 1;

QY    7   PGC6GPRLLLGTDARCCRVHTTRCCHDYPGEECCSEWDCMCVQPEPHCGDPCCCTTCRH 66
       |||||:: :| : ||| :          ||| : : || |::||| | :| :|
Db     26  PGC6GPGKVGSGNNTRCSLYA-----PGKEDCPKERGICVTPEYHCGDPQCCKICKH 78

QY    67  HPCPPGGGVQ 76
       :: || ||| :
Db     79  YPCQPGRQVE 88

```

```

RESULT 7
US-08-097-827-7
; Sequence 7, Application US/08097827
; Patent No. 5457035
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5457035
; TITLE OF INVENTION: OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-097-827-7

```

```
Query Match      19.8%; Score 166.5; DB 1; Length 206;
Best Local Similarity 28.7%; Pred. No. 9.5e-08;
Matches 50; Conservative 12; Mismatches 51; Indels 61; Gaps 9;
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[illegible]

RESULT 8  
US-08-494-574-7  
: Sequence 7, Application US/08494574  
: Patent No. 5783665  
: GENERAL INFORMATION:  
: APPLICANT: Baum, Peter  
: APPLICANT: Goodwin, Ray  
: APPLICANT: Fanslow, William  
: APPLICANT: Gayle, Richard  
: TITLE OF INVENTION: NO. 5783665el Cytokine Which is a Ligand for  
: NUMBER OF SEQUENCES: 13  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Immunex Corporation  
: STREET: 51 University Street  
: CITY: Seattle  
: STATE: WA  
: COUNTRY: USA  
: ZIP: 98101  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/494, 574  
: FILING DATE: 22-JUN-1995  
: CLASSIFICATION: 530  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US/08/097, 827  
: FILING DATE: 23-JUL-1993  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Perkins, Patricia A.  
: REGISTRATION NUMBER: 34,693  
: REFERENCE/DOCKET NUMBER: 2806  
: TELEPHONE: 206-587-0730  
: INFORMATION FOR SEQ ID NO: 7:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 206 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
: US-08-494-574-7

```

Query Match      19.8%; Score 166.5; DB 1; Length 206;
Best Local Similarity 28.7%; Pred. No. 9.5e-08;
Matches 50; Conservative 12; Mismatches 51; Indels 61; Gaps
9;
QY      1  ORPITGGPCGPRLLLG--TGTDA--CCRVHT-----TRCRD-YPG---EECCSEWDC 47
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       6  QOQT-----ALLGLGLTGLTARLNCVKHYTPSGHKCCRECPQGHGMVNRCDHTRT 58
QY      48  MCVQPEFHCGDPC-----CTTCRHP-----CpPQQG 74
      :| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       59  LC-----HPCETGFYNEAVNYDTCKQCTQCNHRSSELKQNCPTQDITVCRCPGTQ 110
QY      75  VQSGCKSFSGFCIDCAGTSGGHEGCKPWTDCQTQGFITVFPGNKTHNAV 128
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      111  PRDSGKYKLVGDCVPCPGHESPGNNQACKPWNTCTLSGKQTRHPASDLSDAVC 164

```

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: September 4, 2001, 15:57:34 ; Search time 65.86 Seconds  
(without alignments)  
42.831 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_26\_162

Perfect score: 841

Sequence: 1 QRPTGGPGCGRLLGTGT.....FPGKTHNAVCPGSPAP 137

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*

2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*

3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*

4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	841	100.0	228	3	US-08-911-423-6
2	841	100.0	241	3	US-08-911-423-4
3	841	100.0	311	3	US-08-911-423-8
4	509	60.5	232	3	US-08-911-423-7
5	465.5	55.4	228	3	US-08-911-423-2
6	219.5	26.1	89	4	US-09-188-930-191
7	166.5	19.8	206	1	US-08-097-827-7
8	166.5	19.8	206	1	US-08-494-574-7
9	166.5	19.8	438	1	US-08-097-827-11
10	166.5	19.8	438	1	US-08-494-574-11
11	160.5	19.1	255	1	US-08-236-918A-8
12	160.5	19.1	255	2	US-08-816-605-9
13	160.5	19.1	255	5	PCT-US96-03965-8
14	158.5	18.8	219	2	US-08-816-605-2
15	158.5	18.8	277	2	US-08-147-784-2
16	158.5	18.8	277	4	US-08-195-967-2
17	153	18.2	191	3	US-08-974-022-52
18	153	18.2	256	1	US-08-236-918A-6
19	153	18.2	256	5	PCT-US96-03965-2
20	151	18.0	205	3	US-08-974-022-51
21	150.5	17.9	300	2	US-08-794-796-2
22	149	17.7	140	4	US-08-477-347-17
23	140	16.6	401	3	US-08-974-022-2
24	139.5	16.6	139	2	US-08-219-237B-8
25	139	16.5	401	3	US-08-974-022-4
26	139	16.5	401	4	US-09-042-785A-13
27	133	15.8	401	3	US-08-974-022-6

28	133	15.8	401	4	US-09-042-785A-12	Sequence 12, Appl
29	131	15.6	451	3	US-08-996-139-4	Sequence 4, Appl
30	131	15.6	451	4	US-08-995-659-4	Sequence 4, Appl
31	131	15.6	591	3	US-08-996-139-2	Sequence 2, Appl
32	131	15.6	591	4	US-08-995-659-2	Sequence 2, Appl
33	131	15.6	616	3	US-08-996-139-6	Sequence 6, Appl
34	131	15.6	616	4	US-08-995-659-6	Sequence 6, Appl
35	129.5	15.4	605	4	US-09-042-785A-4	Sequence 4, Appl
36	129.5	15.4	605	3	US-09-042-785A-23	Sequence 23, Appl
37	129.5	15.4	655	3	US-08-959-382-2	Sequence 2, Appl
38	127.5	15.2	197	3	US-08-974-022-49	Sequence 49, Appl
39	127.5	15.2	289	4	US-09-042-785A-11	Sequence 11, Appl
40	123	14.6	625	3	US-08-996-139-15	Sequence 15, Appl
41	123	14.6	625	4	US-08-995-659-15	Sequence 15, Appl
42	121	14.4	227	3	US-08-974-022-48	Sequence 48, Appl
43	121	14.4	461	4	US-09-042-785A-7	Sequence 7, Appl
44	119	14.1	461	1	US-08-385-229-2	Sequence 2, Appl
45	119	14.1	461	6	5395760-2	Patent No. 5395760

ALIGNMENTS

RESULT 1  
US-08-911-423-6  
; Sequence 6, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-6

Query Match	100.0%	Score 841;	DB 3;	Length 228;
Best Local Similarity	100.0%	Pred. No. 3.2e-66;		
Matches 137;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	QRPRTGGPCGGPGRLLLTGTGDARCCRVHVTTRCCRDYPCGEECCSEWDCMCVQPERHCGDPC	60		
DB 20	QRPRTGGPCGGPGRLLLTGTGDARCCRVHVTTRCCRDYPCGEECCSEWDCMCVQPERHCGDPC	79		
QY 61	CTTCRRHPCPPGQGVQSGKSFQFCIDCASGTFSSGGHGHCKPWTDTCTQGFGLTVFPF	120		
DB 80	CTTCRRHPCPPGQGVQSGKSFQFCIDCASGTFSSGGHGHCKPWTDTCTQGFGLTVFPF	139		
QY 121	NKTHNAVCPGSPPAEP	137		
DB 140	NKTHNAVCPGSPPAEP	156		
RESULT 2				
US-08-911-423-4				
; Sequence 4, Application US/08911423				
; Patent No. 6111090				
; GENERAL INFORMATION:				
; APPLICANT: Gorman, Daniel M.				
; APPLICANT: Randall, Troy D.				
; APPLICANT: Zlotnik, Albert				
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED				
; TITLE OF INVENTION: REAGENTS				
; NUMBER OF SEQUENCES: 8				
; CORRESPONDENCE ADDRESS:				
; ADDRESSEE: DNAX Research Institute				
; STREET: 901 California Avenue				
; CITY: Palo Alto				
; STATE: California				
; COUNTRY: USA				
; ZIP: 94304-1104				
; COMPUTER READABLE FORM:				
; MEDIUM TYPE: Floppy disk				
; COMPUTER: IBM PC compatible				
; OPERATING SYSTEM: PC-DOS/MS-DOS				
; SOFTWARE: PatentIn Release #1.0, Version #1.30				
; CURRENT APPLICATION DATA:				
; APPLICATION NUMBER: US/08/911,423				
; FILING DATE: 14-AUG-1997				
; CLASSIFICATION: 536				
; PRIOR APPLICATION DATA:				
; APPLICATION NUMBER: US 60/023,419				
; FILING DATE: 16-AUG-1996				
; PRIOR APPLICATION DATA:				
; APPLICATION NUMBER: US 60/027,901				
; FILING DATE: 07-OCT-1996				
; ATTORNEY/AGENT INFORMATION:				
; NAME: Ching, Edwin P.				
; REGISTRATION NUMBER: 34,090				
; REFERENCE/DOCKET NUMBER: DX0612K				
; TELECOMMUNICATION INFORMATION:				
; TELEPHONE: 650-852-9196				
; TELEFAX: 650-496-1200				
; INFORMATION FOR SEQ ID NO: 4:				
; SEQUENCE CHARACTERISTICS:				
; LENGTH: 241 amino acids				
; TYPE: amino acid				
; TOPOLOGY: linear				
; MOLECULE TYPE: protein				
US-08-911-423-4				
Query Match	100.0%	Score 841;	DB 3;	Length 241;
Best Local Similarity	100.0%	Pred. No. 3.3e-66;		
Matches 137;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	QRPRTGGPCGGPGRLLLTGTGDARCCRVHVTTRCCRDYPCGEECCSEWDCMCVQPERHCGDPC	60		
DB 26	QRPRTGGPCGGPGRLLLTGTGDARCCRVHVTTRCCRDYPCGEECCSEWDCMCVQPERHCGDPC	85		

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Barnard, Brown & Michaels  
;; STREET: 306 East State Street, Suite 220  
;; CITY: Ithaca  
;; STATE: NY  
;; COUNTRY: USA  
;; ZIP: 14850  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US96/03965  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/122,796  
;; FILING DATE: 16-SEP-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/012,269  
;; FILING DATE: 01-FEB-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/922,996  
;; FILING DATE: 30-JUL-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/267,577  
;; FILING DATE: 07-NOV-1988  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Michaels, Christopher A  
;; REGISTRATION NUMBER: 34,390  
;; REFERENCE/DOCKET NUMBER: KWO5  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 607-273-1711  
;; TELEFAX: 607-273-2609  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 256 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
PCT-US96-03965-2

Query Match 19.7%; Score 140; DB 5; Length 256;  
Best Local Similarity 32.7%; Pred. No. 2.4e-05;  
Matches 36; Conservative 15; Mismatches 41; Indels 18; Gaps 7;  
Qy 9 CGPGLR-LLGTGTDARCCRVHTTRCCRDYPGEECCSEW---DCMGVQPFHCGDPCCTTC 64  
Db 47 CPPFTFSIGQPNICNRV---CAGYFRKFKCSSTHNAECEIE-GFHLGLGQCITRC 101  
Qy 65 RHHPCPGGVQSGQKFSFGQICDASGTFSGGH-EGHCKPWTDTCTQFG 113  
Db 102 -EKDCRPQQLTKG-----CKTCSLGTENDQNGTGVCRPWTNCSLDG 143

RESULT 15  
US-08-477-347-17  
; Sequence 17, Application US/08477347  
; Patent No. 6232446  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: BIGDA, Jacek  
; APPLICANT: BELETSKY, Igor  
; APPLICANT: METT, Igor  
; TITLE OF INVENTION: TNF LIGANDS  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W.  
; CITY: Washington  
; STATE: D.C.

;; COUNTRY: USA  
;; ZIP: 20004  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/477,347  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/115,685  
;; FILING DATE:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: IL 106271  
;; FILING DATE: 08-JUL-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Townsend, G. Kevin  
;; REGISTRATION NUMBER: 34,033  
;; REFERENCE/DOCKET NUMBER: WALLACH-10  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-628-5197  
;; TELEFAX: 202-737-3528  
;; TELEX: 248633  
;; INFORMATION FOR SEQ ID NO: 17:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 140 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-477-347-17

Query Match 19.5%; Score 139; DB 4; Length 140;  
Best Local Similarity 30.1%; Pred. No. 1.8e-05;  
Matches 34; Conservative 7; Mismatches 42; Indels 30; Gaps 5;  
Qy 31 RCRD-YPGEECCSEWD-----CMCVQPFHCG----DPC--CTTCRHH----- 67  
Db 12 KCCRCQPGHGMVSRCDHTRDVTCHPCEPGFYNEAVNYDTCKQCTQCNHRSSELKQNC 71  
Qy 68 -----PCPPGGVQSGQKFSFGQICDASGTFSGGHGCKPWTDTCTQFG 113  
Db 72 PTEDTVCCQCRPGTQPRQDSSHKLGVDVCPGPGHFGSPGNSQACKPWTNCTLSG 124

Search completed: September 4, 2001, 15:57:35  
Job time: 377 sec





; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-974-022-51

Query Match 19.8%; Score 141; DB 3; Length 205;

Best Local Similarity 29.3%; Pred. No. 1.6e-05; Mismatches 9; Indels 44; Gaps 8;

QY 1 QRPFGGPGGGRLLG--TGTDARCCRVHTT-----RCCRD-YPGEECCSEWD----- 46

Db 6 QQPT-----AFLLGLSLGVTVKLVKNCVDTYPSGHKCCRECPGHGMYSRCDHTRDTV 58

QY 47 CMCVQPEFHG----DPC--CTTCRHH-----PCPPGGVQSQGKFSF 83

Db 59 CHPCEGFYNEAVNYDTCKQCTQCNHRSSELKQNCPTPTDVCQCRPGTQPRDSSHKL 118

QY 84 GFQCIDCASTFSGGHEGCHKPWTCTQFG 113

Db 119 GVDVCPGPHFSPGSNQACKPWTNCTLSG 148

## RESULT 12

US-08-974-022-52

; Sequence 52, Application US/08974022

; Patent No. 6015938

; GENERAL INFORMATION:

; APPLICANT: Boyle, William J.

; APPLICANT: Lacey, David L.

; APPLICANT: Calzone, Frank J.

; APPLICANT: Chang, Ming-Shi

; TITLE OF INVENTION: OSTEOPROTEGERIN

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Inc.

; STREET: 1840 Behavilland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: USA

; ZIP: 91320-1789

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/974,022

; FILING DATE: 12-DEC-1995

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/577,788

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Winter, Robert B.

; REFERENCE/DOCKET NUMBER: A-378

; INFORMATION FOR SEQ ID NO: 52:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 191 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-974-022-52

Query Match 19.7%; Score 140; DB 3; Length 191;

Best Local Similarity 32.7%; Pred. No. 1.9e-05;

Mismatches 15; Mismatches 41; Indels 18; Gaps 7;

QY 9 CGPGRLL-LLGTTGTDARCCRVHTTCCRDYPGEECCSEW---DCMCVQPEFHGCDPCCTTC 64

Db 47 CPPSTFSSIGGQPNICRV-----CAGYFRFKFKCSSTHNAECECIE-GFHLGPQCTRC 101

QY 65 RHFCPPCGVQSQKFSFGQCIDCASGTFSGGH-EGHCKPWTCTQFG 113

Db 102 -EKDCRPGQELTKQG-----CKTCSLGTFTNDQNGTGVCRPWTNCSLDG 143

## RESULT 13

US-08-236-918A-6

; Sequence 6, Application US/08236918A

; Patent No. 5674704

; GENERAL INFORMATION:

; APPLICANT: Alderson, Mark R.

; APPLICANT: Goodwin, Raymond G.

; APPLICANT: Smith, Craig A.

; TITLE OF INVENTION: Cytokine Designated 4-LBB Ligand

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: Washington

; COUNTRY: US

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple 7.5.3

; SOFTWARE: Microsoft Word, Version #6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/236,918A

; FILING DATE: 06-May-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/060,843

; FILING DATE: 07-May-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Anderson, Kathryn A.

; REGISTRATION NUMBER: 32,172

; REFERENCE/DOCKET NUMBER: 2801-B

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 587-0430

; TELEFAX: (206) 233-0644

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 256 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-236-918A-6

Query Match 19.7%; Score 140; DB 1; Length 256;

Best Local Similarity 32.7%; Pred. No. 2.4e-05;

Mismatches 15; Mismatches 41; Indels 18; Gaps 7;

QY 9 CGPGRLL-LLGTTGTDARCCRVHTTCCRDYPGEECCSEW---DCMCVQPEFHGCDPCCTTC 64

Db 47 CPPSTFSSIGGQPNICRV-----CAGYFRFKFKCSSTHNAECECIE-GFHLGPQCTRC 101

QY 65 RHFCPPCGVQSQKFSFGQCIDCASGTFSGGH-EGHCKPWTCTQFG 113

Db 102 -EKDCRPGQELTKQG-----CKTCSLGTFTNDQNGTGVCRPWTNCSLDG 143

## RESULT 14

PCT-US96-03965-2

; Sequence 2, Application PC/TUS9603965

; GENERAL INFORMATION:

; APPLICANT: Kwon, Byoung Se

; APPLICANT: Kang, Chang-Yuil

; TITLE OF INVENTION: Monoclonal antibody against human

; TITLE OF INVENTION: receptor 4-1BB

; NUMBER OF SEQUENCES: 10

;; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED

;; TITLE OF INVENTION: REAGENTS

;; NUMBER OF SEQUENCES: 8

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: DNAX Research Institute

;; STREET: 901 California Avenue

;; CITY: Palo Alto

;; STATE: California

;; COUNTRY: USA

;; ZIP: 94304-1104

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/911,423

;; FILING DATE: 14-AUG-1997

;; CLASSIFICATION: 536

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 60/023,419

;; FILING DATE: 16-AUG-1996

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 60/027,901

;; FILING DATE: 07-OCT-1996

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Ching, Edwin P.

;; REGISTRATION NUMBER: 34,090

;; REFERENCE/DOCKET NUMBER: DX0612K

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 650-852-9196

;; TELEFAX: 650-496-1200

;; INFORMATION FOR SEQ ID NO: 7:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 232 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: peptide

;; US-08-911-423-7

Query Match 71.6%; Score 509; DB 3; Length 232;

Best Local Similarity 74.6%; Pred. No. 4.8e-37;

Matches 88; Conservative 5; Mismatches 17; Indels 8; Gaps 3;

QY 1 QRTGGGCGGPRLLLTGTDAACCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60

Db 20 QRTGGGCGGPRLLLTGTDAACCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 79

QY 61 CTTCTRHHPCCPGQVQSGKFSFGQCI----DCASGTFSGGH-BGHCKPWTDCQTQFG 113

Db 80 CTTCTRHHPCCPGQVQSGK---SWRCLWESTQARGSTRARGRHRCPARTCGVWG 134

RESULT 5

US-08-911-423-2

;; Sequence 2, Application US/08911423

;; Patent No. 611090

;; GENERAL INFORMATION:

;; APPLICANT: Gorman, Daniel M.

;; APPLICANT: Randall, Troy D.

;; APPLICANT: Zlotnik, Albert

;; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED

;; TITLE OF INVENTION: REAGENTS

;; NUMBER OF SEQUENCES: 8

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: DNAX Research Institute

;; STREET: 901 California Avenue

;; CITY: Palo Alto

;; STATE: California

;; COUNTRY: USA

;; ZIP: 94304-1104

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/911,423

;; FILING DATE: 14-AUG-1997

;; CLASSIFICATION: 536

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 60/023,419

;; FILING DATE: 16-AUG-1996

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 60/027,901

;; FILING DATE: 07-OCT-1996

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Ching, Edwin P.

;; REGISTRATION NUMBER: 34,090

;; REFERENCE/DOCKET NUMBER: DX0612K

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 650-852-9196

;; TELEFAX: 650-496-1200

;; INFORMATION FOR SEQ ID NO: 2:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 228 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; US-08-911-423-2

Query Match 52.5%; Score 373.5; DB 3; Length 228;

Best Local Similarity 53.7%; Pred. No. 2e-25;

Matches 58; Conservative 19; Mismatches 24; Indels 7; Gaps 1;

QY 7 PGCGPGRLLLTGTDAACCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRH 66

Db 27 PGCGPGRLLLTGTDAACCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRH 79

QY 67 HPCPPGQVQSGKFSFGQCIDCASGTFSGGHEGHCCKPWTDCQTQGF 114

Db 80 YPCQPGRVESQGDIVFGFRVCACAMGTFSGRDLWNTCSQFGF 127

RESULT 6

US-09-188-930-191

;; Sequence 191, Application US/09188930A

;; Patent No. 6150502

;; GENERAL INFORMATION:

;; APPLICANT: Watson, James D.

;; APPLICANT: Strachan, Lorna

;; APPLICANT: Sleeman, Matthew

;; APPLICANT: Onrust, Rene

;; APPLICANT: Murlison, James Greg

;; TITLE OF INVENTION: Compositions Isolated From Skin Cells

;; TITLE OF INVENTION: and Methods For Their Use

;; FILE REFERENCE: 11000.1011c1

;; CURRENT APPLICATION NUMBER: US/09/188,930A

;; CURRENT FILING DATE: 1998-11-09

;; NUMBER OF SEQ ID NOS: 348

;; SOFTWARE: FastSeq for Windows Version 3.0

;; SEQ ID NO 191

;; LENGTH: 89

;; TYPE: PRT

;; ORGANISM: mouse

;; US-09-188-930-191

Query Match 30.9%; Score 219.5; DB 4; Length 89;

Best Local Similarity 48.6%; Pred. No. 1.5e-12;

Matches 34; Conservative 13; Mismatches 16; Indels 7; Gaps 1;

QY 7 PGCGPGRLLLTGTDAACCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRH 66





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2001, 15:57:34 ; Search time 65.86 Seconds  
(without alignments)  
35.641 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_26\_139

Perfect score: 711

Sequence: 1 QPRTGGPGCGPGRLLGTCT.....FSGGHEGCKPWTDCQTQFGF 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued\_Patents\_AA.\*

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2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*

3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*

4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	711	100.0	228	3	US-08-911-423-6
2	711	100.0	241	3	US-08-911-423-4
3	711	100.0	311	3	US-08-911-423-8
4	509	71.6	232	3	US-08-911-423-7
5	373.5	52.5	228	3	US-08-911-423-2
6	219.5	30.9	89	4	US-08-188-930-191
7	147.5	20.7	206	1	US-08-097-827-7
8	147.5	20.7	206	1	US-08-494-574-7
9	147.5	20.7	438	1	US-08-097-827-11
10	147.5	20.7	438	1	US-08-494-574-11
11	141	19.8	205	3	US-08-974-022-51
12	140	19.7	191	3	US-08-974-022-52
13	140	19.7	256	1	US-08-236-918A-6
14	140	19.7	256	5	PCT-US96-03965-2
15	139	19.5	140	4	US-08-477-347-17
16	135.5	19.1	255	1	US-08-236-918A-8
17	135.5	19.1	255	2	US-08-816-605-9
18	135.5	19.1	255	5	PCT-US96-03965-8
19	129.5	18.2	139	2	US-08-219-237B-8
20	129.5	18.2	219	2	US-08-816-605-2
21	123.5	17.4	277	2	US-08-147-784-2
22	123.5	17.4	277	4	US-08-195-967-2
23	117	16.5	300	2	US-08-794-796-2
24	116.5	16.4	197	3	US-08-974-022-49
25	116.5	16.4	289	4	US-09-042-785A-11
26	108.5	15.3	276	4	US-09-041-886-27
27	108.5	15.3	277	4	US-09-042-785A-10

US-08-911-423-6  
; Sequence 6, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-6

ALIGNMENTS

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28 108 15.2 451 3 US-08-996-139-4 Sequence 4, Appl  
29 108 15.2 451 4 US-08-995-659-4 Sequence 4, Appl  
30 108 15.2 591 3 US-08-996-139-2 Sequence 2, Appl  
31 108 15.2 591 4 US-08-995-659-2 Sequence 2, Appl  
32 108 15.2 616 3 US-08-996-139-6 Sequence 6, Appl  
33 108 15.2 616 4 US-08-995-659-6 Sequence 6, Appl  
34 106 14.9 625 3 US-08-996-139-15 Sequence 15, Appl  
35 106 14.9 625 4 US-08-995-659-15 Sequence 15, Appl  
36 104.5 14.7 253 4 US-09-042-785A-4 Sequence 4, Appl  
37 104.5 14.7 605 4 US-09-042-785A-23 Sequence 23, Appl  
38 104.5 14.7 655 3 US-08-959-382-2 Sequence 2, Appl  
39 102 14.3 401 3 US-08-974-022-2 Sequence 2, Appl  
40 101 14.2 401 3 US-08-974-022-4 Sequence 4, Appl  
41 101 14.2 401 4 US-09-042-785A-13 Sequence 13, Appl  
42 99 13.9 401 3 US-08-974-022-6 Sequence 6, Appl  
43 99 13.9 401 4 US-09-042-785A-12 Sequence 12, Appl  
44 98.5 13.9 1345 2 US-08-977-767-3 Sequence 3, Appl  
45 98 13.8 573 4 US-09-042-785A-2 Sequence 2, Appl

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Query Match      100.0%; Score 711; DB 3; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.2e-54;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGPGCGPGRLLLTGTDAACCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
DB 20 QRTGGPGCGPGRLLLTGTDAACCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 79

QY 61 CTTCRHHPCPPGGVQSGQKFSFGFCIDCASGTFSGGHEGCHKPWTDCQTQGF 114
DB 80 CTTCRHHPCPPGGVQSGQKFSFGFCIDCASGTFSGGHEGCHKPWTDCQTQGF 133

RESULT 2
US-08-911-423-4
; Sequence 4, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-911-423-4

Query Match      100.0%; Score 711; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.3e-54;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGPGCGPGRLLLTGTDAACCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
DB 26 QRTGGPGCGPGRLLLTGTDAACCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 85

QY 61 CTTCRHHPCPPGGVQSGQKFSFGFCIDCASGTFSGGHEGCHKPWTDCQTQGF 114
DB 86 CTTCRHHPCPPGGVQSGQKFSFGFCIDCASGTFSGGHEGCHKPWTDCQTQGF 139
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RESULT 3
US-08-911-423-8
; Sequence 8, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 311 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-911-423-8

Query Match      100.0%; Score 711; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 2.8e-54;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRTGGPGCGPGRLLLTGTDAACCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 60
DB 20 QRTGGPGCGPGRLLLTGTDAACCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPC 79

QY 61 CTTCRHHPCPPGGVQSGQKFSFGFCIDCASGTFSGGHEGCHKPWTDCQTQGF 114
DB 80 CTTCRHHPCPPGGVQSGQKFSFGFCIDCASGTFSGGHEGCHKPWTDCQTQGF 133

RESULT 4
US-08-911-423-7
; Sequence 7, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
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QY 145 GNRTHNAVCVBPG-----SPPA---EP 16Z  
| | : | |  
Db 150 GTKERDVVCGPSADLSPGASSVTTPAPAREP 181

RESULT 15  
PCT-US96-03965-8  
; Sequence 8, Application PC/TUS9603965  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung Se  
; APPLICANT: Kang, Chang-Yuil  
; TITLE OF INVENTION: Monoclonal antibody against human  
; TITLE OF INVENTION: receptor 4-1BB  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Barnard, Brown & Michaels  
; STREET: 306 East State Street, Suite 220  
; CITY: Ithaca  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 14850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/03965  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/122,796  
; FILING DATE: 16-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/012,269  
; FILING DATE: 01-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/922,996  
; FILING DATE: 30-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/267,577  
; FILING DATE: 07-NOV-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michaels, Christopher A  
; REGISTRATION NUMBER: 34,390  
; REFERENCE/DOCKET NUMBER: KW05  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 607-273-1711  
; TELEFAX: 607-273-2609  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 255 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US96-03965-8

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Matches	47; Conservative	Mismatches	52; Indels	41; Gaps
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Db	48	CPPNSFSAGG--QRTCDI-----CROCKGVFRTRKECSSTNAECDC---TPGFHCLGA	97	
QY	85	CCTTCRIHHPCPGCGVQVOSQKGFSGFGQICDCASTFGSGHGHCCKPWTDCDTQGFGLVFP	144	
Db	98	GCSCW--EQDCKQGGBELTKKG-----CKDCCGFENDQKRIGICRPWTNCSLDGSKSVLVN	149	
QY	145	GKNTHNACVCPG-----SPPA---EP	162	
Db	150	GTKERDVVYCGSPADLSPGASSVTPPAPAREP	181	

Search completed: September 4, 2001, 15:57:37  
Job time: 379 sec



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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,784
; FILING DATE: 03-NOV-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 05490A-220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-147-784-2

Query Match 16.5%; Score 162; DB 2; Length 277;
Best Local Similarity 29.7%; Pred. No. 3.8e-07;
Matches 51; Conservative 11; Mismatches 92; Indels 18; Gaps 5;

QY 5 GAMGAFRALCGLALCALSLG-----QRPTEGCGPGRLLLGTTDARCRVHT 54
Db 4 GARRLGRPCAAALLLGLSTVTGLHCYVDTPSNDRCCHECR--PGNGMVSRCRSQN 61
QY 55 TRCCRDYPG--EECCSEWDCM-CVQPEFHCGD---PCCTTCRHHPCPPGQGVQSQGKFSF 108
Db 62 TVCRPCGPGFYNDVSSKPCPKCTWCNLSRSGSERKQLCTATQDTCRCRAGTQPLDSYKP 121
QY 109 GFQCIDCASGTFSGGHCGKPTWCTQFGFLTVPFNKTHNAVCPGSPPA 160
Db 122 GVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPA 173

RESULT 12
US-08-195-967-2
; Sequence 2, Application US/08195967
; Patent No. 6242566
; GENERAL INFORMATION:
; APPLICANT: Godfrey, Wayne
; APPLICANT: Engleman, Edgar G.
; TITLE OF INVENTION: LIGAND (ACT-4-L) TO A RECEPTOR ON THE SURFACE OF ACTIVATED
; TITLE OF INVENTION: CD4+ T-CELLS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,967
; FILING DATE: 10-FEB-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 05490A-230
; TELECOMMUNICATION INFORMATION:
```

```
;
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-195-967-2

Query Match 16.5%; Score 162; DB 4; Length 277;
Best Local Similarity 29.7%; Pred. No. 3.8e-07;
Matches 51; Conservative 11; Mismatches 92; Indels 18; Gaps 5;

QY 5 GAMGAFRALCGLALCALSLG-----QRPTEGCGPGRLLLGTTDARCRVHT 54
Db 4 GARRLGRPCAAALLLGLSTVTGLHCYVDTPSNDRCCHECR--PGNGMVSRCRSQN 61
QY 55 TRCCRDYPG--EECCSEWDCM-CVQPEFHCGD---PCCTTCRHHPCPPGQGVQSQGKFSF 108
Db 62 TVCRPCGPGFYNDVSSKPCPKCTWCNLSRSGSERKQLCTATQDTCRCRAGTQPLDSYKP 121
QY 109 GFQCIDCASGTFSGGHCGKPTWCTQFGFLTVPFNKTHNAVCPGSPPA 160
Db 122 GVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPA 173

RESULT 13
US-08-236-918A-8
; Sequence 8, Application US/08236918A
; Patent No. 5674704
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple 7.5.3
; SOFTWARE: Microsoft Word, Version #6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,918A
; FILING DATE: 06-May-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,843
; FILING DATE: 07-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2801-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-236-918A-8
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Db 121 HCKPMTDCTQGFELTVFGKTHNAVCPGSPPAEPLG 158

RESULT 4

US-08-911-423-7

; Sequence 7, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 232 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-7

Query Match 61.8%; Score 605; DB 3; Length 232;

Best Local Similarity 78.1%; Pred. No. 1.4e-45; Mismatches 17; Indels 8; Gaps 3;

Db 7 MGAFRALCGLLALCALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTRCCRDYPGECC 66

Db 1 MGAFRALCGLLALCALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTRCCRDYPGECC 60

Qy 67 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQVQSGKFSFGFQCI----DCASGTFSG 122

Db 61 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQVQSGKFSFGFQCI----SWRCLWESTQARGSTRAR 117

Qy 123 GH-EGHCKPMTDCTQFG 138

Db 118 GRARGHRCPARTCGVWG 134

RESULT 5

US-08-911-423-2

; Sequence 2, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-2

Query Match 52.1%; Score 510; DB 3; Length 228;

Best Local Similarity 54.1%; Pred. No. 2.3e-37; Mismatches 25; Conservative 25; Mismatches 40; Indels 8; Gaps 2;

Qy 7 MGAFRALCGLLALCALSLGQ-RPTGGPGCGPGRLLLTGTGDARCCRVHTRCCRDYPGEE 65

Db 1 MGAWAMLYGVSMCLVLDLQSPVVEEPGCGPGKVGSGNNTRCCSLVA-----PGKE 53

Qy 66 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQVQSGKFSFGFQCIDCASGTFSGGHE 125

Db 54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQVRVESQGDIVFGFRVCACAMGTFSGARD 113

Qy 126 GHCKPMTDCTQFGELTVFGKTHNAVCPGSPPAEPLG 164

Db 114 GHCLWNTNCSQFGELTVFGKTHNAVCPGSPPAEPLG 152

RESULT 6

US-09-188-930-191

; Sequence 191, Application US/09188930A

; Patent No. 6150502

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Strachan, Lorna

; APPLICANT: Sleeman, Matthew

; APPLICANT: Onrust, Rene





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2001, 15:57:36 ; Search time 65.86 Seconds  
(without alignments)  
51.273 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_1\_164

Perfect score: 979  
Sequence: 1 MAOHGAMGAFRALGCLALLC.....GNKTHNAVCPGSPAEPLG 164

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	979	100.0	241	3	US-08-911-423-4
2	947	96.7	228	3	US-08-911-423-6
3	947	96.7	311	3	US-08-911-423-8
4	605	61.8	232	3	US-08-911-423-7
5	510	52.1	228	3	US-08-911-423-2
6	255	26.0	89	4	US-09-188-930-191
7	166.5	17.0	206	1	US-08-097-827-7
8	166.5	17.0	206	1	US-08-494-574-7
9	166.5	17.0	438	1	US-08-097-827-11
10	166.5	17.0	438	1	US-08-494-574-11
11	162	16.5	277	2	US-08-147-784-2
12	162	16.5	277	4	US-08-195-967-2
13	160.5	16.4	255	1	US-08-236-918A-8
14	160.5	16.4	255	2	US-08-816-605-9
15	160.5	16.4	255	5	PCT-US96-03965-8
16	158.5	16.2	219	2	US-08-816-605-2
17	153	15.6	191	3	US-08-974-022-52
18	153	15.6	256	1	US-08-236-918A-6
19	153	15.6	256	5	PCT-US96-03965-2
20	153	15.6	300	2	US-08-794-796-2
21	151	15.4	205	3	US-08-974-022-51
22	149	15.2	140	4	US-08-477-347-17
23	141.5	14.5	401	3	US-08-974-022-2
24	139.5	14.2	139	2	US-08-219-237B-8
25	139.5	14.2	401	3	US-08-974-022-4
26	139.5	14.2	401	4	US-09-042-785A-13
27	138.5	14.1	451	3	US-08-996-139-4

28	138.5	14.1	451	4	US-08-995-659-4	Sequence 4, Appli
29	138.5	14.1	616	3	US-08-996-139-6	Sequence 6, Appli
30	138.5	14.1	616	4	US-08-995-659-6	Sequence 6, Appli
31	137	14.0	401	3	US-08-974-022-6	Sequence 6, Appli
32	137	14.0	401	4	US-09-042-785A-12	Sequence 12, Appli
33	135.5	13.8	197	3	US-08-974-022-49	Sequence 49, Appli
34	135.5	13.8	289	4	US-09-042-785A-11	Sequence 11, Appli
35	131	13.4	591	3	US-08-996-139-2	Sequence 2, Appli
36	131	13.4	591	4	US-08-995-659-2	Sequence 2, Appli
37	129.5	13.2	253	4	US-09-042-785A-4	Sequence 4, Appli
38	129.5	13.2	605	4	US-09-042-785A-23	Sequence 23, Appli
39	129.5	13.2	655	3	US-08-959-382-2	Sequence 2, Appli
40	123	12.6	625	3	US-08-996-139-15	Sequence 15, Appli
41	123	12.6	625	4	US-08-995-659-15	Sequence 15, Appli
42	121	12.4	197	2	US-08-505-606-1	Sequence 1, Appli
43	121	12.4	227	3	US-08-974-022-48	Sequence 48, Appli
44	121	12.4	461	4	US-09-042-785A-7	Sequence 7, Appli
45	119	12.2	461	6	5395760-2	Patent No. 5395760

ALIGNMENTS

RESULT 1  
US-08-911-423-4  
; Sequence 4, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-911-423-4

Query Match 100.0% Score 979; DB 3; Length 241;

Best Local Similarity 100.0%; Pred. No. 5.7e-78;  
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMAGFALCGALCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
DB 1 MAQHGMAGFALCGALCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60  
QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
DB 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTF 120  
QY 121 SGGHEGCHKPWTDCTQFGFLTVFPGNKTHNAVCPGSPPAEPLG 164  
DB 121 SGGHEGCHKPWTDCTQFGFLTVFPGNKTHNAVCPGSPPAEPLG 164

## RESULT 2

US-08-911-423-6  
; Sequence 6, Application US/08911423  
; Patent No. 611090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-6

Query Match 96.7%; Score 947; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 3.2e-75;  
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGAFRALCGALCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 66  
DB 1 MGAFRALCGALCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 60

QY 67 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTFSGGHEG 126  
DB 61 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTFSGGHEG 120  
QY 127 HCKPWTDCCTQFGFLTVFPGNKTHNAVCPGSPPAEPLG 164  
DB 121 HCKPWTDCCTQFGFLTVFPGNKTHNAVCPGSPPAEPLG 158

## RESULT 3

US-08-911-423-8  
; Sequence 8, Application US/08911423  
; Patent No. 611090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 311 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-8

Query Match 96.7%; Score 947; DB 3; Length 311;  
Best Local Similarity 100.0%; Pred. No. 4.3e-75;  
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGAFRALCGALCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 66  
DB 1 MGAFRALCGALCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEEC 60  
QY 67 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTFSGGHEG 126  
DB 61 CSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTFSGGHEG 120  
QY 127 HCKPWTDCCTQFGFLTVFPGNKTHNAVCPGSPPAEPLG 164







US-08-097-827-7

Query Match 21.4%; Score 158; DB 1; Length 206;  
Best Local Similarity 27.4%; Pred. No. 2.5e-07;  
Matches 40; Conservative 11; Mismatches 45; Indels 50; Gaps 6;

QY 5 CRVHT-----TRCCRD-YPG-----ECCSEWDCMCVQPEFHCGDPC----- 40

Db 27 CVKHTYPSGHKCCRECQPGHGMVNRCDHTRDTLC-----HPCETGYNEAVNYDTCK 78

QY 41 -CTTCRRHP-----CPPGQGVQSGKFSFGFCQIDCASGTFSGGHEGH 82

Db 79 QCTOCNHRSGSELKQNCPTQDVTVCRCRPGTQPRDQSGYKLGVDVCPGPPGHFSPGNNOA 138

QY 83 CKPWTDCQTFQGLTVFPGNKTHNAV 108

Db 139 CKPWTNCTLSGKQTRHPASDSLDAVC 164

RESULT 12

US-08-494-574-7

; Sequence 7, Application US/08494574

; Patent No. 5783665

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter

; APPLICANT: Goodwin, Ray

; APPLICANT: Fanslow, William

; APPLICANT: Gayle, Richard

; TITLE OF INVENTION: No. 5783665el Cytokine which is a Ligand for

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/494,574

; FILING DATE: 22-JUN-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/097,827

; FILING DATE: 23-JUL-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia A.

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2806

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-587-0730

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 206 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-494-574-7

Query Match 21.4%; Score 158; DB 1; Length 206;  
Best Local Similarity 27.4%; Pred. No. 2.5e-07;  
Matches 40; Conservative 11; Mismatches 45; Indels 50; Gaps 6;

QY 5 CRVHT-----TRCCRD-YPG-----ECCSEWDCMCVQPEFHCGDPC----- 40

Db 27 CVKHTYPSGHKCCRECQPGHGMVNRCDHTRDTLC-----HPCETGYNEAVNYDTCK 78

QY 41 -CTTCRRHP-----CPPGQGVQSGKFSFGFCQIDCASGTFSGGHEGH 82

Db 79 QCTOCNHRSGSELKQNCPTQDVTVCRCRPGTQPRDQSGYKLGVDVCPGPPGHFSPGNNOA 138

QY 83 CKPWTDCQTFQGLTVFPGNKTHNAV 108

Db 139 CAPWTNCTLSGKQTRHPASDSLDAVC 164

RESULT 13

US-08-097-827-11

; Sequence 11, Application US/08097827

; Patent No. 5457035

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter

; APPLICANT: Goodwin, Ray

; APPLICANT: Fanslow, William

; APPLICANT: Gayle, Richard

; TITLE OF INVENTION: No. 5457035el Cytokine which is a Ligand for

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/097,827

; FILING DATE:

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia A.

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2806

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-587-0730

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 438 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-097-827-11

Query Match 21.4%; Score 158; DB 1; Length 438;  
Best Local Similarity 27.4%; Pred. No. 5.1e-07;

Matches 40; Conservative 11; Mismatches 45; Indels 50; Gaps 6;

QY 5 CRVHT-----TRCCRD-YPG-----ECCSEWDCMCVQPEFHCGDPC----- 40

Db 27 CVKHTYPSGHKCCRECQPGHGMVNRCDHTRDTLC-----HPCETGYNEAVNYDTCK 78

QY 41 -CTTCRRHP-----CPPGQGVQSGKFSFGFCQIDCASGTFSGGHEGH 82

Db 79 QCTOCNHRSGSELKQNCPTQDVTVCRCRPGTQPRDQSGYKLGVDVCPGPPGHFSPGNNOA 138

QY 83 CKPWTDCQTFQGLTVFPGNKTHNAV 108

Db 139 CKPWTNCTLSGKQTRHPASDSLDAVC 164

RESULT 14

US-08-494-574-11

; Sequence 11, Application US/08494574

Qy	1	DARCCRVHTTCCRDPYGEBCCESDCMCVQPERFHCGDPCTTCRRHHPCPGQGVSQSGK
Db	40	DARCCRVHTTCCRDPYGEBCCESDCMCVQPERFHCGDPCTTCRRHHPCPGQGVSQSGK

Query Match	23.8%	Score 175.5	DB 4	Length 89
Best Local Similarity	56.0%	pred. No. 3.3e-09		
Matches : 28	Conservative	8	Mismatches 13	Indels 1
Gaps				1

Query Match 23.8%; Score 175.5; DB 4; Length 89;  
Best Local Similarity 56.0%; Pred. No. 3,3e-09;  
Matches\* 28; Conservative 8; Mismatches 13; Indels

OV 8 HTRCCRDY - GGECCSSEWDCMCVOPEHFGCDPCCTTCRRHHPDPGCGVO 56



Db 39 NNTRCCSLYAPGKEDCPKERCICVTPEYHCGDPQCKICKHYPCQPQGRVE 88

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RESULT 7
US-08-236-918A-8
; Sequence 8, Application US/08236918A
; Patent No. 5674704
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-LBB Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple 7.5.3
; SOFTWARE: Microsoft Word, Version #6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,918A
; FILING DATE: 06-May-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,843
; FILING DATE: 07-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2801-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-236-918A-8

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Query Match	21.6%	Score 159.5	DB 1	Length 255
Best Local Similarity	31.9%	Pred. No. 2.3e-07		
Matches	44	Conservative	12	Mismatches 43
			Indels	39
			Gaps	8

  

Qy	3	RCRHHVTRCRDYPG-----EECCS----	EWDCMCVQPEFHCGDPCTTCRHHPCPGQ	53
Db	60	RTCDI-----CRCKGVFRTRKECSSTNAECDC--	TPGFHCLGAGCSMC-EQDCKGQ	110
Qy	54	GVOSQGFSEFGQICASGTFSGHGEGHKPWTDC	TQGFELTFPGNKTHNACVCPG--	111
Db	111	ELTKKG-----CKDCCFGTFNDQKRGICRPWTNCSLDGKSVLVNGTKERDVCVCGPSPA	163	
Qy	112	-----SPPA---EP	117	
Db	164	DLSPGASSVTPPAPAREP	181	

RESULT 8  
US-08-816-605-9  
; Sequence 9, Application US/08816605  
; Patent No. 5874240  
; GENERAL INFORMATION:  
; APPLICANT: NI, Jian

APPLICANT: Yu, Guo-Liang  
 APPLICANT: Gentz, Reiner  
 TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: MD  
 COUNTRY: USA  
 ZIP: 20850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/816,605  
 FILING DATE: 13-MAR-1997  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brookes, A. Anders  
 REGISTRATION NUMBER: 36,373  
 REFERENCE/DOCKET NUMBER: PF254  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 301-309-8504  
 TELEFAX: 301-309-8512  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 255 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-816-605-9

Query Match	21.6%	Score 159.5	DB 2	Length 255
Best Local Similarity	31.9%	Pred. No. 2.3e-07		
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Qy 3	RCRRVHTTRCCRDYDG----	EECCS----	EWDCMCVQPEFHCGDPCCCTTCRHHPCPPQ	53
Db 60	RVCDI-----	CRQCKGVFTRKRECSSTNAECDC---	TPGFHCLGAGCSMC--EQDCKGQ	110
Qy 54	GVQSQCKFSFGQCIDCAGSTFSGGHEGHCKPWTBCTCGELTFVPFGKNTNNAVCVPG--			111
Db 111	ELTKG-----	CKDCCEGFNDQKRGICRPWTNCSLDGKSVLNGTKERDVVCGPSPA		163
Qy 112	-----	SPPA-----	EP	117
Db 164	DLSPGASSVTTPAPAREP			181

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RESULT          9
PCT-US96-03965-8
; Sequence 8, Application PC/TUS9603965
; GENERAL INFORMATION:
; APPLICANT: Kwon, Young Se
; APPLICANT: Kang, Chang-YuIl
; TITLE OF INVENTION: Monoclonal antibody against human
; TITLE OF INVENTION: receptor 4-1BB
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnard, Brown & Michaels
; STREET: 306 East State Street, Suite 220
; CITY: Ithaca
; STATE: NY
; COUNTRY: USA
; ZIP: 14850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2001, 15:57:35 ; Search time 65.86 Seconds  
(without alignments)  
37.204 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_46\_164

Perfect score: 737

Sequence: 1 DACCRRVHTTRCCRDYPGEE.....GNKTHNAVCPGSPAPPLG 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA.\*

- 1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	737	100.0	311	3	US-08-911-423-8
4	425.5	57.7	228	3	US-08-911-423-2
5	395	53.6	232	3	US-08-911-423-7
6	175.5	23.8	89	4	US-09-188-930-191
7	159.5	21.6	255	1	US-08-236-918A-8
8	159.5	21.6	255	2	US-08-816-605-9
9	158.5	21.5	219	2	US-08-816-605-2
10	158.5	21.5	219	2	US-08-816-605-2
11	158	21.4	206	1	US-08-097-827-7
12	158	21.4	206	1	US-08-494-574-7
13	158	21.4	438	1	US-08-097-827-11
14	158	21.4	438	1	US-08-494-574-11
15	150	20.4	277	2	US-08-147-784-2
16	150	20.4	277	4	US-08-195-967-2
17	149.5	20.3	191	3	US-08-974-022-52
18	149.5	20.3	256	1	US-08-236-918A-6
19	149.5	20.3	256	5	PCT-US96-03965-2
20	149	20.2	140	4	US-08-477-347-17
21	149	20.2	205	3	US-08-974-022-51
22	145	19.7	300	2	US-08-794-796-2
23	139.5	18.9	139	2	US-08-219-237B-8
24	137	18.6	401	3	US-08-974-022-6
25	137	18.6	401	4	US-09-042-785A-12
26	131	17.8	401	3	US-08-974-022-4
27	131	17.8	401	4	US-09-042-785A-13

28	131	17.8	451	3	US-08-996-139-4	Sequence 4, Appl
29	131	17.8	451	4	US-08-995-659-4	Sequence 4, Appl
30	131	17.8	591	3	US-08-996-139-2	Sequence 2, Appl
31	131	17.8	591	4	US-08-995-659-2	Sequence 2, Appl
32	131	17.8	616	3	US-08-996-139-6	Sequence 6, Appl
33	131	17.8	616	4	US-08-995-659-6	Sequence 6, Appl
34	130.5	17.7	401	3	US-08-974-022-2	Sequence 2, Appl
35	128	17.4	253	4	US-09-042-785A-4	Sequence 4, Appl
36	128	17.4	605	4	US-09-042-785A-23	Sequence 23, Appl
37	128	17.4	655	3	US-08-959-382-2	Sequence 2, Appl
38	123	16.7	197	3	US-08-974-022-49	Sequence 49, Appl
39	123	16.7	289	4	US-09-042-785A-11	Sequence 11, Appl
40	123	16.7	625	3	US-08-996-139-15	Sequence 15, Appl
41	123	16.7	625	4	US-08-995-659-15	Sequence 15, Appl
42	119	16.1	227	3	US-08-974-022-48	Sequence 48, Appl
43	119	16.1	461	4	US-09-042-785A-7	Sequence 7, Appl
44	119	16.1	474	2	US-08-650-000-4	Sequence 4, Appl
45	119	16.1	474	6	5395760-4	Patent No. 5395760

ALIGNMENTS

RESULT 1  
US-08-911-423-6  
; Sequence 6, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-6

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	Best Local Similarity	100.0%;	Pred. No. 1.2e-58;		
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Qy	61	FSFGQCIDCASGTF	SGSGHEGCHRPWT	DCTQFGFLTV	PPGNKTHNAVCPGSPPAEP
Db	106	FSFGQCIDCASGTF	SGSGHEGCHRPWT	DCTQFGFLTV	PPGNKTHNAVCPGSPPAEP

RESULT 4  
US-08-911-423-2  
; Sequence 2, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Albert  
; APPLICANT: Zlotnik, Albert

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2001, 15:57:35 ; Search time 65.86 Seconds  
(without alignments)  
38.142 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_33\_154

Perfect score: 753

Sequence: 1 GCGPRLLLGTGTARCCRV.....TQFCFLTVFPGNKTHNAVCV 122

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA.\*

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2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*

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4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	753	100.0	228	3	US-08-911-423-6
2	753	100.0	241	3	US-08-911-423-4
3	753	100.0	311	3	US-08-911-423-8
4	468	62.2	232	3	US-08-911-423-7
5	445.5	59.2	228	3	US-08-911-423-2
6	212.5	28.2	89	4	US-09-188-930-191
7	164	21.8	206	1	US-08-097-827-7
8	164	21.8	206	1	US-08-494-574-7
9	164	21.8	438	1	US-08-097-827-11
10	164	21.8	438	1	US-08-494-574-11
11	152.5	20.3	255	1	US-08-236-918A-8
12	152.5	20.3	255	2	US-08-816-605-9
13	152.5	20.3	255	5	PCT-US96-03965-8
14	149.5	19.9	205	3	US-08-974-022-51
15	149	19.8	140	4	US-08-477-347-17
16	149	19.8	191	3	US-08-974-022-52
17	149	19.8	256	1	US-08-236-918A-6
18	149	19.8	256	5	PCT-US96-03965-2
19	146.5	19.5	219	2	US-08-816-605-2
20	145.5	19.3	277	2	US-08-147-784-2
21	145.5	19.3	277	4	US-08-195-967-2
22	145	19.3	300	2	US-08-794-796-2
23	140	18.6	401	3	US-08-974-022-2
24	139.5	18.5	139	2	US-08-219-237B-8
25	139	18.5	401	3	US-08-974-022-4
26	139	18.5	401	4	US-09-042-785A-13
27	133	17.7	401	3	US-08-974-022-6

28 133 17.7 401 4 US-09-042-785A-12 Sequence 12, Appl  
29 128.5 17.1 253 4 US-09-042-785A-4 Sequence 4, Appl  
30 128.5 17.1 605 4 US-09-042-785A-23 Sequence 23, Appl  
31 128.5 17.1 655 3 US-08-959-382-2 Sequence 2, Appl  
32 127.5 16.9 197 3 US-08-974-022-49 Sequence 49, Appl  
33 127.5 16.9 289 4 US-09-042-785A-11 Sequence 11, Appl  
34 121 16.1 451 3 US-08-996-139-4 Sequence 4, Appl  
35 121 16.1 451 4 US-08-995-659-4 Sequence 4, Appl  
36 121 16.1 591 3 US-08-996-139-2 Sequence 2, Appl  
37 121 16.1 591 4 US-08-995-659-2 Sequence 2, Appl  
38 121 16.1 616 3 US-08-996-139-6 Sequence 6, Appl  
39 121 16.1 616 4 US-08-995-659-6 Sequence 6, Appl  
40 121 16.1 625 3 US-08-996-139-15 Sequence 15, Appl  
41 121 16.1 625 4 US-08-995-659-15 Sequence 15, Appl  
42 117 15.5 573 4 US-09-042-785A-2 Sequence 2, Appl  
43 114.5 15.2 276 4 US-09-041-886-27 Sequence 27, Appl  
44 114.5 15.2 277 4 US-09-042-785A-10 Sequence 10, Appl  
45 113 15.0 227 3 US-08-974-022-48 Sequence 48, Appl

#### ALIGNMENTS

RESULT 1  
US-08-911-423-6  
; Sequence 6, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-6

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QY	121	CV 122	
Db	153	CV 154	
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; Sequence 8, Application US/08911423			
; Patent No. 6111090			
; GENERAL INFORMATION:			
; APPLICANT: Gorman, Daniel M.			
; APPLICANT: Randall, Troy D.			
; APPLICANT: Ziocnik, Albert			
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED			
; NUMBER OF SEQUENCES: 8			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: DNAX Research Institute			
; STREET: 901 California Avenue			
; CITY: Palo Alto			
; STATE: California			
; COUNTRY: USA			
; ZIP: 94304-1104			
; COMPUTER READABLE FORM:			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/911,423			
; FILING DATE: 14-AUG-1997			
; CLASSIFICATION: 536			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 60/023,419			
; FILING DATE: 16-AUG-1996			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 60/027,901			
; FILING DATE: 07-OCT-1996			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Ching, Edwin P.			
; REGISTRATION NUMBER: 34,090			
; REFERENCE/DOCKET NUMBER: DX0612K			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 650-852-9196			
; TELEFAX: 650-496-1200			
; INFORMATION FOR SEQ ID NO: 8:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 311 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: peptide			
US-08-911-423-8			
Query Match         100.0%; Score 753; DB 3; Length 311;			
Best Local Similarity 100.0%; Pred. No. 7.9e-60;			
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps			
QY	1	GCGPGRLLLTGTDAACCRVHTTRCCRDYPGBECCSEWDCMCVPFFHCGDPCCCTTCRHH	60
Db	27	GCGPGRLLLTGTDAACCRVHTTRCCRDYPGBECCSEWDCMCVPFFHCGDPCCCTTCRHH	86
QY	61	PCPPGGVQSOGKFSFGFCIDCASGTFSGGHGCHKPMTDCTQGFLTVFPGNKTNNAV	120
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QY	121	CV 122	

SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-03965-8

Query Match 20.3%; Score 152.5; DB 5; Length 255;  
Best Local Similarity 31.8%; Pred. No. 9.6e-07;  
Matches 41; Conservative 11; Mismatches 50; Indels 27; Gaps 7;

QY 2 CGPGRLLLTGTGDARCCRVHTTRCCRDYPG-----ECCS-----EWDCCMCVQPEFHCGDP 52  
DB 48 CPPNSFSAGG--QRTCDI-----CROKGVFTRKECSSTSNACDC---TPGFHCLGA 97  
QY 53 CTTTCRRHPCPGQVQSGKFSFGQCIDCASGTRSGGHEGCKPWTCTQFGELTVFP 112  
DB 98 GCSMC-EQDCKQGOELTKG-----CKDCGFTFNDQKRGICRPWTNCSLDGKSLVN 149  
QY 113 GNKTHNAV 121  
DB 150 GYKRDVVC 158

RESULT 14  
US-08-974-022-51  
Sequence 51, Application US/08974022  
Patent No. 6015938  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Beverlyland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,022  
FILING DATE: 12-DEC-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 205 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-974-022-51

Query Match 19.9%; Score 149.5; DB 3; Length 205;  
Best Local Similarity 28.9%; Pred. No. 1.5e-06;  
Matches 44; Conservative 11; Mismatches 60; Indels 37; Gaps 7;  
QY 7 LLLG--TGTDAACRRVHTT-----RCCRD-YPGECCSEWD-----CMCVQPEFHCG-- 50

DB 12 LLLGLSLGVTVKLNCVADTYPGSHKCCRCQPGHGMVSRCDHTRDTVCHPCPEPGFYNEAV 71  
QY 51 --DPC--CTTCRRH-----PCPPGQVQSGKFSFGQCIDCASGTF 89  
DB 72 NYDTCKQCTQCNHRSGSELKQNCPTFTEDTVCCQRPQTQPRODSSHKLGVDVCPGPHFS 131  
QY 90 GGHEGCKPWTCTQFGELTVFPGNKTHNAV 121  
DB 132 PGSNQACKPWTNCTLSGKQIRHPASNSLDTVC 163  
RESULT 15  
US-08-477-347-17  
Sequence 17, Application US/08477347  
Patent No. 6232446  
GENERAL INFORMATION:  
APPLICANT: WALLACH, David  
APPLICANT: BIGDA, Jacek  
APPLICANT: BELETSKY, Igor  
APPLICANT: METT, Igor  
TITLE OF INVENTION: TNF LIGANDS  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,347  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/115,685  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 106271  
FILING DATE: 08-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, G. Kevin  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: WALLACH-10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 140 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-477-347-17

Query Match 19.8%; Score 149; DB 4; Length 140;  
Best Local Similarity 28.9%; Pred. No. 1.1e-06;  
Matches 37; Conservative 10; Mismatches 51; Indels 30; Gaps 5;  
QY 24 RCCRD-YPGECCSEWD-----CMCVQPEFHCG-----DPC--CTTCRRH----- 60  
DB 12 KCCRCQPGHGMVSRCDHTRDTVCHPCPEPGFYNEAVNYDTCKQCTQCNHRSGSELKQNC 71  
QY 61 -----PCPPGQVQSGKFSFGQCIDCASGTFSGGHEGCKPWTCTQFGELTVFP 113

Db 72 PTEDTVCCRRGTQPRODSSHKLGVDCVPCPPGHFSPGSNOACKPWTNCTLSGKQIRHPA 131

Qy 114 NKTHNAVC 121

Db 132 SNSLDTV 139

Search completed: September 4, 2001, 15:57:35  
Job time: 377 sec

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RESULT 9
US-08-097-827-11
; Sequence 11, Application US/08097827
; Patent No. 5457035
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for
; TITLE OF INVENTION: OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-097-827-11

Query Match 21.8%; Score 164; DB 1; Length 438;
Best Local Similarity 29.2%; Pred. No. 1.5e-07;
Matches 47; Conservative 11; Mismatches 49; Indels 54; Gaps 8;

Qy 7 LLLG--TGTAR--CCRVHT---TRCCRD--YPG---BECCSEWDCMCVQPEFHCGDPC 53
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Db 12 LLLGLTGVTAARRLNCVKHTYPSGHKCCRCQPGHGMVNRCDHTRDTLC-----HPC 63

Qy 54 -----CTTCRHHP-----CPPGGVQSQGKFSFGQC 80
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Db 64 ETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCPTQDTVCRCPGTQPRQDSGYKLGVC 123

Qy 81 IDCASSTSGGHEGCHKPWTCTQFGFLTVFPNKNTHNAV 121
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Db 124 VPCPPGHFSPGNNAQKPNWTNCTLSGKQTRHPASDSLDAVC 164

RESULT 10
US-08-494-574-11
; Sequence 11, Application US/08494574
; Patent No. 5783665
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand for
; TITLE OF INVENTION: OX40
; NUMBER OF SEQUENCES: 13
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,574
; FILING DATE: 22-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE: 23-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-494-574-11

Query Match 21.8%; Score 164; DB 1; Length 438;
Best Local Similarity 29.2%; Pred. No. 1.5e-07;
Matches 47; Conservative 11; Mismatches 49; Indels 54; Gaps 8;

Qy 7 LLLG--TGTAR--CCRVHT---TRCCRD--YPG---BECCSEWDCMCVQPEFHCGDPC 53
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 12 LLLGLTGVTAARRLNCVKHTYPSGHKCCRCQPGHGMVNRCDHTRDTLC-----HPC 63

Qy 54 -----CTTCRHHP-----CPPGGVQSQGKFSFGQC 80
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Db 64 ETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCPTQDTVCRCPGTQPRQDSGYKLGVC 123

Qy 81 IDCASSTSGGHEGCHKPWTCTQFGFLTVFPNKNTHNAV 121
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Db 124 VPCPPGHFSPGNNAQKPNWTNCTLSGKQTRHPASDSLDAVC 164

RESULT 11
US-08-236-918A-8
; Sequence 8, Application US/08236918A
; Patent No. 5674704
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple 7.5.3
; SOFTWARE: Microsoft Word, Version #6.0.1
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;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/236,918A  
;; FILING DATE: 06-May-1994  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/060,843  
;; FILING DATE: 07-May-1993  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Anderson, Kathryn A.  
;; REGISTRATION NUMBER: 32,172  
;; REFERENCE/DOCKET NUMBER: 2801-B  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206) 587-0430  
;; TELEFAX: (206) 233-0644  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 255 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-236-918A-8

Query Match 20.3%; Score 152.5; DB 1; Length 255;  
Best Local Similarity 31.8%; Pred. No. 9.6e-07;  
Matches 41; Conservative 11; Mismatches 50; Indels 27; Gaps 7;

QY 2 CGPGRLLLGTTDARCCRVHTTRCCRDYPG-----EECCS----EWDCCMCVQPEFHCGDP 52  
DB 48 CPNPSFSSAGG--QRTCDI-----CROCKGVTRTRKESSTNSAECDC---TPGFHCLGA 97  
QY 53 CTTCTRHHPGPPGQGVQSGKFSFGFCIDCASGTFSGHGHGCKPWTDCDTQGFGLTVFP 112  
DB 98 GCSMC-EQDCKQOGLTKKG-----CKDCCFGTFNDQKRGICRPWTNCSLDGKSLV 149  
QY 113 GNKTHNAV 121  
DB 150 GTRKRDVVC 158

RESULT 12  
US-08-816-605-9  
; Sequence 9, Application US/08816605  
; Patent No. 5874240  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Gentz, Reiner  
; TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/816,605  
; FILING DATE: 13-MAR-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF254  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504

;; TELEFAX: 301-309-8512  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 255 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-816-605-9  
  
Query Match 20.3%; Score 152.5; DB 2; Length 255;  
Best Local Similarity 31.8%; Pred. No. 9.6e-07;  
Matches 41; Conservative 11; Mismatches 50; Indels 27; Gaps 7;  
  
QY 2 CGPGRLLLGTTDARCCRVHTTRCCRDYPG-----EECCS----EWDCCMCVQPEFHCGDP 52  
DB 48 CPNPSFSSAGG--QRTCDI-----CROCKGVTRTRKESSTNSAECDC---TPGFHCLGA 97  
QY 53 CTTCTRHHPGPPGQGVQSGKFSFGFCIDCASGTFSGHGHGCKPWTDCDTQGFGLTVFP 112  
DB 98 GCSMC-EQDCKQOGLTKKG-----CKDCCFGTFNDQKRGICRPWTNCSLDGKSLV 149  
QY 113 GNKTHNAV 121  
DB 150 GTRKRDVVC 158  
  
RESULT 13  
PCT-US96-03965-8  
; Sequence 8, Application PC/TUS9603965  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung Se  
; APPLICANT: Kang, Chang-Yul  
; TITLE OF INVENTION: Monoclonal antibody against human  
; TITLE OF INVENTION: receptor 4-IBB  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Barnard, Brown & Michaels  
; STREET: 306 East State Street, Suite 220  
; CITY: Ithaca  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 14850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/03965  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/122,796  
; FILING DATE: 16-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/012,269  
; FILING DATE: 01-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/922,996  
; FILING DATE: 30-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/267,577  
; FILING DATE: 07-NOV-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michaels, Christopher A  
; REGISTRATION NUMBER: 34,390  
; REFERENCE/DOCKET NUMBER: KWO5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 607-273-1711  
; TELEFAX: 607-273-2609  
; INFORMATION FOR SEQ ID NO: 8:





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Query Match      100.0%; Score 255; DB 3; Length 228;
Best Local Similarity 100.0%; Pred. No. 3.6e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTGTCRCRVTTCRCRDYPCGECCEWDCM 41
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Db 27 GCGPGRLLLTGTGTCRCRVTTCRCRDYPCGECCEWDCM 67

RESULT 2
US-08-911-423-7
; Sequence 7, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-496-1200
; TELEFAX: 650-852-9196
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-911-423-7

Query Match      100.0%; Score 255; DB 3; Length 232;
Best Local Similarity 100.0%; Pred. No. 3.6e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTGTCRCRVTTCRCRDYPCGECCEWDCM 41
    |||||
Db 27 GCGPGRLLLTGTGTCRCRVTTCRCRDYPCGECCEWDCM 67

RESULT 3
US-08-911-423-4
; Sequence 4, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
US-08-911-423-4

Query Match      100.0%; Score 255; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 3.8e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGPGRLLLTGTGTCRCRVTTCRCRDYPCGECCEWDCM 41
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Db 33 GCGPGRLLLTGTGTCRCRVTTCRCRDYPCGECCEWDCM 73

RESULT 4
US-08-911-423-8
; Sequence 8, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
US-08-911-423-8
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:57:35 ; Search time 65.86 Seconds  
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12.818 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_33\_73

Perfect score: 255

Sequence: 1 GCGFGRLLLTGTGDARCRV.....TTCCRDYVGECCSEWDCM 41

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Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA:\*

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- 2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*
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- 6: /cgn2\_6/ptodata/2/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	255	100.0	232	3	US-08-911-423-7
3	255	100.0	241	3	US-08-911-423-4
4	255	100.0	311	3	US-08-911-423-8
5	87.5	34.3	89	4	US-09-188-930-191
6	87.5	34.3	228	3	US-08-911-423-2
7	64.5	25.3	788	2	US-08-918-914-4
8	64	25.1	109	2	US-08-527-044-2
9	64	25.1	109	3	US-09-013-780-2
10	64	25.1	443	4	US-08-821-994-65
11	64	25.1	801	1	US-07-906-349A-6
12	61.5	24.1	434	2	US-08-815-718-3
13	61.5	24.1	559	2	US-08-884-072-6
14	58.5	22.9	430	3	US-08-997-897-2
15	58.5	22.9	430	4	US-09-156-836B-2
16	56.5	22.2	263	1	US-07-927-071-2
17	56.5	22.2	1063	1	US-08-093-453B-3
18	56.5	22.2	1063	1	US-08-127-499A-8
19	55.5	22.2	1063	1	US-08-482-847-8
20	55.5	21.8	94	3	US-08-851-843A-215
21	55.5	21.8	94	4	US-08-974-549A-334
22	55.5	21.8	323	4	US-08-878-474-7
23	55.5	21.8	4544	1	US-08-469-486-52
24	55.5	21.8	4544	2	US-08-469-658-52
25	55	21.6	143	4	US-08-990-823-112
26	55	21.6	861	1	US-08-346-455B-67
27	55	21.6	861	3	US-08-977-221-67

28	55	21.6	861	5	PCT-US95-06613-67	Sequence 67, Appl
29	55	21.6	915	1	US-08-346-455B-69	Sequence 69, Appl
30	55	21.6	915	3	US-08-977-221-69	Sequence 69, Appl
31	55	21.6	915	5	PCT-US95-06613-69	Sequence 69, Appl
32	55	21.6	979	1	US-08-346-455B-38	Sequence 38, Appl
33	55	21.6	979	3	US-08-977-221-38	Sequence 38, Appl
34	55	21.6	979	5	PCT-US95-06613-38	Sequence 38, Appl
35	54.5	21.4	1345	2	US-08-977-767-3	Sequence 3, Appl
36	54	21.2	359	2	US-08-586-165-4	Sequence 4, Appl
37	52.5	20.6	87	2	US-08-465-380-44	Sequence 44, Appl
38	52.5	20.6	87	2	US-08-486-397-44	Sequence 44, Appl
39	52.5	20.6	87	2	US-08-486-399-44	Sequence 44, Appl
40	52.5	20.6	87	2	US-08-461-965-44	Sequence 44, Appl
41	52.5	20.6	87	2	US-08-634-641-44	Sequence 44, Appl
42	52.5	20.6	87	3	US-09-249-471-44	Sequence 44, Appl
43	52.5	20.6	87	3	US-09-249-472-44	Sequence 44, Appl
44	52.5	20.6	87	3	US-09-249-451-44	Sequence 44, Appl
45	52.5	20.6	87	3	US-08-809-455-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1  
US-08-911-423-6  
; Sequence 6, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911.423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Chang, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-6

RESULT 10  
US-08-821-994-65

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RESULT      7
US-08-918-914-4
; Sequence 4, Application US/08918914
; Patent No. 5876963
;
; GENERAL INFORMATION:
; APPLICANT: Mitchell, Peter
; APPLICANT: Hutchinson, Nancy
; APPLICANT: Lawton, Michael
; APPLICANT: Magna, Holly
; APPLICANT: Yocum, Sue
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN NUCLE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals
; STREET: 3174 Porter Dr.

```

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; TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,072
; FILING DATE: Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0333 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 559 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 496120
; US-08-884-072-6

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Query Match      24.18; Score 61.5; DB 2; Length 559;
Best Local Similarity 37.88; Pred. No. 12;
Matches 14; Conservative 3; Mismatches 19; Indels 1; Gaps 1;

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QY 2 CGPGRLLLTGTDAKRCRVTTCRCR-DYGECCSE 37
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Db 445 CGSGRVLKHKQIPGLIQTNRCCCLPYPEQACCGE 481

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RESULT 14
US-08-997-897-2
; Sequence 2, Application US/08997897C
; Patent No. 6114514
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, RANJANA
; APPLICANT: KUMAR, DEEPAK
; APPLICANT: SRIVASTAVA, BRAHM SHANKER
; TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS SPECIFIC DNA FRAGMENT
; FILE REFERENCE: u011469-7
; CURRENT APPLICATION NUMBER: US/08/997,897C
; CURRENT FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (4)
; FEATURE:
; NAME/KEY: UNSURE

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; LOCATION: (6)
; FEATURE: UNSURE
; NAME/KEY: (20)
; LOCATION: (20)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (29)
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; NAME/KEY: UNSURE
; LOCATION: (54)
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; LOCATION: (99)
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; NAME/KEY: UNSURE
; LOCATION: (356)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (366)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (410)

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; Sequence 65, Application US/08821994A  
; Patent No. 6228643  
; GENERAL INFORMATION:  
; APPLICANT: Greenland, Andrew J  
; APPLICANT: Thomas, Didier RP  
; APPLICANT: Jepson, Ian  
; TITLE OF INVENTION: Promoters  
; FILE REFERENCE: PPD 50108  
; CURRENT APPLICATION NUMBER: US/08/821,994A  
; CURRENT FILING DATE: 1997-03-22  
; EARLIER APPLICATION NUMBER: PCT/GB97/00729  
; EARLIER FILING DATE: 1997-03-18  
; EARLIER APPLICATION NUMBER: GB 9606062.9  
; EARLIER FILING DATE: 1996-03-22  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 65  
; LENGTH: 443  
; TYPE: PRT  
; ORGANISM: Brassica napus  
US-08-821-994-65

Query Match 25.1%; Score 64; DB 4; Length 443;  
Best Local Similarity 35.3%; Pred. No. 5.2;  
Matches 12; Conservative 4; Mismatches 16; Indels 2; Gaps 1;  
QY 2 CGPGRLLGTGTDARCCRVHTTRCCRDYPGECC 35  
Db 368 CCCARNLFLCFSWKCELESVAVCKD--GRHCC 399

RESULT 11  
US-07-906-349A-6  
; Sequence 6, Application US/07906349A  
; Patent No. 5434064  
; GENERAL INFORMATION:  
; APPLICANT: Schlessinger, Joseph  
; APPLICANT: Skolnik, Edward Y.  
; APPLICANT: Margolis, Benjamin L.  
; TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR  
; TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINASES AND  
; TITLE OF INVENTION: TARGET PROTEINS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/906,349A  
; FILING DATE: 30-JUN-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/643,237  
; FILING DATE: 18-JAN-1991  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 801 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-07-906-349A-6

Query Match 25.1%; Score 64; DB 1; Length 801;  
Best Local Similarity 37.1%; Pred. No. 8.8;  
Matches 13; Conservative 1; Mismatches 21; Indels 0; Gaps 0;  
QY 2 CGPGRLLGTGTDARCCRVHTTRCCRDYPGECCS 36  
Db 326 CACGTCCTGTGTGGCGCGGTACCCCTGTGACCT 360

RESULT 12  
US-08-815-718-3  
; Sequence 3, Application US/08815718  
; Patent No. 5981220  
; GENERAL INFORMATION:  
; APPLICANT: NI, JIAN  
; APPLICANT: FENG, PING  
; APPLICANT: DILLON, PATRICK  
; APPLICANT: GENTZ, REINER  
; TITLE OF INVENTION: EPIDERMAL DIFFERENTIATION FACTOR  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
; ADDRESSEE: STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NJ  
; COUNTRY: US  
; ZIP: 07069  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/815,718  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME:  
; REGISTRATION NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (201) 994-1700  
; TELEFAX: (201) 994-1744  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 434 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-815-718-3

Query Match 24.1%; Score 61.5; DB 2; Length 434;  
Best Local Similarity 37.8%; Pred. No. 9.6;  
Matches 14; Conservative 3; Mismatches 19; Indels 1; Gaps 1;  
QY 2 CGPGRLLGTGTDARCCRVHTTRCCRDYPGECCSE 37  
Db 320 CGSGRVLKHKQIPGLIQNTVRCCLPYPQACCGE 356

RESULT 13  
US-08-884-072-6  
; Sequence 6, Application US/08884072  
; Patent No. 5872234  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.



FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (421)  
US-08-997-897-2

Query Match 22.9%; Score 58.5; DB 3; Length 430;  
Best Local Similarity 40.0%; Pred. No. 20;  
Matches 10; Conservative 1; Mismatches 7; Indels 7; Gaps 1;

Qy 17 CCRVHTTRCCRDYPGECCEWDCM 41  
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Db 200 CCRWTRCC-----CCRCWQSL 217

RESULT 15  
US-09-156-836B-2  
Sequence 2, Application US/09156836B  
Patent No. 6242585  
GENERAL INFORMATION:  
APPLICANT: Srivastava, Ranjana  
APPLICANT: Kumar, Deepak  
APPLICANT: Srivastava, Brahm Shanker  
TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS SPECIFIC DNA FRAGMENT  
FILE REFERENCE: U 011876-4  
CURRENT APPLICATION NUMBER: US/09/156,836B  
CURRENT FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 08/997,897  
PRIOR FILING DATE: 1997-12-24  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 430  
TYPE: PRT  
ORGANISM: Mycobacterium tuberculosis  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (4)  
OTHER INFORMATION: amino acid has not been identified  
NAME/KEY: UNSURE  
LOCATION: (6)  
OTHER INFORMATION: amino acid has not been identified  
NAME/KEY: UNSURE  
LOCATION: (20)  
OTHER INFORMATION: amino acid has not been identified  
NAME/KEY: UNSURE  
LOCATION: (29)  
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LOCATION: (159)  
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NAME/KEY: UNSURE  
LOCATION: (366)  
OTHER INFORMATION: amino acid has not been identified  
NAME/KEY: UNSURE  
LOCATION: (410)  
OTHER INFORMATION: amino acid has not been identified  
NAME/KEY: UNSURE  
LOCATION: (421)  
OTHER INFORMATION: amino acid has not been identified  
US-09-156-836B-2

Query Match 22.9%; Score 58.5; DB 4; Length 430;  
Best Local Similarity 40.0%; Pred. No. 20;  
Matches 10; Conservative 1; Mismatches 7; Indels 7; Gaps 1;

Qy 17 CCRVHTTRCCRDYPGECCEWDCM 41  
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Db 200 CCRWTRCC-----CCRCWQSL 217

Search completed: September 4, 2001, 15:57:36  
Job time: 378 sec

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Query Match      100.0%; Score 252; DB 3; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.4e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCTTCRRHPCPPGGVQSQGKFSFGFCI 40
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Db 68 CVQPEFHCGDPCCTTCRRHPCPPGGVQSQGKFSFGFCI 107

RESULT 2
US-08-911-423-4
; Sequence 4, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; NUMBER OF INVENTION: REAGENTS
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0., Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-496-1200
; TELEFAX: 650-852-9196
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-911-423-4

Query Match      100.0%; Score 252; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.5e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCTTCRRHPCPPGGVQSQGKFSFGFCI 40
   |||||||
Db 74 CVQPEFHCGDPCCTTCRRHPCPPGGVQSQGKFSFGFCI 113

RESULT 3
US-08-911-423-8
; Sequence 8, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
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; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; NUMBER OF INVENTION: REAGENTS
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 311 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-911-423-8

Query Match      100.0%; Score 252; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 3.1e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCTTCRRHPCPPGGVQSQGKFSFGFCI 40
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Db 68 CVQPEFHCGDPCCTTCRRHPCPPGGVQSQGKFSFGFCI 107

RESULT 4
US-08-911-423-7
; Sequence 7, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; NUMBER OF INVENTION: REAGENTS
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:57:36 ; Search time 65.86 Seconds  
(without alignments)  
12.506 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_74\_113

Perfect score: 252

Sequence: 1 CVQEFHGGDPCCTCRHPCPGGVQSGKSFSGFCI 40

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

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2: /cgn2\_6/ptodata/2/laa/5B\_COMB.pep.\*

3: /cgn2\_6/ptodata/2/laa/6A\_COMB.pep.\*

4: /cgn2\_6/ptodata/2/laa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/2/laa/PCTUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/2/laa/backfilesi.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	252	100.0	228	3 US-08-911-423-6	Sequence 6, Appli
2	252	100.0	241	3 US-08-911-423-4	Sequence 4, Appli
3	252	100.0	311	3 US-08-911-423-8	Sequence 8, Appli
4	207.5	82.3	232	3 US-08-911-423-7	Sequence 7, Appli
5	168	66.7	228	3 US-08-911-423-2	Sequence 2, Appli
6	125	49.6	89	4 US-09-188-930-191	Sequence 191, App
7	67	26.6	191	3 US-08-974-022-52	Sequence 52, Appl
8	67	26.6	256	1 US-08-236-918A-6	Sequence 6, Appli
9	67	26.6	256	5 PCT-US96-03965-2	Sequence 2, Appli
10	63	25.0	283	5 PCT-US96-12374-2	Sequence 2, Appli
11	60	23.8	644	1 US-08-336-708A-9	Sequence 9, Appli
12	60	23.8	1210	2 US-08-484-438-7	Sequence 7, Appli
13	60	23.8	1210	2 US-08-475-035-4	Sequence 4, Appli
14	59.5	23.6	1104	2 US-08-327-832-5	Sequence 5, Appli
15	59.5	23.6	1104	2 US-08-828-584-5	Sequence 5, Appli
16	58	23.0	140	4 US-08-477-347-17	Sequence 17, Appl
17	58	23.0	205	3 US-08-974-022-51	Sequence 51, Appl
18	57.5	22.8	197	3 US-08-974-022-49	Sequence 49, Appl
19	57.5	22.8	289	4 US-09-042-785A-11	Sequence 11, Appl
20	57.5	22.8	961	5 PCT-US93-11725-4	Sequence 4, Appli
21	56.5	22.4	41	1 US-08-050-319B-39	Sequence 39, Appl
22	56.5	22.4	41	2 US-08-465-982-39	Sequence 39, Appl
23	56.5	22.4	162	2 US-08-219-237B-7	Sequence 7, Appli
24	56.5	22.4	162	4 US-08-477-347-16	Sequence 16, Appl
25	56.5	22.4	276	4 US-09-041-886-27	Sequence 27, Appl
26	56.5	22.4	277	4 US-09-042-785A-10	Sequence 10, Appl
27	55.5	22.0	277	2 US-08-147-784-2	Sequence 2, Appli

28 55.5 22.0 277 4 US-08-195-967-2 Sequence 2, Appli  
29 55.5 22.0 426 4 US-09-082-092-6 Sequence 6, Appli  
30 55 21.8 623 4 US-09-029-348-3 Sequence 3, Appli  
31 55 21.8 626 4 US-09-029-348-2 Sequence 2, Appli  
32 54 21.4 73 2 US-08-972-008-5 Sequence 5, Appli  
33 54 21.4 263 2 US-08-972-008-2 Sequence 2, Appli  
34 54 21.4 300 2 US-08-794-796-2 Sequence 2, Appli  
35 54 21.4 317 4 US-09-383-586-20 Sequence 20, Appli  
36 53.5 21.2 1833 3 US-08-479-722B-2 Sequence 2, Appli  
37 53.5 21.2 1833 5 PCT-US95-02251-18 Sequence 18, Appli  
38 53 21.0 292 2 US-08-403-852D-26 Sequence 26, Appli  
39 53 21.0 292 3 US-08-510-646B-26 Sequence 26, Appli  
40 53 21.0 292 4 US-09-231-818-25 Sequence 25, Appli  
41 53 21.0 366 4 US-08-857-076-103 Sequence 103, App  
42 53 21.0 486 3 US-08-746-559A-5 Sequence 5, Appli  
43 53 21.0 516 3 US-08-746-559A-4 Sequence 4, Appli  
44 53 21.0 1367 2 US-08-249-687C-2 Sequence 2, Appli  
45 53 21.0 1367 2 US-08-625-819-2 Sequence 2, Appli

#### ALIGNMENTS

RESULT 1  
US-08-911-423-6  
; Sequence 6, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911.423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-6

COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patencin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 12-DEC-1995  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
PRIORITY APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 191 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-974-022-52

Query Match 26.6%; Score 67; DB 3; Length 191;  
Best Local Similarity 45.2%; Pred. No. 1.5;  
Matches 14; Conservative 3; Mismatches 12; Indels 2; Gaps 2;

QY 1 CVQPEFHCGDPCCTTCHRHPCPPGGVQSQG 31  
DB 87 CIE-GFHLGPQCTRC-EKDCRPGQELTKQG 115

RESULT 8  
US-08-236-918A-6  
Sequence 6, Application US/08236918A  
Patent No. 5674704  
GENERAL INFORMATION:  
APPLICANT: Alderson, Mark R.  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple 7.5.3  
SOFTWARE: Microsoft Word, Version #6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/236,918A  
FILING DATE: 06-May-1994  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
PRIORITY APPLICATION NUMBER: US 08/060,843  
FILING DATE: 07-May-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2801-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-236-918A-6

Query Match 26.6%; Score 67; DB 1; Length 256;  
Best Local Similarity 45.2%; Pred. No. 1.9;  
Matches 14; Conservative 3; Mismatches 12; Indels 2; Gaps 2;

QY 1 CVQPEFHCGDPCCTTCHRHPCPPGGVQSQG 31  
DB 87 CIE-GFHLGPQCTRC-EKDCRPGQELTKQG 115

RESULT 9  
PCT-US96-03965-2  
Sequence 2, Application PC/TUS9603965  
GENERAL INFORMATION:  
APPLICANT: Kwon, Byoung Se  
APPLICANT: Kang, Chang-yull  
TITLE OF INVENTION: Monoclonal antibody against human  
TITLE OF INVENTION: receptor 4-1BB  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Barnard, Brown & Michaels  
STREET: 306 East State Street, Suite 220  
CITY: Ithaca  
STATE: NY  
COUNTRY: USA  
ZIP: 14850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/03965  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
PRIORITY APPLICATION NUMBER: US 08/122,796  
FILING DATE: 16-SEP-1993  
PRIORITY APPLICATION DATA:  
PRIORITY APPLICATION NUMBER: US 08/012,269  
FILING DATE: 01-FEB-1993  
PRIORITY APPLICATION DATA:  
PRIORITY APPLICATION NUMBER: US 07/922,996  
FILING DATE: 30-JUL-1992  
PRIORITY APPLICATION DATA:  
PRIORITY APPLICATION NUMBER: US 07/267,577  
FILING DATE: 07-NOV-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Michaels, Christopher A.  
REGISTRATION NUMBER: 34,390  
REFERENCE/DOCKET NUMBER: KWO5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 607-273-1711  
TELEFAX: 607-273-2609  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-03965-2

Query Match 26.6%; Score 67; DB 5; Length 256;  
Best Local Similarity 45.2%; Pred. No. 1.9;

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,419  
FILING DATE: 16-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/027,901  
FILING DATE: 07-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K  
TELEPHONE: 650-496-1200  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-911-423-7

Query Match 82.3%; Score 207.5; DB 3; Length 232;  
Best Local Similarity 82.5%; Pred. No. 1.4e-15;  
Matches 33; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 CVQPEFHCGDPCCCTCRHHPCPPGQGVQSGKFSFGQCI 40  
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DB 68 CVQPEFHCGDPCCCTCRHHPCPPGQGVQSGKFSFGQCI 104  
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RESULT 5  
US-08-911-423-2  
Sequence 2, Application US/08911423  
Patent No. 6111090  
GENERAL INFORMATION:  
APPLICANT: Gorman, Daniel M.  
APPLICANT: Randall, Troy D.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
TITLE OF INVENTION: REAGENTS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/911,423  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,419  
FILING DATE: 16-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/027,901  
FILING DATE: 07-OCT-1996  
ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0612K  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 228 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-911-423-2

Query Match 66.7%; Score 168; DB 3; Length 228;  
Best Local Similarity 62.5%; Pred. No. 2.5e-11;  
Matches 25; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCCTCRHHPCPPGQGVQSGKFSFGQCI 40  
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DB 62 CVTPEYHCGDPQCKICKHYPCQGVQSGDIVGFRVCV 101  
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RESULT 6  
US-09-188-930-191  
Sequence 191, Application US/09188930A  
Patent No. 6150502  
GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Onrust, Rene  
APPLICANT: Murison, James Greg  
TITLE OF INVENTION: Compositions Isolated From Skin Cells  
TITLE OF INVENTION: and Methods For Their Use  
FILE REFERENCE: 11000.1011c1  
CURRENT APPLICATION NUMBER: US/09/188,930A  
CURRENT FILING DATE: 1998-11-09  
NUMBER OF SEQ ID NOS: 348  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 191  
LENGTH: 89  
TYPE: PRT  
ORGANISM: mouse  
US-09-188-930-191

Query Match 49.6%; Score 125; DB 4; Length 89;  
Best Local Similarity 64.3%; Pred. No. 4.4e-07;  
Matches 18; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 CVQPEFHCGDPCCCTCRHHPCPPGQGVQ 28  
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DB 61 CVTPEYHCGDPQCKICKHYPCQGVQ 88  
|||||

RESULT 7  
US-08-974-022-52  
Sequence 52, Application US/08974022  
Patent No. 6015938  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California







;; ZIP: 20001  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/828,584  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Posorske, Laurence H.  
;; REGISTRATION NUMBER: 34,698  
;; REFERENCE/DOCKET NUMBER: 1107.46362  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 20-2 508-9153  
;; TELEFAX: 202 508-9299  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1104 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-828-584-5

Query Match 23.6%; Score 59.5; DB 2; Length 1104;  
Best Local Similarity 43.5%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 12; Indels 1; Gaps 1;  
QY 1 CVOPEFHCGDPCCTTCR-HHPCP 22  
Db 840 CTTPRADCGHPCMAPCHTSSPCP 862

Search completed: September 4, 2001, 15:57:36  
Job time: 378 sec

Query Match 100.0%; Score 246; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 1.2e-23;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DCASGTFSGGHEGCKPWTCTQFGFLTVPFGNKTTHNAVCV 41  
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DB 108 DCASGTFSGGHEGCKPWTCTQFGFLTVPFGNKTTHNAVCV 148

RESULT 2  
US-08-911-423-4  
; Sequence 4, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; FILING DATE: 07-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-911-423-4

Query Match 100.0%; Score 246; DB 3; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1.3e-23;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DCASGTFSGGHEGCKPWTCTQFGFLTVPFGNKTTHNAVCV 41  
|||||  
DB 114 DCASGTFSGGHEGCKPWTCTQFGFLTVPFGNKTTHNAVCV 154

RESULT 3  
US-08-911-423-8  
; Sequence 8, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.

; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 311 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-8

Query Match 100.0%; Score 246; DB 3; Length 311;  
Best Local Similarity 100.0%; Pred. No. 1.7e-23;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DCASGTFSGGHEGCKPWTCTQFGFLTVPFGNKTTHNAVCV 41  
|||||  
DB 108 DCASGTFSGGHEGCKPWTCTQFGFLTVPFGNKTTHNAVCV 148

RESULT 4  
US-08-911-423-2  
; Sequence 2, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 15:57:36 ; Search time 65.86 Seconds  
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12.818 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_114\_154

Perfect score: 246

Sequence: 1 DCASGTFSGHGCHKPWT.....TQFGFLTVFPGKTHNAVCV 41

Scoring table: BLOSUM62

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Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	246	100.0	228	3	US-08-911-423-6
2	246	100.0	241	3	US-08-911-423-4
3	246	100.0	311	3	US-08-911-423-8
4	192	78.0	228	3	US-08-911-423-2
5	96	39.0	277	2	US-08-147-784-2
6	96	39.0	277	4	US-08-195-967-2
7	95	38.6	206	1	US-08-097-827-7
8	95	38.6	206	1	US-08-494-574-7
9	95	38.6	438	1	US-08-097-827-11
10	95	38.6	438	1	US-08-494-574-11
11	93	37.8	219	2	US-08-816-605-2
12	93	37.8	255	1	US-08-236-918A-8
13	93	37.8	255	1	US-08-816-605-9
14	93	37.8	255	5	PCT-US96-03965-8
15	84	34.1	41	1	US-08-050-319B-44
16	84	34.1	41	2	US-08-465-982-44
17	84	34.1	139	2	US-08-219-237B-8
18	84	34.1	140	4	US-08-477-347-17
19	84	34.1	205	3	US-08-974-022-51
20	83	33.7	401	3	US-08-974-022-2
21	83	33.7	401	3	US-08-974-022-4
22	83	33.7	401	4	US-09-042-785A-13
23	78	31.7	300	2	US-08-794-796-2
24	77	31.3	401	3	US-08-974-022-6
25	77	31.3	401	4	US-09-042-785A-12
26	75	30.5	625	3	US-08-996-139-15
27	75	30.5	625	4	US-08-995-659-15

28	74	30.1	253	4	US-09-042-785A-4	Sequence 4, Appli
29	74	30.1	451	3	US-08-996-139-4	Sequence 4, Appli
30	74	30.1	451	4	US-08-995-659-4	Sequence 4, Appli
31	74	30.1	591	3	US-08-996-139-2	Sequence 2, Appli
32	74	30.1	591	4	US-08-995-659-2	Sequence 2, Appli
33	74	30.1	605	4	US-09-042-785A-23	Sequence 23, Appli
34	74	30.1	616	3	US-08-996-139-6	Sequence 6, Appli
35	74	30.1	616	4	US-08-995-659-6	Sequence 6, Appli
36	74	30.1	655	3	US-08-959-382-2	Sequence 2, Appli
37	70.5	28.7	191	3	US-08-974-022-52	Sequence 52, Appli
38	70.5	28.7	256	1	US-08-236-918A-6	Sequence 6, Appli
39	70.5	28.7	256	5	PCT-US96-03965-2	Sequence 2, Appli
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41	63	25.6	227	3	US-08-974-022-48	Sequence 48, Appli
42	63	25.6	461	4	US-09-042-785A-7	Sequence 7, Appli
43	61	24.8	39	1	US-08-050-319B-41	Sequence 41, Appli
44	61	24.8	39	2	US-08-465-982-41	Sequence 41, Appli
45	61	24.8	163	2	US-08-219-237B-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1  
US-08-911-423-6  
; Sequence 6, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911.423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Chang, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-911-423-6

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; FILING DATE: 22-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE: 23-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-494-574-7

Query Match          38.6%; Score 95; DB 1; Length 206;
Best Local Similarity 46.2%; Pred. No. 7.9e-05;
Matches 18; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY      2 CASGTFSGGHGCKPWTCTQFGFLTVFFGNKTHNAVC 40
Db       | ||| : ||||| | | | : |||
        126 CPGHFSPGNQACKPWNTCTLSGKQTRHPASDSLDAVC 164

RESULT      9
US-08-097-827-11
; Sequence 11, Application US/08097827
; Patent No. 5457035
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for
; TITLE OF INVENTION: OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-097-827-11

Query Match          38.6%; Score 95; DB 1; Length 438;

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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-911-423-2

Query Match 78.0%; Score 192; DB 3; Length 228;
Best Local Similarity 75.0%; Pred. No. 6.8e-17;
Matches 30; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CASGTFSGHGCHKPTWDTCTQFGFLTVFPGNKTHNAVCV 41
Db 103 CAMGTFSGAGRCHRLWNCISGFLTFMFPGNKTHNAVCI 142

RESULT 5
US-08-147-784-2
; Sequence 2, Application US/08147784
; Patent No. 5821332
; GENERAL INFORMATION:
; APPLICANT: Godfrey, Wayne
; APPLICANT: Buck, David
; APPLICANT: Engleman, Edgar G.
; TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED
; TITLE OF INVENTION: CD4+ T-CELLS: ACT-4
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,784
; FILING DATE: 03-NOV-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 05490A-220
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-147-784-2
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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-147-784-2

Query Match 39.0%; Score 96; DB 2; Length 277;
Best Local Similarity 43.6%; Pred. No. 8.1e-05;
Matches 17; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Qy 2 CASGTFSGHGCHKPTWDTCTQFGFLTVFPGNKTHNAVVC 40
Db 128 CPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAIC 166

RESULT 6
US-08-195-967-2
; Sequence 2, Application US/08195967
; Patent No. 6242566
; GENERAL INFORMATION:
; APPLICANT: Godfrey, Wayne
; APPLICANT: Engleman, Edgar G.
; TITLE OF INVENTION: LIGAND (ACT-4-L) TO A RECEPTOR ON THE SURFACE OF ACTIVATED
; TITLE OF INVENTION: CD4+ T-CELLS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,967
; FILING DATE: 10-FEB-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 05490A-230
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-195-967-2

Query Match 39.0%; Score 96; DB 4; Length 277;
Best Local Similarity 43.6%; Pred. No. 8.1e-05;
Matches 17; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Qy 2 CASGTFSGHGCHKPTWDTCTQFGFLTVFPGNKTHNAVVC 40
Db 128 CPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAIC 166

RESULT 7
US-08-097-827-7
; Sequence 7, Application US/08097827
; Patent No. 5457035
; GENERAL INFORMATION:
```

REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2801-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-236-918A-8

Query Match 37.8%; Score 93; DB 1; Length 255;  
Best Local Similarity 40.0%; Pred. No. 0.00018;  
Matches 16; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 1 DCASGTFSGHGEGHCKPWTDCQTQFGFLTVFPGNKTHNAV 40  
DB 119 DCCFGTFNDQKRGICRPWTNCSLDGKSVLVNGTKRDRVVC 158

RESULT 13  
US-08-816-605-9  
Sequence 9, Application US/08816605  
Patent No. 5874240  
GENERAL INFORMATION:  
APPLICANT: NI, Jian  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Gentz, Reiner  
TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/816.605  
FILING DATE: 13-MAR-1997

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF254  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8512  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-816-605-9

Query Match 37.8%; Score 93; DB 2; Length 255;  
Best Local Similarity 40.0%; Pred. No. 0.00018;  
Matches 16; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 1 DCASGTFSGHGEGHCKPWTDCQTQFGFLTVFPGNKTHNAV 40  
DB 119 DCCFGTFNDQKRGICRPWTNCSLDGKSVLVNGTKRDRVVC 158

RESULT 14  
PCT-US96-03965-8  
Sequence 8, Application PC/TUS9603965  
GENERAL INFORMATION:  
APPLICANT: Kwon, Byoung Se  
APPLICANT: Kang, Chang-Yull  
TITLE OF INVENTION: Monoclonal antibody against human  
TITLE OF INVENTION: receptor 4-1BB  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Barnard, Brown & Michaels  
STREET: 306 East State Street, Suite 220  
CITY: Ithaca  
STATE: NY  
COUNTRY: USA  
ZIP: 14850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/03965  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/122,796  
FILING DATE: 16-SEP-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/012,269  
FILING DATE: 01-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/922,996  
FILING DATE: 30-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/267,577  
FILING DATE: 07-NOV-1988

ATTORNEY/AGENT INFORMATION:  
NAME: Michaels, Christopher A  
REGISTRATION NUMBER: 34,390  
REFERENCE/DOCKET NUMBER: KW05  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 607-273-1711  
TELEFAX: 607-273-2609  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-03965-8

Query Match 37.8%; Score 93; DB 5; Length 255;  
Best Local Similarity 40.0%; Pred. No. 0.00018;  
Matches 16; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 1 DCASGTFSGHGEGHCKPWTDCQTQFGFLTVFPGNKTHNAV 40  
DB 119 DCCFGTFNDQKRGICRPWTNCSLDGKSVLVNGTKRDRVVC 158

RESULT 15  
US-08-050-319B-44  
Sequence 44, Application US/08050319B  
Patent No. 5633145  
GENERAL INFORMATION:  
APPLICANT: M. Feldmann, P.W. Gray  
APPLICANT: M.J.C. Turner, F.M. Brennan  
TITLE OF INVENTION: Modified human TNFalpha (Tumor  
TITLE OF INVENTION: Necrosis Factor alpha) Receptor

```
Best Local Similarity 46.2%; Pred. No. 0.00017;
Matches 18; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 2 CASGTFSGGHEGCKPWTCTQFGFLTVPFGKTHNAV 40
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 126 CPPGHFSPGNQACKPWTNCTLSGKQTRHPASDSD 164

RESULT 10
US-08-494-574-11
; Sequence 11, Application US/08494574
; Patent No. 5783665
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5783665el Cytokine which is a Ligand for
; TITLE OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,574
; FILING DATE: 22-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE: 23-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-494-574-11

Query Match 38.6%; Score 95; DB 1; Length 438;
Best Local Similarity 46.2%; Pred. No. 0.00017;
Matches 18; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 2 CASGTFSGGHEGCKPWTCTQFGFLTVPFGKTHNAV 40
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 126 CPPGHFSPGNQACKPWTNCTLSGKQTRHPASDSD 164

RESULT 11
US-08-816-605-2
; Sequence 2, Application US/08816605
; Patent No. 5874240
; GENERAL INFORMATION:
; APPLICANT: NL, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant
; NUMBER OF SEQUENCES: 9
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,605
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF254
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-816-605-2

Query Match 37.8%; Score 93; DB 2; Length 219;
Best Local Similarity 40.0%; Pred. No. 0.00015;
Matches 16; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

Qy 1 DCASGTFSGGHEGCKPWTCTQFGFLTVPFGKTHNAV 40
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 83 DCCFGTFNDQKRGICRPWTNCSLDGKSVLVNGTKERD 122

RESULT 12
US-08-236-918A-8
; Sequence 8, Application US/08236918A
; Patent No. 5674704
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple 7.5.3
; SOFTWARE: Microsoft Word, Version #6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,918A
; FILING DATE: 06-May-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,843
; FILING DATE: 07-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
```



NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Reed & Robbins  
STREET: 635 Bryant Street  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/050.319B  
FILING DATE: 10-May-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Robbins, Roberta L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 5150-0030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 41 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-050-319B-44

Query Match 34.1%; Score 84; DB 1; Length 41;  
Best Local Similarity 41.0%; Pred. No. 0.00035;  
Matches 16; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Oy 2 CASGTFSGGHEGCKPWTCTQFGFLTFPPGNKTHNAV 40  
| | | | | | | | | | | | | | | | | | | | | |  
Db 2 CPPGHFPGSNQACKPWTNCTLSGRQIRHPASNSLD 40  
| | | | | | | | | | | | | | | | | | | | | |

Search completed: September 4, 2001, 15:57:36  
Job time: 378 sec



Db 117 TSKRTQRC-QPMFCAAWALECHTCELLSDCPGTEAELEKDEVGKGNHCVPCAGHF 175  
 QY 121 --SGHEGHCRTWDTCTGFGFLTVPGNKNTHNAVCPGSPRAEPLG-----WLTVVLL 171  
 Db 176 QNTSPSARCQPHTRCENQGLVEAAPGTAQSTTC---KNLEPLPPMSGTMLMLAVLL 232  
 QY 172 AVAACVLLTSAQLGLHIWQ-----LRKTQLLEVPSPSTE 206  
 Db 233 PLAPFLLLATVFC---INWKSHPSLCKRLGSLKKRRPQGE 269

RESULT 10  
 MWRTS  
 laminin beta-2 chain precursor - rat  
 N:Alternate names: laminin chain B3; S:laminin  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 10-Dec-1999  
 C:Accession: S03539  
 R:Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.  
 Nature 338, 229-234, 1989  
 A:Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neuro  
 A:Reference number: S03539; MUID:89159410  
 A:Accession: S03539  
 A:Molecule type: mRNA  
 A:Residues: 1-1801 <HUN>  
 A:Cross-references: EMBL:X16563; NID:Q57250; PIDN:CAA34561.1; PID:G57251  
 C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
 C:Function:  
 A:Description: Interact with cells and with other basement membrane proteins to promote  
 C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
 C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
 F:1-35/Domain: signal sequence #status predicted <SIG>  
 F:36-1801/Product: laminin beta-2 chain #status predicted <MAT>  
 F:36-285/Domain: VI <DOM>  
 F:286-535/Domain: V <DOM>  
 F:286-347/Domain: laminin-type EGF-like homology <LE01>  
 F:350-410/Domain: laminin-type EGF-like homology <LE02>  
 F:413-470/Domain: laminin-type EGF-like homology <LE03>  
 F:473-522/Domain: laminin-type EGF-like homology <LE04>  
 F:525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>  
 F:556-784/Domain: IV <DOM>  
 F:785-831/Domain: laminin-type EGF-like homology <LE06>  
 F:788-1196/Domain: laminin-type EGF-like homology <LE07>  
 F:834-877/Domain: laminin-type EGF-like homology <LE08>  
 F:880-927/Domain: laminin-type EGF-like homology <LE09>  
 F:930-986/Domain: laminin-type EGF-like homology <LE10>  
 F:989-1038/Domain: laminin-type EGF-like homology <LE11>  
 F:1041-1095/Domain: laminin-type EGF-like homology <LE12>  
 F:1098-1143/Domain: laminin-type EGF-like homology <LE13>  
 F:1146-1190/Domain: laminin-type EGF-like homology <LE14>  
 F:1197-1412/Domain: laminin-type EGF-like homology <LE15>  
 F:1197-1412/Region: heptad repeats  
 F:1413-1445/Domain: alpha <ALP>  
 F:1446-1801/Region: heptad repeats  
 F:1446-1801/Domain: I <DOM1>  
 F:45-50/Disulfide bonds: #status predicted  
 F:251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status p  
 F:1193,1196,1800/Disulfide bonds: Interchain #status predicted

Query Match 10.0%; Score 134.5; DB 1; Length 1801;  
 Best Local Similarity 26.9%; Pred. No. 0.0063;  
 Matches 63; Conservative 6; Mismatches 60; Indels 105; Gaps 15;

QY 8 GAFRALC-GLALLCALSLG-----QRPTGG-PGCGP-----GRLLLGTTDARCCRV 52  
 Db 840 GALSALCEGTSQCLCRTGAFGLRCDHCQGWGFNCRPCVCNGR-----ADECCA 891

QY 53 HTTRC--CRDYPGECCSWDCMCVQPEFHCGDPCT---TCRHHPCPGQVQSGKFS 107  
 Db 892 HTGACLGCRDVTGGBHCEH-----CI-AGFH-GDPLRYPVGQCRPCPCPEPG--SORHEA 943

QY 108 -----FGQCIDCASGTF----- 120  
 Db 944 TSCHRDGYSOIVCHCRAGVTGLRCEACAPGHGDPKPGRCQCLBCSGNIDTPDCAC 1003  
 QY 121 -----SGHEGHCRTWDTCTGFGFLTVPGNKNTHNAVCPGSPRAEPLG 159  
 Db 1004 DPHTGQCLRLHHTGPHGCHKRP-----GFHQGAARQSHRCTCNLLGTDP 1050

RESULT 11  
 A60771  
 B-cell activation protein CD40 precursor - human  
 N:Alternate names: B-cell surface antigen Bp50  
 C:Species: Homo sapiens (man)  
 C>Date: 03-Jun-1993 #sequence\_revision 03-Feb-1994 #text\_change 21-Jul-2000  
 C:Accession: S04460; A60771  
 R:Stamenkovic, I.; Clark, E.A.; Seed, B.  
 EMBO J. 8, 1403-1410, 1989  
 A:Title: A B-lymphocyte activation molecule related to the nerve growth factor recept  
 A:Reference number: S04460; MUID:89356608  
 A:Accession: S04460  
 A:Molecule type: mRNA  
 A:Residues: 1-277 <STA>  
 A:Cross-references: EMBL:X60592; NID:G29850; PIDN:CAA43045.1; PID:G29851  
 R:Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.  
 J. Immunol. 142, 562-567, 1989  
 A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-  
 A:Reference number: A60771; MUID:89093941  
 A:Accession: A60771  
 A:Molecule type: protein  
 A:Residues: 21-50 <BRA>  
 A:Experimental source: Burkitt lymphoma cell line Raji  
 C:Genetics:  
 A:Gene: GDB:CD40  
 A:Cross-references: GDB:215268; OMIM:109535  
 A:Map position: 20q12-20q13.2  
 C:Superfamily: CD27 antigen; NGF receptor repeat homology  
 C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane prot  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>  
 F:21-193/Domain: extracellular #status predicted <EXT>  
 F:194-215/Domain: transmembrane #status predicted <TM>  
 F:216-277/Domain: intracellular #status predicted <CYT>  
 F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.4%; Score 126.5; DB 2; Length 277;  
 Best Local Similarity 24.0%; Pred. No. 0.0069;  
 Matches 48; Conservative 27; Mismatches 102; Indels 23; Gaps 9;

QY 34 CGPGRLLLTGTDCRCRVHTTRCCRDYPG----EECCSEWDCMCVQPE-FHCGDPCTT 88  
 Db 62 CGSEFELDTWNRETHC---HQHYCDPNLGLRVQOKTSETDTICTCEGWHCTSEACES 118  
 QY 89 C-RHHPCPGQVQSGKFSFGQCIDCASGTFSGGHEG--HCKPMTDCTQFGFLTVFP 145  
 Db 119 CVLHRSCEPGFGVKQIATGSDICEPCPVGFFSNVSSAFKCHPWTSCETKDLVQOAG 178  
 QY 146 NKTTHNAVCPGSPAPPLGLWTV--VLLAVAACVLLTSAQLGLHIWQLRKTKQLLEVP 203  
 Db 179 TNKTDVVC-----GPQDRLRALVPIIFILFALLVL-----VFIRKVAK-KPTNKAPH 228  
 QY 204 STEDARSCQFPEEERGERSA 223  
 Db 229 PKOEPQEIFPDPLPGSNTA 248

RESULT 12  
 I48854  
 gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 23-Jul-1999  
 C:Accession: I48854

[illegible]



QY 72 -CMCVQPEFHC-----GDCCTTCRHHPGPGGQVOSQKFSFGFCIDCASGTFSS-- 122  
Db 117 ICTC-RPGWYCALSKQBGRCLCAPLR--KCRPGFGVARPGTETSDVYCKPCAPGTFSTNT 173  
QY 123 GHEGCHKPWTDCQTFGLTVFPNGKTHNVC-----VPG----- 156  
Db 174 SSTDICRPHQICN-----VVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQP 229  
QY 157 -----SPPAE-----PLGW-----LTVLLAAVACVLLLTSAQ 184  
Db 230 TPEPSTAPSTSLFLPMGPPSPABEGSTGDFALPVGLIIVGTALGILLIIGVNCVIMT----- 285  
QY 185 LGHIWQLRKTQLLE-----VPSTED-ARSCQFPPEE 217  
Db 286 -----QVRKKPLCLQREAKVPHLPADKARGTQGPQQ 317

RESULT 7  
JC5559  
lectin-B - Virginian pokeweed  
C:Species: Phytolacca americana (Virginian pokeweed)  
C>Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 17-Mar-2000  
C:Accession: JC5559  
R:Yamaguchi, K.; Yurino, N.; Kino, M.; Ishiguro, M.; Funatsu, G.  
Biosci. Biotechnol. Biochem. 61, 690-698, 1997  
A:Title: The amino acid sequence of mitogenic lectin-B from the roots of pokeweed (Phytolacca americana)  
A:Reference number: JC5559; MUID:97290889  
A:Accession: JC5559  
A:Molecule type: protein  
A:Residues: 1-295 <YAM>  
A:Experimental source: root  
C:Comment: This protein is a lectin specific for N-acetylglucosamine-containing saccharides  
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; plant lectins  
C:Keywords: glycoprotein  
F:96,139/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.4%; Score 139; DB 2; Length 295;  
Best Local Similarity 28.8%; Pred. No. 0.00077;  
Matches 36; Conservative 18; Mismatches 41; Indels 30; Gaps 8;

QY 20 CALSLGQRTGGP-----GCGPRLLLGTGTDAACRCRVHTTRCCRDYDYG-----EECC 67  
Db 133 CGVDFGNRTCPNDLCSSEWGWCGITGEGYCGGCSQC---NHQRCKGDFAGRTCLNDLCC 189  
QY 68 SEWDCMCVQPEFHCQDPCTTCRHHPGPGGQVOSQKFSFGFCIDCASGTFSSG 123  
Db 190 SEWG-WCGSSEAHCGGCGGCSNCRNRC-----GR-NFGFRTCPNELCCSSGGWCGS 238  
QY 124 HEGHC 128  
Db 239 NDAHC 243

RESULT 8  
A46476  
B cell-associated surface molecule CD40, long splice form - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Nov-2000  
C:Accession: A46476; A46515  
R:Torres, R.M.; Clark, E.A.  
J. Immunol. 148, 620-626, 1992.  
A:Title: Differential increase of an alternatively polyadenylated mRNA species of murine CD40  
A:Reference number: A46476; MUID:92105763  
A:Accession: A46476  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-305 <TOR>  
A:Cross-references: GB:M83312; NID:g1553058  
A:Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)  
A:Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0  
R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Howard, M.; Cockayne, J.

J. Immunol. 149, 3921-3926, 1992  
A:Title: Genomic structure and chromosome mapping of the murine CD40 gene.  
A:Reference number: A46515; MUID:93094586  
A:Accession: A46515  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-287, 'LV' <GRI>  
A:Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126  
A:Experimental source: BALB/c, liver  
A:Note: sequence extracted from NCBI backbone (NCBIP:120357)  
C:Comment: For an alternative splice form, see PIR:A46515.  
C:Comment: For an alternative splice form, see PIR:A46476.  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: alternative splicing; transmembrane protein  
F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 10.4%; Score 139; DB 2; Length 305;  
Best Local Similarity 23.3%; Pred. No. 0.00079;  
Matches 65; Conservative 23; Mismatches 107; Indels 84; Gaps 11;

QY 13 LCGL--ALLCALSLGQRTGGPGRLLLTGTGTDAACRCRVHTTRCCRDYDYG----- 50  
Db 7 LCALWGCLLTAVHLGQCVT-----CSDKQYL-----HDGCCDLCPGSLTSHCTALEKTQ 58  
QY 51 -----RVHTTRCCRDYDYG-----EECCSEWDCMCVQPE-FHCQDPCTT 88  
Db 59 CHPCDSGEFSAQWNRCHQRHCEPNOGLRVKKEGTAESDTVCTCKEGHCTSKDCEA 118  
QY 89 C-RHHPGPGGQVOSQKFSFGFCIDCASGTFSSGHE--GHCKPWTCTDCTGFLTVFPV 145  
Db 119 CAQHTPCIPGFGVMEMATETDTTVCHPCPVGFFNQSSSLFEKCYPMWTSCEKNLEVLQK 178  
QY 146 NKTNAVCPGSPAPPLGLWLTVVLLAAVACVLLLTSAQLGLHIWOLRK----- 194  
Db 179 TSQTNVTCGLKSR-----MRALLVIVPMVGLITFGVFLYIKVVKPKDNEMLP 231

QY 195 -----TQLLEVP-----PSTEDARSCQFPEERERS 222  
Db 232 ARRDQPMEDYPCGHNTAAAPVQETLHGCPVTVQSDGKES 270

RESULT 9  
I54182  
tumor necrosis factor receptor 2-related protein - human  
C:Species: Homo sapiens (man)  
C>Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 17-Mar-2000  
C:Accession: I54182  
R:Baens, M.; Chafanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.  
Genomics 16, 214-218, 1993  
A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed seq  
A:Reference number: I54182; MUID:93252381  
A:Accession: I54182  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-435 <RES>  
A:Cross-references: GB:I04270; NID:g339761; PIDN:AAA36757.1; PID:g339762  
C:Genetics:  
A:Gene: GDB:LTBR  
A:Cross-references: GDB:1230195; OMIM:600979  
A:Map position: 12p13.3-12p13.1  
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 10.0%; Score 134.5; DB 2; Length 435;  
Best Local Similarity 26.4%; Pred. No. 0.0023;  
Matches 58; Conservative 17; Mismatches 86; Indels 59; Gaps 13;

QY 34 CGPGRLLLTGTDAACRCRVHTTRC-----CRDYPGEE---C 66  
Db 62 CPP-----GYVSAKSRIRDTVCAENSYNHNWYLTICQLCRPCDPVWGLEETAPC 116  
QY 67 CS--EWDCCMCVQPEFHCQDPCTTCR-HHPCPPGGVOSQKFSFG-FOCIDCASGTF 120

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2001, 15:53:43 ; Search time 80.15 Seconds  
(without alignments)  
222.394 Million cell updates/sec

Title: US-09-512-363-2

Perfect score: 1340

Sequence: 1 MAQHGMGAFRALGLALIC.....EEEGERSABEKRGLGLWV 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_68.\*

1: pirl.\*

2: pirl2.\*

3: pirl3.\*

4: pirl4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	201.5	15.0	256	2 B32393	T-cell antigen 4-1
2	197	14.7	255	2 I38426	lymphocyte activat
3	188.5	12.6	272	2 I48700	gene ox40 protein
4	165	12.3	277	2 I37552	OX40 homolog - hum
5	160.5	12.0	271	2 S12783	OX40 antigen precu
6	139.5	10.4	461	1 A35356	tumor necrosis fac
7	139	10.4	295	2 J05559	lectin-B - Virgini
8	139	10.4	305	2 A46476	B cell-associated
9	134.5	10.0	435	2 I54182	tumor necrosis fac
10	134.5	10.0	1801	1 NMRTS	laminin beta-2 cha
11	126.5	9.4	277	2 A60771	B-cell activation
12	120.5	9.0	459	2 I48854	gene murine tumour
13	119.5	8.9	1798	2 S53869	laminin beta-2 cha
14	119	8.9	474	2 B38634	tumor necrosis fac
15	119	8.9	1574	2 T13954	MEGF6 protein - ra
16	115.5	8.6	1371	2 A33837	insulin-like transme
17	115	8.6	1687	2 T30176	EGF repeat transme
18	114.5	8.5	329	2 A48805	insulin-like growt
19	112.5	8.4	1797	2 A55677	laminin beta-2 cha
20	112	8.4	152	2 T18975	hypothetical prote
21	112	8.4	2318	2 S45306	notch 3 protein -
22	111	8.3	1111	2 T26972	hypothetical prote
23	110.5	8.2	2907	2 A57278	fibrillin-2 precu
24	109.5	8.2	164	2 T24272	hypothetical prote
25	109.5	8.2	2531	2 A46019	Notch-1 protein -
26	109	8.1	3635	2 T10053	laminin alpha 5 ch
27	108.5	8.1	3566	1 A40701	tenascin-X precurs
28	106.5	7.9	2918	2 A54105	fibrillin-2 precu
29	105	7.8	188	2 T15651	hypothetical prote

30	105	7.8	1172	1 TSHUP2	thrombospondin 2 p
31	105	7.8	1364	2 T00250	MEGF2 protein - hu
32	104.5	7.8	2825	2 T14271	Doc4 protein - stre
33	103.5	7.7	1737	2 T00209	MEGF8 protein - hu
34	102.5	7.6	956	1 A46016	thrombospondin 3 -
35	102.5	7.6	2871	2 A55567	fibrillin I - bovi
36	102	7.6	186	2 A28401	agglutinin isolect
37	102	7.6	680	2 P05010	integrin beta-3 ch
38	101.5	7.6	1367	1 IGHUR1	insulin-like growt
39	101.5	7.6	1820	2 A55494	latent transformin
40	101	7.5	788	2 T25061	hypothetical prote
41	101	7.5	4543	1 A53102	alpha-2-macroglobu
42	100.5	7.5	656	2 JC2005	integrin beta-5 ch
43	100.5	7.5	2531	2 S18188	notch protein homo
44	100.5	7.5	3002	2 A47221	fibrillin 1 precu
45	100	7.5	213	1 AEWT2	agglutinin isolect

ALIGNMENTS

RESULT 1

B32393

T-cell antigen 4-1BB precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 21-Jul-2000

C:Accession: B32393; I48879

R:Kwon, B.S.; Weissman, S.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989

A:Title: cDNA sequence of two inducible T-cell genes.

A:Reference number: A32393; MUID:89184547

A:Accession: B32393

A:Molecule type: mRNA

A:Residues: 1-256 <KWD>

A:Cross-references: GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122

R:Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.

J. Immunol. 152, 2256-2262, 1994

A:Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1B

A:Reference number: I48879; MUID:94179805

A:Accession: I48879

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-256 <RES>

A:Cross-references: EMBL:U02567; NID:g117783; PIDN:AAA93113.1; PID:g409178

C:Genetics:

A:Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1

C:Superfamily: CD27 antigen; NGF receptor repeat homology

C:Keywords: transmembrane protein

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-256/Product: 4-1BB protein #status predicted <MAT>

Query Match 15.0%; Score 201.5; DB 2; Length 256;

Best Local Similarity 28.7%; Pred. No. 9.8e-09;

Matches 62; Conservative 26; Mismatches 85; Indels 43; Gaps 10;

QY 34 CGPGRLL-LGTGTDARCCRVHTTRCCRDYFGEECCSEW---DCMCVQPEFHCGDPCCTTC 89

DB 47 CPTTFSSIGGGQNCNICRV---CAGYFRFKFCSTHNAECEIE-GFHCLGPGQCTRC 101

QY 90 RHHPCCPPGGVQSGQKFSFGFCIDCASGTGSGGH-EGHCKPWTDCFTQFGFLTVFPCNKT 148

DB 102 -EKDVRPGGELTKQG-----CKTCSLGTFFNDQNGTGVCRPWTNCSLDGRSVLKTGTTT 153

QY 149 HNACVCP-----GSPPAEPLGWLTVVLLAVAAACVLLLTSAQLGLHI--W 190

DB 154 KDVVCPPVVPVFSFSPSTISVTPEGGPGGSHLQVLTFLTAULTSALLALITITLLFSVLKW 213

QY 191 QURKTOLLLEVP-----PSTEDARSCQFPPEERG 219

DB 214 IRKKFPHIFKQPKTKTGAQAQEDACSCRPQEEG 249

```
RESULT 2
I38426
Lymphocyte activation-induced receptor ILA precursor - human
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000
C:Accession: I38426; J07052
R:Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; H
Eur. J. Immunol. 24, 2219-2227, 1994
A:Title: Molecular and biological characterization of human 4-1BB and its ligand.
A:Reference number: I38426; MUID:94374434
A:Accession: I38426
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-255 <RES>
A:Cross-references: EMBL:003397; NID:g571320; PIDN:AAA53133.1; PID:g571321
R:Schwarz, H.; Tuckwell, J.; Lotz, M.
Gene 134, 295-298, 1993
A:Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne
A:Reference number: J07052; MUID:94085794
A:Accession: J07052
A:Molecule type: mRNA
A:Residues: 1-106,'R',108-255 <SCH>
C:Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necro
C:Comment: This receptor recognizes soluble, cell-surface bound or extracellular matrix
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-255/Product: lymphocyte activation-induced receptor <MAT>
F:187-213/Domain: transmembrane #status predicted <TM>
F:138,149/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:234,235/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predict
F:242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 14.7%; Score 197; DB 2; Length 255;
Best Local Similarity 30.2%; Pred. No. 2.2e-08;
Matches 67; Conservative 20; Mismatches 81; Indels 54; Gaps 12;

QY 34 CGPGRLLGTGDARCCRVHTTCCRDYPG-----ECCS-----EWDGMCVQPFHCGDP 84
DB 48 CPNPSFSSAGG--QRTCDI-----CRQKGVFTRKECSSTSNACDC---TPGFHCLGA 97

QY 85 CCTTCRHHPCCPGQVQSQKFGFCIDCASGTSFGGHEGCKPWTCTQFGFLTVFP 144
DB 98 GCSMC-EQDCKQGOELTKG-----CKDCFGTFNDQKRGICRPWTNGLDGKSLVN 149

QY 145 GNKTHNAVCPG-----SPPA---EPLGLTVV--LLAVACVLLLTSAQLGLH 188
DB 150 GTERDVVCGPSADLSPGASSVTPPAPAREGHSQIISFFLALTSTALLFLFLTLR 209

QY 189 ---IWQLRKTQLLEVP-----STEDARSCQPFEEERG 219
DB 210 FSVVGRKKLLYIFQKPMRPVQTTQEDGCSRPPEERG 251

RESULT 3
I48700
gene ox40 protein - mouse
N:Alternate names: Ox40 antigen
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
R:Calderhead, D.M.; Buhlmann, J.B.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.;
J. Immunol. 151, 5261-5271, 1993
A:Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell int
A:Reference number: I48700; MUID:94044750
A:Accession: I48700
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-272 <RES>
A:Cross-references: EMBL:221674; NID:g312827; PIDN:CAA79772.1; PID:g312828
R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
```

```
A:Title: Gene structure and chromosomal localization of the mouse homologue of rat Ox
A:Reference number: I48334; MUID:95255413
A:Accession: I48334
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-14,'G',16-272 <RE2>
A:Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
C:Genetics:
A:Gene: Ox40
A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 12.6%; Score 168.5; DB 2; Length 272;
Best Local Similarity 24.9%; Pred. No. 3.7e-06;
Matches 60; Conservative 18; Mismatches 70; Indels 93; Gaps 11;

QY 39 LLLGTGTGDAR--CCRVHT---TRCCRD-YPG-----ECCSEWDCMCVQPFHCGDPC-- 85
DB 14 LALTLGVTARLNCVKHTYPSGHKCCRECPGHGMVSRCDHTRDTLC-----HPCET 65

QY 86 -----CTTCRRHP-----CPPGQGVQSQKFSFGFCID 114
DB 66 GFYNEAVNYDFCKQCTQCNHRSSELKONCTPTQDTVCRCPGTQPRODSGKGLGVDCVP 125

QY 115 CASGTFSGGHEGCKPWTCTQFGFLTVFPGNKTHNAV----- 153
DB 126 CPPGHFSPGNNAQCKPWTNCTLSGKQTRHPASDSLDVACEDRSLLATLLWETQRTFRPT 185

QY 154 -----VPGSP--AEPLGLTVVLLAVACVLLLTSAQLGLHI----WOLRK 194
DB 186 TVQSTTVMPRTSELP-SPPTLVTPGPAFVLLGLGLLAPLTVLLALYLLRKAMRLPN 244

QY 195 T 195
DB 245 T 245

RESULT 4
Ox40 homologue - human
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
R:Latza, U.; Durkop, H.; Schmittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fo
Eur. J. Immunol. 24, 677-683, 1994
A:Title: The human Ox40 homologue: cDNA structure, expression and chromosomal assignmen
A:Reference number: I37552; MUID:94170844
A:Accession: I37552
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-277 <RES>
A:Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 12.3%; Score 165; DB 2; Length 277;
Best Local Similarity 25.2%; Pred. No. 7e-06;
Matches 63; Conservative 18; Mismatches 113; Indels 56; Gaps 7;

QY 5 GAGAFRALCGLALLCALSLG-----ORPTGGPGCGPGRLLLTGTGDARCCRVHT 54
DB 4 GARRLGRGPCAALLLGLGLSTVTLGHCVDGTYPSNDRCCHECR--PGNGMVSRCSRQSN 61

QY 55 TRCCRDYPG--EECCSEWDCM-CVQPFHCGD---PCCTTCRHHPCPPGQGVQSQKFSF 108
DB 62 TVCRPCPGFYNDVVSCKPKCTWNCNLSRGSERKQJCTATQDTVCRCRAGTQPLDSYKP 121

QY 109 GFQICDCASGTFSGGHEGCKPWTCTQFGFLTVFPGNKTHNAVCPGSPPA----- 161
DB 122 GVDCAFCPPGHFSGPDNQACKPWTNCTLQAGKHTLQPASNSDAICEDRDPTATQPTQ 181

QY 162 -----PLGWLTVVLLAVAAACVLLLTSAQLGLHIWOLR 193
```







```
[3]
RP SEQUENCE OF 1-26 FROM N.A.
RC STRAIN=NOD;
RA Jacob C.O., Liu J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE OF 1-22 FROM N.A.
RC TISSUE=Liver;
RA Kissenerghis M., Fellowes R., Feldmann M., Chernaiovsky Y.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
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CC
CC EMBL; M60469; AAA39752.1; -
DR EMBL; M59378; AAA40463.1; -
DR EMBL; U39488; AAA85021.1; -
DR EMBL; X87128; CAA60618.1; -
DR PIR; B38634; B38634.
DR HSSP; P19438; INCF.
DR MGD; MGI:1314883; Tnfrsf1b.
DR InterPro; IPR001368; -
DR Pfam; PF00020; TNFR_c6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 22
FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT DOMAIN 23 238 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 259 288 POTENTIAL.
FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 39 203 4 X TNFR-CYS.
FT REPEAT 39 77 TNFR-CYS 1.
FT REPEAT 78 119 TNFR-CYS 2.
FT REPEAT 120 164 TNFR-CYS 3.
FT REPEAT 165 203 TNFR-CYS 4.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 55 68 BY SIMILARITY.
FT DISULFID 136 145 BY SIMILARITY.
FT DISULFID 139 163 BY SIMILARITY.
FT DISULFID 166 181 BY SIMILARITY.
FT CARBOHYD 69 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Query Match 8.9%; Score 119; DB 1; Length 474;
Best Local Similarity 31.0%; Pred. No. 0.0047;
Matches 36; Conservative 8; Mismatches 54; Indels 18; Gaps 5;

QY 46 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDCPCTTC-RHHPCPPGGVGSQ 104
DB 107 EIRACTKQNRVCACAGRYCAL-----KTHSGS--CROCMRLSKCGPFGVASSR 155
QY 105 KFSFGQCIDCAGTSG--GHEGCHKPWTCTQGFGLTVFPNGKTHNAVCPESP 158
DB 156 APNGNVLRCACAPGTSTSTSDVCRPHRICS----ILAIPGNASTDAVCAPESP 207

RESULT 15
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IGIR_RAT
ID IGIR_RAT STANDARD; PRT; 1370 AA.
AC P24062;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR (EC 2.7.1.112).
GN IGFLR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95277910; PubMed=7758167;
RA Du J., Delafontaine P.;
RT "Inhibition of vascular smooth muscle cell growth through antisense
transcription of a rat insulin-like growth factor I receptor cDNA.";
RL Circ. Res. 76:963-972(1995).
RN [2]
RP SEQUENCE OF 1-364 FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=90017496; PubMed=2477843;
RA Warner H., Woloschak M., Adamo M., Shen-Orr Z., Roberts C.T. Jr.,
RA Leroith D.;
RT "Developmental regulation of the rat insulin-like growth factor I
receptor gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:7451-7455(1989).
RN [3]
RP SEQUENCE OF 913-1017 FROM N.A.
RX MEDLINE=92412145; PubMed=1530648;
RA Kurachi H., Jobo K., Ohta M., Kawasaki T., Itoh N.;
RT "A new member of the insulin receptor family, insulin
receptor-related receptor, is expressed preferentially in the
kidney.";
RL Biochem. Biophys. Res. Commun. 187:934-939(1992).
CC -1- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)
WITH A HIGH AFFINITY AND IGF II WITH A LOWER AFFINITY. IT HAS A
TYROSINE-PROTEIN KINASE ACTIVITY.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE
BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-
BINDING DOMAIN, WHILE THE BETA CHAIN CARRIES THE KINASE DOMAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
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CC
CC EMBL; L29232; AAA41392.1; -
DR EMBL; M27293; AAA41384.1; -
DR PIR; A33837; A33837.
DR HSSP; P06213; IIRK.
DR InterPro; IPR000494; -
DR InterPro; IPR007119; -
DR InterPro; IPR001245; -
DR InterPro; IPR001777; -
DR InterPro; IPR002011; -
DR InterPro; IPR002174; -
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
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FT	CHAIN	20	289		CD40L RECEPTOR.
FT	DOMAIN	20	193		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	194	215		POTENTIAL.
FT	DOMAIN	216	289		CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	25	187		4 X TNFR-CYS.
FT	REPEAT	25	60		TNFR-CYS 1.
FT	REPEAT	61	103		TNFR-CYS 2.
FT	REPEAT	104	144		TNFR-CYS 3.
FT	REPEAT	145	187		TNFR-CYS 4.
FT	CARBOHYD	153	153		N-LINKED (GLCNAC..) (POTENTIAL).
SQ	SEQUENCE	289 AA;	32111 MW;		C791CB6D2FEA574E CRC64;

  

Query Match	10.4%;	Score 139;	DB 1;	Length 289;
Best Local Similarity	23.3%;	Pred. No. 6.6e-05;		
Matches	65;	Conservative 23;	Mismatches 107;	Indels 84; Gaps

  

QY	13	LCCLG--ALICALSLGRPTGGPGCGPGRLLLGTTGTARCC-----	50
		:           :	
Db	7	LCAIWGCLLTAVHLGCQV-----CSDKQYL-----HDQCDCDLCPGSRILTSHCTALEKTQ	58
QY	51	-----RVHTTRCCRDPG-----EECCSEWDMCMQPE-FHCGDPCCTT	88
Db	59	CHPCDSGEFSAQNREIRCHQRHCNPQGLRKYKKEGTAESDTVTCTCKEGQHCTSKDCEA	118
QY	89	C-RHHPCPPCQGVSOGKSFSGFCIDCASGFISGGHE--GHCKPMTDCTQGFLLTVFG	145
		:           :           :	
Db	119	CAOHTFCIPFGVMEMATEETDITVCHPCVPVGFSNOSSLFEKCYPMTCEDKNLEVLQKG	178
QY	146	NKTHNAVCPGSPPAEPGLWLTVVLLAVAACVULLTSAGLGLHIWLKR-----	194
		:           :           :	
Db	179	TSQTNVICGLKSR-----MRALLVIPVMGLIITIFGVFLYIKKKVKPKDNMLPPA	231
QY	195	-----TQLLEVP-----PSTEDARKSCQFPBEERS	222
		:           :           :	
Db	232	ARRQDPQMEDYPGHNTAAPVQVETLHGCGPVPTQEDGKES	270

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RESULT 9
TNRC_HUMAN TNRC_HUMAN STANDARD; PRT; 435 AA.
ID TNRC_HUMAN
AC P36941;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
DE 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
GN LTBR OR TNFCR OR TNFRSF3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93252381; PubMed=8486360;
RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT "Construction and evaluation of a hncDNA library of human 12p
RT transcribed sequences derived from a somatic cell hybrid.";
RL Genomics 16:214-218(1993).
RN [2]
RP FUNCTION.
RX MEDLINE=94225209; PubMed=8171323;
RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-beta-specific receptor.";
RL Science 264:707-710(1994).
CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> .	
CC	-----	
CC	EMBL; L04270; AAA36757.1; ..	
CC	HSSP; P25942; ICDF.	
DR	MIM; 600979; ..	
DR	InterPro; IPR001368; ..	
DR	Pfam; PF00020; TNFR_C6; 4.	
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.	
DR	PROSITE; PS00030; TNFR_NGFR_2; 3.	
KW	Receptor; Transmembrane; Glycoprotein; Repeat; Signal.	
FT	SIGNAL	1 30
FT	CHAIN	31 435
FT	DOMAIN	31 227
FT	TRANSMEM	228 248
FT	DOMAIN	249 435
FT	DOMAIN	42 211
FT	REPEAT	42 81
FT	REPEAT	82 124
FT	REPEAT	125 168
FT	REPEAT	169 211
FT	DISULFID	43 58
FT	DISULFID	59 72
FT	DISULFID	62 80
FT	DISULFID	83 98
FT	DISULFID	101 116
FT	DISULFID	104 124
FT	DISULFID	126 132
FT	DISULFID	139 148
FT	DISULFID	142 167
FT	DISULFID	170 185
FT	CARBOHYD	40 40
FT	CARBOHYD	177 177
FT	SEQUENCE	435 AA; 46709 MW; 624626E022F656F CRC64;
SO		







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QY 157 -----SPAE-----PLGW-----LTWLLAVAAACVLLLSAQ 184
Db 230 TPESTAPSTSFLLPMGSPAGSGDFALPGLVGVGTALGLLIIGVNCVIMT----- 285
QY 185 LGLHIWLRKTKQLLE-----VPPSTED-ARSCQFPPEE 217
Db 286 -----QVKKKPLCLQREAKVPHLPADKARGTQGPQQ 317

RESULT 7
CD40_BOVIN
ID CD40_BOVIN STANDARD; PRT; 269 AA.
AC Q28203;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).
GN TNFRSF5 OR CD40.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97281252; PubMed=9135560;
RA Hirano A., Brown W.C., Estes D.M.;
RT "Cloning, expression and biological function of the bovine CD40
RT homologue: role in B-lymphocyte growth and differentiation in
RT cattle."
RL Immunology 90:294-300(1997).
CC -|- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC -----
DR EMBL; U57745; AAC48710.1; -.
DR HSSP; P25942; ICDF.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
DR Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
KW SIGNAL.
FT SIGNAL.
FT CHAIN.
FT DOMAIN.
FT DOMAIN.
FT TRANSMEM.
FT DOMAIN.
FT DOMAIN.
FT REPEAT.
FT REPEAT.
FT REPEAT.
FT REPEAT.
FT REPEAT.
FT CARBOHYD.
FT CARBOHYD.
FT NON_TER.
SQ SEQUENCE 269 AA; 29983 MW; 746903F30F95F387 CRC64;
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Query Match
Best Local Similarity 10.4%; Score 139; DB 1; Length 269;
Matches 52; Conservative 17; Mismatches 82; Indels 36; Gaps 9;

QY 34 CGPGRLLTGTDARCCRVHTTRCCRDYDECCSEWD-----CMQVQPEFHCGDPCCT 87
Db 62 CGKGEFLSTWNRKYC---HEHYRCVNPNLGLRTQSEGLNTDTCVCEQ-HCTSHCE 117
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```
QY 88 TCRHHP-CPPECQVQSOGKSFQCIDCASGTSGGHEG--HCKPWTDCQFGFLTVEP 144
Db 118 SCTPHSLCLPGFGKQIATGLDVTCEPCPLGFGFFSNVSSAFKCHRWTSCKRGKLVQHV 177
QY 145 GNKTHNAV-----VPGSPPAEPLGLWLTWLLAVAAACVLLLSAQGLGLHWLR 193
Db 178 GTNKTDVVCGFQSRMRLVIVPVT-----MGVLFAVLL-VSACIRNITKKR-----QLR 225
QY 194 KTQLLE 200
Db 226 PCTLWLK 232

RESULT 8
CD40_MOUSE
ID CD40_MOUSE STANDARD; PRT; 289 AA.
AC P27512;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
GN TNFRSF5 OR CD40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92105763; PubMed=1370315;
RA Torres R.M., Clark E.A.;
RT "Differential increase of an alternatively polyadenylated mRNA
RT species of murine CD40 upon B lymphocyte activation."
RL J. Immunol. 148:620-626(1992).
RN [2]
RP REVISIONS.
RC STRAIN-BALB/C;
RA Torres R.M.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-BALB/C; TISSUE=Liver;
RX MEDLINE=93094586; PubMed=1281194;
RA Gimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.;
RA Howard M., Cockayne D.A.;
RT "Genomic structure and chromosomal mapping of the murine CD40 gene."
RL J. Immunol. 149:3921-3926(1992).
CC -|- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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CC -----
DR EMBL; M83312; AAB08705.1; -.
DR EMBL; M94126; AAA37404.1; -.
DR EMBL; M94129; AAA37404.1; JOINED.
DR EMBL; M94128; AAA37404.1; JOINED.
DR EMBL; M94127; AAA37404.1; JOINED.
DR PIR; A46476; A46476.
DR HSSP; P25942; ICDF.
DR MGD; MGI:88336; Tnfrsf5.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL.
FT CHAIN.
FT DOMAIN.
FT DOMAIN.
FT TRANSMEM.
FT DOMAIN.
FT DOMAIN.
FT REPEAT.
FT REPEAT.
FT REPEAT.
FT REPEAT.
FT REPEAT.
FT CARBOHYD.
FT CARBOHYD.
FT NON_TER.
SQ SEQUENCE 289 AA; 29983 MW; 746903F30F95F387 CRC64;
```

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RESULT 3
OX40_MOUSE
ID OX40_MOUSE STANDARD; PRT; 272 AA.
AC P47741;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).
GN TNFRSF4 OR TXGP1 OR OX40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=94044750; PubMed=8228223;
RA Calderhead D.M., Buhmann J.E., van den Eertwegh A.J.,
RA Claassen E., Noelle R.J., Fell H.;
RT "Cloning of mouse OX40: a T cell activation marker that may mediate
RT T-B cell interactions.";
RL J. Immunol. 151:5261-5271(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95255413; PubMed=7737295;
RA Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Barclay A.N.;
RT "Gene structure and chromosomal localization of the mouse homologue
RT of rat OX40 protein.";
RL Eur. J. Immunol. 25:926-930(1995).
CC -!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC -----
CC EMBL; Z21674; CAA79772.1; -
CC DR EMBL; X85214; CAA59476.1; -
CC DR HSP; P25942; ICDF.
CC DR MGD; MGI:104512; Tnfrsf4.
CC DR InterPro; IPR001368; -
CC DR PROSITE; PS00652; TNFR_NGFR_1; 3.
CC DR PROSITE; PS50050; TNFR_NGFR_2; 2.
CC KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
CC Signal.
FT SIGNAL 1 19
FT CHAIN 20 272
FT DOMAIN 20 211
FT TRANSMEM 212 236
FT DOMAIN 237 272
FT DOMAIN 26 165
FT REPEAT 26 61
FT REPEAT 62 103
FT REPEAT 104 124
FT REPEAT 125 165
FT CARBOHYD 144 144
FT CONFLICT 15 15
SQ SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;

Query Match 12.6%; Score 168.5; DB 1; Length 272;
Best Local Similarity 24.9%; Pred. No. 2.le-07;
Matches 60; Conservative 18; Mismatches 70; Indels 93; Gaps 11;
QY 39 LLLGTGTADAR--CCRVHT-----TRCCRD-YPG-----ECCSSEWDCMCVQPEFHCGDPC-- 85

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Db 14 LALTGLVTARRLNCVRYHTYPSGHKKCCRECPGHGMVSRCDHTRTDLC-----HPCET 65
QY 86 -----CTTCRHP-----CPPGGVQSOGCKFSFGFOCID 114
Db 66 GFYNEAVNYDTCKQCTQCNRHSSELKQNCPTPTQDTVCRRCRPGTQPDQSGYKLGVDVCP 125
QY 115 CASGTFSGGHEGCKPWTCTQFGFLTTFEGNKTHNAV----- 153
Db 126 CPPGHPSPGNQACKPWTNCTLSGKQTRHPASDSLDVAVCEDSRLLATLLWETQRTFRPT 185
QY 154 -----VPGSP--APPLGLWLTVLLAVACVLLLTSAQLGLHI-----WOLRK 194
Db 186 TVQSTTVWPTSELP-SPPTLVTPGPAFAVLGLGLGLLAPLTVLLALYLLRKAWRLPN 244
QY 195 T 195
Db 245 T 245

RESULT 4
OX40_HUMAN
ID OX40_HUMAN STANDARD; PRT; 277 AA.
AC P43489; Q13663;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY
DE ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).
GN TNFRSF4 OR TXGP1L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94170844; PubMed=7510240;
RA Latza U., Duerkop H., Schnittger S., Ringeling J., Eitelbach F.,
RA Hummel M., Fonatsch C., Stein H.;
RT "The human OX40 homolog: cDNA structure, expression and chromosomal
RT assignment of the ACT35 antigen.";
RL Eur. J. Immunol. 24:677-683(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95219871; PubMed=7704935;
RA Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A.,
RA Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.;
RT "Identification of OX40 ligand and preliminary characterization of
RT its activities on OX40 receptor.";
RL Circ. Shock 44:30-34(1994).
CC -!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD134 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd134.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X75962; CAA53576.1; -
CC DR EMBL; S76792; AAB33944.1; ALT_INIT.
CC DR HSP; P25942; ICDF.
CC DR MIM; 600315; -
CC DR InterPro; IPR001368; -
CC DR Pfam; PF00020; TNFR_c6; 3.
CC DR PROSITE; PS00652; TNFR_NGFR_1; 3.
CC DR PROSITE; PS50050; TNFR_NGFR_2; 2.
CC KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;

```

```
KW SIGNAL.
FT CHAIN 1 28 POTENTIAL.
FT CHAIN 29 277 OX40L RECEPTOR.
FT DOMAIN 29 214 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 215 235 POTENTIAL.
FT DOMAIN 236 277 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 30 169 4 X TNFR-CYS.
FT REPEAT 30 65 TNFR-CYS 1.
FT REPEAT 66 107 TNFR-CYS 2.
FT REPEAT 108 126 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 127 167 TNFR-CYS 4.
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 277 AA; 29340 MW; 49F15525941550BF CRC64;

Query Match 12.3%; Score 165; DB 1; Length 277;
Best Local Similarity 25.2%; Pred. No. 4.2e-07;
Matches 63; Conservative 18; Mismatches 113; Indels 56; Gaps 7;

QY 5 GANGAFRALCGLALLCALSLG-----QRTGPGGCGPGRLLLTGTGDARCCRVHT 54
   || || || || || || || || || || || || || || || || || || || ||
Db 4 GARRLGRGCAALLLLGLSTVGLHCVDGTPSNDRCHECR--PGNGMVSRCRSQN 61

QY 55 TRCRDYPG--ECCSBDWM--CQVPEFHGD---PCITTCRHHPCPPGQVQSGKFSF 108
   || || || || || || || || || || || || || || || || || || || ||
Db 62 TVCRPCPGFYNDVYVSKPKCTWCLNSGSRKQLCTATQDTCRCRAGTQPLDSYKP 121

QY 109 GFQICDCASGTFSGHGCHKPTDCTQFGFLTVFPGNKNHNAVCPGSPPAE----- 161
   || || || || || || || || || || || || || || || || || || || ||
Db 122 GVDCAPCPPGHFSGDNQACKPWTNCTLAKGHTLPASNSDAICEDRDPPATQPTQ 181

QY 162 -----PLGWLTVLLAAVACVLLLTSAQLGLHIWQLR 193
   || || || || || || || || || || || || || || || || || || || ||
Db 182 PPARPIVQTEAMPRTSQGSTPRVPEVPGGRAVAILGLGLVLGLLPLAILLALLR 241

QY 194 KTQOLLEVP 203
   || || || || || || || || || || || || || || || || || || || ||
Db 242 RDQRL-----PP 248

RESULT 5
OX40_RAT STANDARD; PRT; 271 AA.
AC P15725;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).
GN TNFRSF4 OR TXGPIL OR OX40.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=90214614; PubMed=2157591;
RA Mallett S., Fossum S., Barclay A.N.;
RT "Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes -- a molecule related to nerve growth factor receptor.";
RL EMBO J. 9:1063-1068(1990).
CC -!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
CC -!- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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or send an email to license@isb-sib.ch).
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CC EMBL; X17037; CAA34897.1; -.
CC PIR; S08036; S08036.
DR PIR; S12783; S12783.
DR HSP; P25942; ICDF.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00652; TNFR_NGFR_2; 2.
KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 271 OX40L RECEPTOR.
FT DOMAIN 20 210 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 211 235 POTENTIAL.
FT DOMAIN 236 271 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 164 4 X TNFR-CYS.
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 102 TNFR-CYS 2.
FT REPEAT 103 123 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 124 164 TNFR-CYS 4.
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 271 AA; 29895 MW; C06465136816821 CRC64;

Query Match 12.0%; Score 160.5; DB 1; Length 271;
Best Local Similarity 26.0%; Pred. No. 9.9e-07;
Matches 59; Conservative 18; Mismatches 79; Indels 71; Gaps 11;

QY 26 QRPFGGCGPGRLLG--TGTDAKCCRVHT-----RCCRD-YPGECCSBDW----- 71
   || || || || || || || || || || || || || || || || || || || ||
Db 6 QQPT-----AFLLLGLSLGTVKLNCKVDTPSGHKRCRCQPGHGMVSRCDTRDTV 58

QY 72 CMCVQPEFHCG---DPC--CTTCRHH-----PCPPGQVQSGKFSF 108
   || || || || || || || || || || || || || || || || || || || ||
Db 59 CHPCEPGFYNEAVNYDCKQCTQCNHRSSELKQNCQCTEDTVCCRCGTQPRQSSHL 118

QY 109 GFQICDCASGTFSGHGCHKPTDCTQFGFLTVFPGNKNHNAVCPGSPPAELGLWLT 168
   || || || || || || || || || || || || || || || || || || || ||
Db 119 GVDCAVCPGPHFSGDNQACKPWTNCTLAKGHTLPASNSDLTVCEDRS----- 167

QY 169 VLLAVACVLLLTSAQLGLHIWQLRKTOLL--LEVPPTEDARSQFP 214
   || || || || || || || || || || || || || || || || || || || ||
Db 168 -LLATL-----LWETQRTTFRPTTVPSTTTPWPTSQLP 199

RESULT 6
TNR2_HUMAN STANDARD; PRT; 461 AA.
ID TNR2_HUMAN
AC P20333;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 2) (TNFRII) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).
GN TNFRSF1B OR TNFR2 OR TNFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90260639; PubMed=2160731;
RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA Dower S.K., Cosman D., Goodwin R.G.;
RT "A receptor for tumor necrosis factor defines an unusual family of cellular and viral proteins.";
RL Science 248:1019-1023(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91045991; PubMed=2172983;
RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
```

GenCore version 4.5  
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OM protein - protein search; using sw model

Run on: September 4, 2001, 15:56:28 ; Search time 43.78 Seconds  
(without alignments)  
183.092 Million cell updates/sec

Title: US-09-512-363-2

Perfect score: 1340

Sequence: 1 MAQHGMGAPRALGLALLC.....EEERGSAREEKGRLGLWY 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	201.5	15.0	256	1 41BB_MOUSE	P20334 mus musculus
2	197	14.7	255	1 41BB_HUMAN	Q07011 homo sapien
3	168.5	12.6	272	1 41BB_MOUSE	P47741 mus musculus
4	165	12.3	277	1 0X40_HUMAN	P43489 homo sapien
5	160.5	12.0	271	1 0X40_RAT	P15725 rattus norv
6	141.5	10.6	461	1 TNR2_HUMAN	P20333 homo sapien
7	139	10.4	269	1 CD40_BOVIN	Q28203 bos taurus
8	139	10.4	289	1 CD40_MOUSE	P27512 mus musculus
9	134.5	10.0	435	1 TNRC_HUMAN	P36941 homo sapien
10	134.5	10.0	1801	1 LMB2_RAT	P15800 rattus norv
11	127.5	9.5	1799	1 LMB2_MOUSE	Q61292 mus musculus
12	126.5	9.4	277	1 CD40_HUMAN	P25942 homo sapien
13	123	9.2	415	1 TNRC_MOUSE	P50284 mus musculus
14	119	8.9	474	1 TNR2_MOUSE	P25119 mus musculus
15	115.5	8.6	1370	1 IGR_RAT	P24062 rattus norv
16	112	8.4	2318	1 NTC3_MOUSE	Q61982 mus musculus
17	111.5	8.3	1798	1 LMB2_HUMAN	P55268 homo sapien
18	110.5	8.2	2907	1 FBN2_MOUSE	Q61555 mus musculus
19	109.5	8.2	2531	1 NTC1_MOUSE	Q01705 mus musculus
20	109	8.1	3635	1 LMA5_MOUSE	Q61001 mus musculus
21	108.5	8.1	1373	1 IGR_MOUSE	Q60751 mus musculus
22	106.5	7.9	2911	1 FBN2_HUMAN	P35556 homo sapien
23	105	7.8	1172	1 TSP2_HUMAN	P35442 homo sapien
24	104.5	7.8	684	1 FBL1_CHICK	O73775 gallus gall
25	103.5	7.7	417	1 WSL1_HUMAN	Q93038 h wsl-1 pro
26	102.5	7.6	956	1 TSP3_MOUSE	Q05895 mus musculus
27	102.5	7.6	2871	1 FBN1_BOVIN	P98133 bos taurus
28	102	7.6	186	1 AGI3_WHEAT	P10969 triticum ae
29	102	7.6	787	1 ITB3_MOUSE	O54890 mus musculus
30	101.5	7.6	1367	1 IGR_HUMAN	P08069 homo sapien
31	101	7.5	4543	1 LRP1_CHICK	P98157 gallus gall
32	100.5	7.5	655	1 ITB5_PAPCY	Q07441 papio cynoc
33	100.5	7.5	2531	1 NTC1_RAT	Q07008 rattus norv

## ALIGNMENTS

RESULT	ID	41BB_MOUSE	STANDARD;	PRT;	256 AA.
1	41BB_MOUSE				
AC	P20334;				
DT	01-FEB-1991 (Rel. 17, Created)				
DT	01-FEB-1991 (Rel. 17, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB).				
GN	TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
[1]	SEQUENCE FROM N.A.				
RP	MEDLINE=89184547; PubMed=2784565;				
RX	Kwon B.S., Weissman S.M.;				
RA	"cDNA sequences of two inducible T-cell genes.;"				
RT	Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).				
RL	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BALB/C;				
RX	MEDLINE=94179805; PubMed=8130309;				
RA	Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;				
RT	"Genomic organization and chromosomal localization of the T-cell antigen 4-1BB.;"				
RL	J. Immunol. 152:2256-2262(1994).				
[3]					
RP	CHARACTERIZATION, AND SEQUENCE OF 25-29.				
RX	MEDLINE=93139510; PubMed=7678621;				
RA	Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T.,				
RT	Kwon B.S.;				
RT	"Inducible T cell antigen 4-1BB. Analysis of expression and function.;"				
RL	J. Immunol. 150:771-781(1993).				
CC	- - FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY				
CC	ACTIVE DURING T CELL ACTIVATION.				
CC	- - SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.				
CC	ASSOCIATES WITH P56-LCK.				
CC	- - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.				
CC	TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.				
CC	- - INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.				
CC	- - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
CC	EMBL; J04492; AAA0167.1; -				
DR	EMBL; U02567; AAA93113.1; -				
DR	PIR; B32393; B32393.				
DR	HSSP; P25942; 1CDF.				

34	100.5	7.5	2871	1	FBN1_HUMAN	P35555 homo sapien
35	100	7.5	213	1	AGI2_WHEAT	P02876 triticum ae
36	100	7.5	581	1	IRR_RAT	Q64716 rattus norv
37	100	7.5	1106	1	STC_DROME	P40798 drosophila
38	99.5	7.4	169	1	KRUA_HUMAN	P26371 homo sapien
39	99.5	7.4	227	1	AGI_ORYZA	P11219 oryza sativ
40	99.5	7.4	2569	1	LMA3_MOUSE	Q61789 mus musculu
41	99	7.4	4544	1	LRP1_HUMAN	Q07954 homo sapien
42	98.5	7.4	755	1	COMP_RAT	P35444 rattus norv
43	98.5	7.4	1408	1	SERR_DROME	P18168 drosophila
44	98.5	7.4	2139	1	CRB_DROME	P10040 drosophila
45	98	7.3	212	1	AGI_HORVU	P15312 hordeum vul





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68 rGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspProc 85
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235 AAAGAAGAGGTGCATATGTCACACCTGAGTACCACCTGTGGAGACCCCTC 284

85 ysCysThrThrCysArgHisHisProCysProProGlyGlnGlyValGln 101
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285 AGTCACAGATCTGCAAGCACTACCCCTGCCAACCCAGCCAGGGTGGAG 334

102 SerGlnGlyLysPheSerPheGlnCysIleAspCysAlaSerGln 118
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335 TCTCAAGGGGATATGTGTTGGCTTCGGTGTGTGCTGTGCCATGGG 384

118 yThrPheSerGlyHisGluGlyHisCysLysProTrpThrAspCyst 135
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435 CTCAGTTTGGATTCTCACCATTGTCCTGGGAACAAGACCCACAATGCT 484

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485 GTGTGCATCCCGAGGCCACTGCCCACTGAGCAATACGGCCATTGACTGT 534

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535 CATCTTCTGTCATGCTGCATGCTATTTCTTCTTAACCACAGTCCAGC 584

185 euGlyLeuHisIleTrpGlnLeuArgLys..... 194
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585 TCGGCTGCACATATGGCAGCTGAGGAGGCAACACATGTGTCCCGAGAG 634

195 ThrGlnLeuLeuLeuGluValProProSerThrGluAspAlaArgSerCy 211
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635 ACCAGCCATTTCGGGAGGTGCAGTTGTCAGTGAGGATGCTGCAGCTT 684

211 sGlnPheProGluGluArgGlyGluArgSerAlaGluGlyLysGlyA 228
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685 CCAGTTCCCTGAGGAGGAACCGGGGAGCAGACA...GAAGAAAGTGTG 731

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732 ATCTGGGGGTCTGGTGG 748
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70 rPaspCysMetCysValGlnProGluPheHisCysGlyAspProCysCys 86  
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104 .....GlyLysPheSerPheG 109  
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155 roGlySerProProAlaGluProLeuGlyTrpLeuThrValValLeu 171  
16604 CAGGGTCCCCCGGCGAGCGCTTGGGTGGCTGACCGTCTGCTCTCTG 16653  
172 AlaValAlaAlaCysValLeuLeuLeuThrSerAlaGlnLeuGlyLeuH1 188  
16654 GCCGTGGCGGCTGCTGCTCTCTCTGACCTCGGCCAGCTTGGACTGCA 16703  
188 sileTrpGlnLeuArg..... 193  
16704 CATCTGCAGCTGAGGAGTCAGTGCATGTGCCCCCGAGGTCTGTACACAGC 16753  
193 ..... 193  
16754 CTGCTGGGGAGGTGGGAGCATGGCTGCCCTGCTGACCGTGGCCCCCTG 16803  
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16804 CAGAGACCCAGCTGCTGCTGGAGGTGCGCGCTGACCGAAGAGCCGAGA 16853  
210 SerCysGlnPheProGluGluGluArgGlyGluArgSerAlaGluGlu 226  
16854 AGCTGCCAGTTCCCCGAGGAAGAGCGGGCGAGCGATCGGCAGAGGAGAA 16903  
226 sGlyArgLeuGlyAspLeuTrpVal 234  
16904 GGGCGGCTGGGAGACCTGTGGGTG 16928

seq\_name: gb\_pat1:A91704

seq\_documentation\_block:

LOCUS A91704 1020 bp DNA  
DEFINITION Sequence 1 from Patent WO9824895.  
ACCESSION A91704  
VERSION A91704.1 GI:6740652

PAT

22-JAN-2000





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LOCUS       AL390719      184184 bp      DNA      HTG              22-MAR-2001
DEFINITION  Homo sapiens chromosome 1 clone RP11-465B22, *** SEQUENCING IN
PROGRESS ***, 33 unordered pieces.
ACCESSION   AL390719
VERSION     AL390719.15  GI:13445418
KEYWORDS    HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MELAY.K.
Direct Submission
Submitted (21-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequests@sanger.ac.uk
On Mar 24, 2001 this sequence version replaced gi:13396610.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: bm465B22
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 3% of reads Chemistry:
Dye-terminator Big Dye; 96% of reads
Consensus quality: 172641 bases at least Q40
Consensus quality: 176408 bases at least Q30
Consensus quality: 178512 bases at least Q20
Insert size: 180984; sum-of-contigs
Quality coverage: 4.53x in Q20 bases; agarose-fp
Coverage: 4.07x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 5627: contig of 5627 bp in length
* 5628 5727: gap of 100 bp
* 5728 8009: contig of 2282 bp in length
* 8010 8109: gap of 100 bp
* 8110 11014: contig of 2905 bp in length
* 11015 11114: gap of 100 bp
* 11115 23404: contig of 12290 bp in length
* 23405 23504: gap of 100 bp
* 23505 26139: contig of 2635 bp in length
* 26140 26239: gap of 100 bp
* 26240 29766: contig of 3527 bp in length
* 29767 29866: gap of 100 bp
* 29867 33003: contig of 3136 bp in length
* 33003 33102: gap of 100 bp
* 33103 48262: contig of 15160 bp in length
* 48263 48362: gap of 100 bp
* 48363 52129: contig of 3767 bp in length
* 52130 52229: gap of 100 bp
* 52230 61454: contig of 9225 bp in length
* 61455 61554: gap of 100 bp
* 61555 63812: contig of 2258 bp in length
* 63813 63912: gap of 100 bp
* 63913 68103: contig of 4191 bp in length
* 68104 68203: gap of 100 bp
* 68204 73002: contig of 4799 bp in length
* 73003 73102: gap of 100 bp
* 73103 79538: contig of 6436 bp in length
* 79539 79638: gap of 100 bp
*
* 79539 83620: contig of 3982 bp in length
* 83621 83720: gap of 100 bp
* 83721 97596: contig of 13876 bp in length
* 97597 97696: gap of 100 bp
* 97697 104680: contig of 6984 bp in length
* 104681 104780: gap of 100 bp
* 104781 107164: contig of 2384 bp in length
* 107165 107264: gap of 100 bp
* 107265 113440: contig of 6176 bp in length
* 113441 113540: gap of 100 bp
* 113541 121563: contig of 8023 bp in length
* 121564 121663: gap of 100 bp
* 121664 124320: contig of 2657 bp in length
* 124321 124420: gap of 100 bp
* 124421 128583: contig of 4163 bp in length
* 128584 128683: gap of 100 bp
* 128684 131527: contig of 2844 bp in length
* 131528 131627: gap of 100 bp
* 131628 134673: contig of 3046 bp in length
* 134674 134773: gap of 100 bp
* 134774 139103: contig of 4330 bp in length
* 139104 139203: gap of 100 bp
* 139204 145549: contig of 6346 bp in length
* 145550 145649: gap of 100 bp
* 145650 148007: contig of 2358 bp in length
* 148008 148107: gap of 100 bp
* 148108 151671: contig of 3564 bp in length
* 151672 151771: gap of 100 bp
* 151772 157223: contig of 5452 bp in length
* 157224 157323: gap of 100 bp
* 157324 161601: contig of 4278 bp in length
* 161602 161701: gap of 100 bp
* 161702 170342: contig of 8641 bp in length
* 170343 170442: gap of 100 bp
* 170443 180911: contig of 10469 bp in length
* 180912 181011: gap of 100 bp
* 181012 184184: contig of 3173 bp in length.
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                        /clone="RP11-465B22"
                        /clone_lib="RPCI-11.2"
     misc_feature       1..5627
                        /note="assembly_fragment:02136"
                        fragment_chain:1
                        clone_end:T7
                        vector_side:left"
     misc_feature       5728..8009
                        /note="assembly_fragment:00136"
                        fragment_chain:1"
     misc_feature       8110..11014
                        /note="assembly_fragment:00300"
                        fragment_chain:1"
                        11115..23404
                        /note="assembly_fragment:02856"
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                        fragment_chain:2"
     misc_feature       26240..29766
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* 62419 68116: contig of 5698 bp in length
* 68117 68216: gap of 100 bp
* 68217 87865: contig of 19649 bp in length
* 87866 87965: gap of 100 bp
* 87966 95832: contig of 7867 bp in length
* 95833 95932: gap of 100 bp
* 95933 98546: contig of 2614 bp in length
* 98547 98646: gap of 100 bp
* 98647 104772: contig of 6126 bp in length
* 104773 104872: gap of 100 bp
* 104873 110195: contig of 5323 bp in length.

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## FEATURES

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## misc\_feature

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## misc\_feature

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## misc\_feature

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/note="assembly_fragment:00683"
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## misc\_feature

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/note="assembly_fragment:02210"
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## misc\_feature

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## misc\_feature

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## misc\_feature

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## misc\_feature

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## misc\_feature

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## misc\_feature

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## misc\_feature

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BASE COUNT 21407 a 33601 c 33207 g 20768 t 1212 others
ORIGIN

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## alignment\_scores:

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  Quality: 905.50      Length: 910
  Ratio: 3.870         Gaps: 7
  Percent Similarity: 25.714  Percent Identity: 25.385

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## alignment\_block:

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US-09-512-363-2 x AL162741/rev ..

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Align seg 1/1 to reverse of: AL162741 from: 1 to: 110195

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1 MetAlaGlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAl 17
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```

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16852 ATGGCACAGACACGGCGATGGCGGCTTCCGGCCCTGTGCGGCTGGC 16803

```

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17 aLeuLeuCysAlaIaLeuSerLeuGlnArgProThrGlyGlyProGlyC 34
|||||
16802 GCTCCTGTGCGCGCTCAGCCTGGGTGAGCGCCACCGGGGGTCCCGGT 16753

34 ySGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys 50
|||||
16752 CGGCGCCTGGCGGCTCCTGCTTGGGACGGGACGACGCGCGCTGTGTC 16703

51 ArgValHisThrThrArgCysCysArgAspTyr..... 61
|||||
16702 CGGTTTCACACAGACGCGCTGCTGCCGGGATTACCGGGGTAAGTAACCGC 16653

61 ..... 61

16652 GTTTACTTAACGGGACCGGCCAAGCGGTCCCGCGGAAGCGGGATGGGT 16603

61 ..... 61

16602 GGGCGCCCCCTTCCCGTGTCTCAGACCGCGCTTGTCTGAGTCTAAGGAGG 16553

61 ..... 61

16552 GTGGGCACAGACGCGCCAGCAGCGGGAGCCCTTCCGGAGGGAGGAGGATC 16503

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16502 CCAGAGGGAGGCGGAGGTGTGCCAGCTCCAGCCAGTGGCCCCCGCGGA 16453

61 ..... 61

16452 GCAGGGGTGAGCCAGGTGGGAGCGCCCTCAAGAGGGGTCTGGGGTCTGGA 16403

61 ..... 61

16402 GGTGGAGGACGGCTGTTCAGGTCTCTGCGGGCGGTCTGTAGCCCTTGG 16353

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61 ..... 61

16302 CTGCGCTGTCTGCTCTGACCTGCACCTGGGGATGAGGGTTTCAGCTG 16253

61 ..... 61

16252 ACAGGCTGTCTGAGAGGAAGCTGGCAGGGAAGTCAACCCAGAGCTTC 16203

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16102 TGAGGTTCGACGGGCTCCAGGGGACTGTGCACCTGTGGGGGCCACCC 16053

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15952 GGAGAAAGACAGACAGCTGGATAAACCCAGGGTCCAGACTCCAGCCAGGAG 15903

61 ..... 61

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15902 CCCTCTGCTCCTGGAGCCAACTGTGGGTGAGAACGACAAACCTCACTC 15853  
61 ..... 61  
15852 CCCTGGAGGGCCGAGGGAGGCCTGGGAGGAGGGGGCTCAGCCAGCT 15803  
62 .....Pro. GlyGluGluCysCysSerGluT 70  
15802 GCTGGGGGGCTGGGCTGTCTCTGCCCCAGGCGAGGAGTGTCTTCCGAGT 15753  
70 rPAspCysMetCysValGlnProGluPheHisCysGlyAspProCysCys 86  
15752 GGGACTGCATGTGTCTCAGCCTGAATTCCTGCGGAGACCTTGTCTGC 15703  
87 ThrThrCysArgHisHisProCysProGlyGlnGlyValGlnSer. G 103  
15702 ACGACCTGCCGGCACCACCTTGTCCCCAGGCCAGGGGGGTACAGTCCA 15653  
103 ln ..... 103  
15652 GGGTAAGTCCTGGAGTGCCTCTGGGAGTCCACACAGGCCAGGGGTTCCA 15603  
103 ..... 103  
15602 CTAGGGCCCGAGGACAGACTCGTGGGCACAGGTGTCCGGCGAGGACATGT 15553  
103 ..... 103  
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103 ..... 103  
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103 ..... 103  
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103 ..... 103  
15252 TCCTCTTAGCGGCTTGTTTACCTGACAGGAGAGGTACGGCTAGGGACATG 15203  
103 ..... 103  
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103 ..... 103  
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103 ..... 103  
15102 TGTTCCTCAACCTCTGTGTTCTACTGGGTCTGCTGGCTTCTGCCAACCT 15053  
103 ..... 103  
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15002 TCGGCACCTCCCCAGGTGCCCTCACTGGGCCCCACCCAGAGGCCCCAC 14953  
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103 ..... 103  
14852 CCCCTGCACTGGCCTGACGCCCTCTCTATCCATCCAGCAACTCCACCAG 14803  
104 .....GlyLysPheSerPheG 109  
14802 CCTCCCTCCCTCCCTCCCCACACCCACACAGGGAATTCAGTTTGG 14753  
109 lypheGlnCysIleAspCysAlaSerGlyThrPheSerGlyGlyHisGlu 125  
14752 GCTTCCAGTGATCGACTGTGCTCGGGAGCCTTCTCCGGGGGCCACGAA 14703  
126 GlyHisCysLysProTirPThrAsp ..... 133  
14702 GGCCTCAAAACCTTGGACAGAGTGAGTCTCTGGTGGGCCCTGCCGGTG 14653  
133 ..... 133  
14652 GCCGGTGTCCAGGCCACCTCTGAGGAAGGTCTCTCTCTGTCCCTTGC 14603  
133 ..... 133  
14602 CCCACAGACACGAGGCGAGCAGCGGGGGGTGATCGGAGGCCGTGCC 14553  
134 .....CysThrGlnPheG 138  
14552 GGGGCTGATAGGAGCGCGTCCATGTATCCAGCTGCACCCAGTTCCG 14503  
138 yPheLeuThrValPheProGlyAsnLysThrHisAsnAlaValCysValP 155  
14502 GTTTCCTCACTGTGTTCCCTGGGAACAAGACCCACAACGCTGTGTGCTCC 14453  
155 roGlySerProProAlaGluProLeuGlyTirPLeuThrValValLeuLeu 171  
14452 CAGGCTCCCGCGCGCAGAGCGCTTGGGTGGCTGACCGTCTCTCTCTG 14403  
172 AlaValAlaAlaCysValLeuLeuLeuThrSerAlaGlnLeuGlyLeuHi 188  
14402 GCGGTGGCGCGCTGCTCTCTCTGACCTCGGCCACGCTTGGACTGCA 14353  
188 sileTirPGLnLeuArg ..... 193  
14352 CATCTGGCAGCTGAGGAGTCACTGTCATGTGGCCCCGAGGTCTGTACAGC 14303  
193 ..... 193  
14302 CTGTGTGGGGAGGTGGAGCATGCTGCTGCTGACCGTGGCCCCCCTG 14253  
194 Lys...ThrGlnLeuLeuLeuGluValProProSerThrGluAspAlaArg 209  
14252 CAGAGCCCCAGCTGTCTGTGGAGGTGCCCGCTCGACCCAGAACGCCAGA 14203  
210 SerCysGlnPheProGluGluGluArgGlyGluArgSerAlaGluGluLy 226  
14202 AGCTCCAGTTCCCCGAGGAAGAGGGGGCGGCGCATCGCAGAGAGGAA 14153  
226 sglyArgLeuGlyAspLeuTirPVal 234  
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GenBank Accession Number AF229434"

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BASE COUNT 141 a 272 c 312 g 140 t

ORIGIN

## alignment\_scores:

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Quality: 948.50 Length: 234
Ratio: 5.579 Gaps: 1
Percent Similarity: 72.650 Percent Identity: 72.650
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## alignment\_block:

US-09-512-363-2 x AF241229 ..

Align seg 1/1 to: AF241229 from: 1 to: 865

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17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34
|||||
51 GCTGCTGTGGCGGCTACGCTGGGTCAGCGGCCACCGGGGGTCCCGGGT 100
|||||
34 ysGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys 50
|||||
101 CGCGCCCTGGCGGCTCTCTGCTGGACGGGAACGACGCGCGCTGCTGC 150
|||||
51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCy 67
|||||
151 CGGGTTCACACGACGCGCTGCTGCGCGGATACCGGGCGGAGAGTGCTG 200
|||||
67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspP 84
|||||
201 TTCGAGTGGGACATGCTGTGTCACGCCCTGAATCCACATCCGCGGAGACC 250
|||||
84 roCysCysThrThrCysArgHisProCysProGlyGlnGlyVal 100
|||||
251 CTGTGCTGACGACCTGCGCGGACCACTTGTCCCGCCAGCCAGCGGGGTA 300
|||||
101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSe 117
|||||
301 CAGTCCCAAGGGAAATTCAGTTTGGCTTCCAGTGTATCGACTGTGCTC 350
|||||
117 rGlyThrPheSerGlyGlyHisGluGlyHisCysLysProThrAspC 134
|||||
351 GGGGACCTTCTCCGGGGCCACGAGGCGCACTGCAAACTTGGACAGACT 400
|||||
134 ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150
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401 GCTG..... 404
|||||
151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167
|||||
404 ..... 404
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184 lnLeuGlyLeuHisIleTrpGlnLeuArgLysThrGlnLeuLeuGlu 200
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461 GCGGGCGAGCGATCGGCAGAGGAGAGGGCGGCTGGGAGACCTGTGGG 510
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234 al 234
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511 TG 512

seq_name: gb_htg20:AL162741

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DEFINITION Homo sapiens chromosome 1 clone RP5-902P8, *** SEQUENCING IN
PROGRESS ***, 13 unordered pieces.
ACCESSION AL162741
VERSION AL162741.11 GI:13273625
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 110195)
AUTHORS McIay, K.
TITLE Direct Submission
JOURNAL Submitted (04-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Mar 11, 2001 this sequence version replaced gi:13234857.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: dj902P8
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 23% of reads Chemistry:
Dye-terminator Big Dye; 76% of reads
Consensus quality: 106361 bases at least Q40
Consensus quality: 107393 bases at least Q30
Consensus quality: 108133 bases at least Q20
Insert size: 108995; sum-of-contigs
Insert size: 160089; 6.7% error; agarose-fp
Quality coverage: 6.79x in Q20 bases; sum-of-contigs Quality
coverage: 4.76x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 3573 3672: contig of 3572 bp in length
* 3573 3672: gap of 100 bp
* 7178 7277: contig of 3505 bp in length
* 7178 7277: gap of 100 bp
* 7278 11454: contig of 4177 bp in length
* 11455 11554: gap of 100 bp
* 11555 22201: contig of 10647 bp in length
* 22202 22301: gap of 100 bp
* 22302 35252: contig of 12951 bp in length
* 35253 35352: gap of 100 bp
* 35353 42069: contig of 6717 bp in length
* 42070 42169: gap of 100 bp
* 42170 62318: contig of 20149 bp in length
* 62319 62418: gap of 100 bp
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167 rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184  
 621 CCGTCGCTCCCTGGCGGTGGCGCGCTGCTCCTCCTGACCTCGGCCC 670  
 184 InLeuGlyLeuHisIleTrpGlnLeu.....Arg 193  
 671 ACCTTGGACTGCACATCTGGCAGCTGAGGAGTCAGTCATGTGGCCCCGA 720  
 194 LysThrGlnLeuLeuLeuGluValProProSerThrGluAspAlaArgSe 210  
 721 GAGACCCAGCTGCTGTGAGGTGGCGCGTCGACCGAAGAGCCGAGAAG 770  
 210 rCysGlnPheProGluGluGluArgGlyGluArgSerAlaGluGlySG 227  
 771 CTGCCAGTTCCCGAGGAAGAGCGGGCGGAGGATCGGCAGAGGAGAAG 820  
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seq\_name: gb\_pat2:AX074381

seq\_documentation\_block: 1008 bp DNA PAT 06-FEB-2001  
 LOCUS AX074381  
 DEFINITION Sequence 1 from Patent WO0103720.  
 ACCESSION AX074381  
 VERSION AX074381.1 GI:12710522  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 1 (bases 1 to 1008)  
 AUTHORS Williams, P.M. and Gerritsen, M.E.  
 TITLE Promotion or inhibition of angiogenesis and cardiovascularization  
 by tumor necrosis factor ligand/receptor homologs  
 JOURNAL Patent: WO 0103720-A 1 18-JAN-2001;  
 Genentech, Inc. (US)  
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 Location/Qualifiers  
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 ORIGIN

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 Ratio: 5.652 Gaps: 1  
 Percent Similarity: 97.095 Percent Identity: 96.680  
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 US-09-512-363-2 x AX074381 ..  
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 121 ATGGGCACACACGCGGCGATGGCGCGTTTCGGGCCCTGTGGCGCTGGC 170  
 17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34  
 171 GCTGTGTCGGGCTCAGCCTGGGTGACGGCCCGCCCGGGGTCCCGGGT 220  
 34 ysGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys 50  
 221 GCGGCCCTGGCGCCTCCTGCTGTGGACGGGAACGACGCGCGCTGCTGC 270  
 51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCy 67  
 271 CGGGTTACACACGCGCTGCTGCCGCGATTACCGGGCGGAGGAGTGCTG 320  
 67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAsp 84

321 TTCGAGTGGGACTGCATGTGTCCAGCCTGAATTCACATCGCGAGACC 370  
 84 roCysCysThrThrCysArgHisHisProCysProProGlyGlnGlyVal 100  
 371 CTTGCTGCACGACCTGCGCGCACCACTTGTCCCCAGGCGCGGGGTA 420  
 101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSe 117  
 421 CAGTCCACGGGAAATTCAGTTTGGCTTCCAGTGTATCGACTGTGCTC 470  
 117 rGlyThrPheSerGlyGlyHisGluGlyHisCysLysLysProThrThrAspC 134  
 471 GGGACCTTCTCCGGGGCCACGAGGCCACTGCAAACTTTGGACAGACT 520  
 134 ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150  
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 151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167  
 571 GCTGTGTGCTCCAGGTTCCCGCGCGCAGAGCGCTTGGTGGCTGAC 620  
 167 rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184  
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 DEFINITION Sequence 15 from Patent WO0105972.  
 ACCESSION AX077027  
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 REFERENCE  
 1 (bases 1 to 1008)  
 AUTHORS Ashkenazi, A.J., Baker, K.P., Fong, S., Goddard, A., Godowski, P.J.,  
 Gurney, A.L., Hillan, K.J., Mark, M.R., Marsters, S.A., Pitti, R.M.,  
 Tumas, D., Watanabe, C.K. and Wood, W.I.  
 TITLE Compositions and methods for the treatment of immune related  
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 JOURNAL Patent: WO 0105972-A 15 25-JAN-2001;  
 Genentech, Inc. (US)  
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VERSION AX074384.1 GI:12710524  
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ORGANISM Homo sapiens  
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1 (bases 1 to 951)  
AUTHORS Williams,P.M. and Gerritsen,M.E.  
TITLE Promotion or inhibition of angiogenesis and cardiovascularization  
by tumor necrosis factor ligand/receptor homologs  
JOURNAL Patent: WO 0103720-A 4 18-JAN-2001;  
Genentech, Inc. (US)  
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ACCESSION   AF125304
VERSION     AF125304.1  GI:4558502
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REFERENCE   1 (bases 1 to 726)
AUTHORS    Gurney,A.L., Masters,S.A., Huang,A., Pitti,R.M., Mark,M.,
            Baldwin,D.T., Gray,A.M., Dowd,P., Brush,J., Heldens,S., Schow,P.,
            Goddard,A.D., Wood,W.I., Baker,K.P., Godowski,P.J. and Ashkenazi,A.
            Identification of a new member of the tumor necrosis factor family
            and its receptor, a human ortholog of mouse GITR
            Curr. Biol. (1999) In press
REFERENCE   2 (bases 1 to 726)
AUTHORS    Gurney,A.L., Masters,S.A., Huang,A., Pitti,R.M., Mark,M.,
            Baldwin,D.T., Gray,A.M., Dowd,P., Brush,J., Heldens,S., Schow,P.,
            Goddard,A.D., Wood,W.I., Baker,K.P., Godowski,P.J. and Ashkenazi,A.
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VERSION     AR108738.1  GI:12824225
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ORGANISM    Unknown.
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AUTHORS    Gorman,D.M., Randall,T.D. and Zlotnik,A.
TITLE      Mammalian cell surface antigens; related reagents
JOURNAL    Patent: US 611090-A 3 29-AUG-2000;
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1008)  
AUTHORS Ashkenazi,A.J., Baker,K.P., Chan,B., Goddard,A., Godowski,P.J.,  
Gurney,A.L., Hebert,C., Henzel,W., Kabakoff,R.C., Shelton,D.L.,  
Tumas,D., Watanabe,C.K. and Wood,W.I.  
TITLE Compositions and methods for the treatment of immune related  
diseases  
JOURNAL Patent: WO 0073452-A 38 07-DEC-2000;  
Genentech, Inc. (US)  
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ACCESSION AX074382
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 (bases 1 to 723)
AUTHORS Williams,P.M. and Gerritsen,M.E.
TITLE Promotion or inhibition of angiogenesis and cardiovascularization
by tumor necrosis factor ligand/receptor homologs
JOURNAL Patent: WO 0103720-A 2 18-JAN-2001;
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117 rGlyThrPheSerGlyGlyHisGluGlyHisCysLysProThrAsp 134
|||||
351 GGGACCTTCTCCGGGGCCACGAGGCCACTGCAAACTTGGACAGACT 400
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134 ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150
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401 GCACCCAGTTCGGGTTCCTACTGTGTTCCCTGGGAACAAGACCCACAAC 450
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151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167
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451 GCTGTGTGCTGCCAGGCTCCCGCGCAGAGCGCTTGGGTGGCTGAC 500
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167 rValValLeuLeuAlaValAlaCysValLeuLeuLeuThrSerAlag 184
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501 CGTGTCTCTCGCGGTGGCGGCTGGTCTCTCTGACCTCGGCCCC 550
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184 lnLeuGlyLeuHisIleTrpGlnLeuArgLysThrGlnLeuLeuGlu 200
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551 AGCTTGGACTGCACATCTGGCAGCTGAGAGAGACCCACAGCTGCTGGAG 600
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201 ValProSerThrGluAspAlaArgSerCysGlnPheProGluGluG 217
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601 GTGCCGCGCTCGACCGAGAGAGCCAGAGCTGCCAGTTCCCGCGAGGAAGA 650
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217 uArgGlyGluArgSerAlaGluGluLysGlyArgLeuGlyAspLeuTrp 234
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651 CGGGGGCAGCGATCGGCAGAGAGAGGGGGCGCTGGGAGACCTGTGGG 700
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234 al 234
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701 TG 702

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Date: Sep 4, 2001 4:21 PM  
About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

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gb_pat2:AX074382	+ 1322.50	1584.38	5.2e-80	723	AX074382 Sequence 2 from Patent
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gb_pat1:AX055408	+ 1322.50	1582.28	6.8e-80	1008	AX055408 Sequence 38 from Patent
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gb_pat2:AX077027	+ 1322.50	1582.28	6.8e-80	1008	AX077027 Sequence 15 from Patent
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gb_btq2:AL162741	+ 905.50	1054.68	1.6e-50	110195	AL162741 Homo sapiens chromo
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gb_pat1:AF229432	+ 683.50	819.18	2.2e-37	1031	AF229432 Mus musculus GTR-B
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gb_pat1:AR003911	+ 182.50	222.02	0.0004	877	AB003911 Rabbit mRNA for OX40 R
gb_pat1:AR019521	+ 175.50	211.09	0.0016	1317	AR019521 Sequence 10 from paten
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gb_pat1:MM0X40	+ 168.50	205.26	0.0034	883	I21674 M.musculus OX40. 12/1993
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seq\_documentation\_block:  
LOCUS AF117297 705 bp mRNA PRI 09-MAR-1999  
DEFINITION Homo sapiens TNF receptor superfamily activation-inducible protein  
ACCESSION AF117297  
VERSION AF117297.1 GI:4378799  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 705)  
AUTHORS Kwon,B., Yu,K.Y., Ni,J., Yu,G.L., Jang,I.K., Kim,Y.J., Xing,L.,  
Liu,D., Wang,S.X. and Kwon,B.S.  
TITLE Identification of a novel activation-inducible protein of the tumor  
necrosis factor receptor superfamily and its ligand  
J. Biol. Chem. 274 (10), 6056-6061 (1999)  
REFERENCE 2 (bases 1 to 705)  
AUTHORS Kwon,B.S.  
TITLE Direct Submission  
J. Biol. Chem. 274 (10), 6056-6061 (1999)  
JOURNAL Submitted (30-DEC-1998) Micro. & Immunol., Indiana University, 635  
Barnhill Dr., Indianapolis, IN 46202, USA

FEATURES  
Location/Qualifiers  
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BASE COUNT 104 a 230 c 247 g 124 t  
ORIGIN

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Quality: 1340.00 Length: 234  
Ratio: 5.726 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

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US-09-512-363-2 x AF117297

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1 ATGCACAGACGCGGGGATGGGCGCTTTCGGGCCCTGTGCGCGCTGGC 50  
17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34  
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51 GCTGCTGTCGCGCTCAGCTGGGTGAGCGCCACCGGGGGTCCCGGGT 100  
34 ysGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys 50  
|||||  
101 GCGGCCCTGGCGCTCTCTGTTGGGACGGAGACGGCGCGCTGCTGTC 150

228 rgLeuGlyAspLeuTrpVal 234  
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702 GGCTGGGGAAACTGTGGGTG 721

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184 InLeuGlyLeuHisIleTrpGlnLeu.....Arg 193  
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 671 AGCTTGAGACTGCACATCTGCAGCTGAGGAGTCAGTGCATGTGGCCCGA 720  
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 194 LysThrGlnLeuLeuGluValProProSerThrGluAspAlaArgSe 210  
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 721 GAGACCCAGCTGCTGTGAGGTGCGCGCTGCACCGAAGACCCAGAG 770  
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 210 rCysGlnPheProGluGluGluArgGlyGluArgSerAlaGluGluLysG 227  
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 771 CTGCGCAGTTCCTCCGAGAGAGCGGGCGCGAGCATCGGCAGAGGAGAGG 820  
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 227 LysArgLeuGlyAspLeuTrpVal 234  
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seq\_documentation\_block:

ID AAA58588 standard; DNA; 813 BP.

XX AC AAA58588;

XX DT 20-OCT-2000 (first entry)

XX DE DNA encoding tumour necrosis factor receptor ztnfr10.

XX KW Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;  
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;  
 KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;  
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;  
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;  
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;  
 KW renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;  
 KW immune response; immunosuppression; graft rejection; joint pain;  
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;  
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;  
 KW renal artery stenosis; occlusion; cholesterol; renal emboli; ztnfr10;  
 KW PCR primer; ss.

XX OS Homo sapiens.

XX PN WO2000040716-A2.

XX PD 13-JUL-2000.

XX PF 07-JAN-2000; 2000WO-US00396.

XX PR 07-JAN-1999; 99US-0226533.

XX PA (ZYMO ) ZYMOGENETICS INC.

XX PI Gross JA, Xu W, Madden K, Yee DP;

XX DR WPI; 2000-452538/39.

XX PT Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,  
 PT renal disease, graft versus host disease, and inflammation, comprises  
 PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide -  
 XX Example 10; Page 169; 175pp; English.

CC The present sequence encodes tumour necrosis factor receptor  
 CC ztnfr10. The specification describes extracellular domains of  
 CC BR43x2 (an isoform of the transmembrane activator and CAML-interactor  
 CC (TACI) receptor), TACI or BCMA (a related B cell protein). These contain  
 CC a cysteine rich domain, and are used for inhibiting ztnf4 activity. They  
 CC may also be used for inhibiting BR43x2, TACI or BCMA receptor-ligand  
 CC engagement associated with activated or resting B lymphocytes, effector  
 CC T-cells, or with antibody production. The antibody production is  
 CC associated with an autoimmune disease selected from systemic lupus  
 CC erythematosus, myasthenia gravis, multiple sclerosis and rheumatoid

CC arthritis. The ztnf4 activity and BR43x2, TACI or BCMA receptor-ligand  
 CC engagement is associated with asthma, bronchitis, emphysema, and stage  
 CC renal failure, glomerulonephritis, vasculitis, nephritis, pyelonephritis,  
 CC renal neoplasms, multiple myelomas, lymphomas, light chain neuropathy,  
 CC amyloidosis, moderating immune response, immunosuppression, graft  
 CC rejection, graft versus host disease, inflammation, insulin dependent  
 CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or  
 CC septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,  
 CC agonists or antagonists can be used to treat hypertension, renal artery  
 CC stenosis, or occlusion, and cholesterol or renal emboli.  
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SQ Sequence 813 BP; 114 A; 276 C; 283 G; 140 T; 0 other;

alignment\_scores:

Quality: 1317.50 Length: 240

Ratio: 5.655 Gaps: 1

Percent Similarity: 97.083 Percent Identity: 96.667

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US-09-512-363-2 x AAA58588

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 102 GCCCTGGGGCGCTCTGCTGGGAGCGGAGCGCGCGCTGCTGCCGG 151  
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52 ValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCys 68  
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 152 GTTCACAGCAGCGCTGCTGCCGGATACCCGGCGGAGGAGTCTGTC 201  
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68 rGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspProc 85  
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 202 CGAGTGGGACTGCATGTGTCTCCAGCCTGAATTCACCTGCGGAGACCTT 251  
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85 yCysThrThrCysArgHisProCysProProGlyGlnGlyValGln 101  
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 252 GCTGCACGACTGCCGGCACACACCTTGTCCCCAGGCCAGGGGGTACAG 301  
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102 SerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSerG 118  
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 302 TCCAGGGGAAATTCAGTTTGGCTTCCAGTGTATCGACTGTGCTCGGG 351  
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118 yThrPheSerGlyGlyHisGluGlyHisCysLysProThrThrAspCys 135  
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135 hrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsnAla 151  
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152 ValCysValProGlySerProAlaGluProLeuGlyTrpLeuThrVa 168  
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168 lValLeuLeuAlaValAlaLacCysValLeuLeuLeuThrSerAlaGlnL 185  
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seq\_name: /SDS8/gcdata/geneseq/geneseq/NA2000.DAT:AAZ49948

seq\_documentation\_block:

ID AAZ49948 standard; cDNA; 763 BP.

XX AC AAZ49948;

DT 18-MAY-2000 (first entry)

DE Human molecule associated with cell proliferation, MACP-5 cDNA.

XX Human: molecule associated with cell proliferation; MACP-5;

XX Incyte clone 2809903; antiarteriosclerotic; hepatotropic; cytostatic;  
 KW anti-inflammatory; antipruritic; anti-HIV; antiasthmatic; anaemia;  
 KW dermatological; antidiabetic; nephrotropic; antithyroid; thyromimetic;  
 KW immunosuppressive; osteopathic; antiarthritic; uropathic; antileuker;  
 KW ophthalmological; diagnosis; treatment; prevention; immune disorder;  
 KW cell proliferative disorder; actinic keratosis; arteriosclerosis;  
 KW atherosclerosis; bursitis; hepatitis; Crohn's disease; amyloidosis; ss.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

XX CDS 17..724

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FT /product= "MACP-5"

FT misc\_feature 1..763

FT /\*tag= b

FT /label= MACP-5 cDNA

FT /note= "This sequence is described as 764 bases long

FT in the Sequence Listing but a sequence of only 763 bases

FT is shown"

XX W0200005374-A2.

XX PD 03-FEB-2000.

XX PF 21-JUL-1999; 99WO-US16637.

XX PR 22-JUL-1998; 98US-0093827.

XX PA (INCY-) INCYTE PHARM INC.

XX PI Tang YT, Lal P, Hillman JL, Corley NC, Patterson C, Baughn MR;

XX WPI; 2000-182699/16.

XX DR P-PSDB; AAY44825.

XX PT Polypeptides and polynucleotides useful for treating and detecting cell

XX proliferation disorders e.g. actinic keratosis, and immune disorders

XX e.g. Crohn's disease

XX Claim 7; Page 67; 67pp; English.

XX The present sequence is a cDNA encoding molecule associated with cell

XX proliferation, MACP-5 from Incyte clone 2809903 isolated from TLYMN0706

XX cDNA library. This sequence is expressed in cardiovascular and

XX haematopoietic/immune tissues. MACP shows antiarteriosclerotic, anti-HIV,

XX hepatotropic, antiinflammatory, antipruritic, cytostatic, antiasthmatic,

XX dermatological, antidiabetic, nephrotropic, antithyroid, thyromimetic,

XX immunosuppressive, osteopathic, antiarthritic, uropathic, antileuker,

XX and ophthalmological activities. The present sequence is useful in the

CC diagnosis, treatment and prevention of cell proliferative disorders e.g.  
 CC actinic keratosis, arteriosclerosis, bursitis and  
 CC hepatitis, and immune disorders e.g. Crohn's disease, amyloidosis and  
 CC anaemia.

XX  
 SQ Sequence 763 BP; 114 A; 252 C; 264 G; 133 T; 0 other;

alignment\_scores:

Quality: 1310.50 Length: 240

Ratio: 5.649 Gaps: 1

Percent Similarity: 96.667 Percent Identity: 96.250

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US-09-512-363-2 x AAZ49948 ..

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 18 uLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyCysG 35  
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 52 GCTGTGGCGGCTCAGCTGGGTGACGCGCCCGGCGGTCCGGGTGCG 101  
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 35 lyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysArg 51  
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 102 GCCTTGGGCGCTCTCTGCTTGGGACGGAACGACGCGCGCTGCTCGCG 151  
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 202 CCAGTGGGACTCATGTGTCTCAGCTTCAATTCACCTCGGAGACCCCT 251  
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 85 yCysThrThrCysArgHisHisProCysProGlyGlnGlyValGln 101  
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XX WO200073452-A2.  
XX 07-DEC-2000.  
XX 02-JUN-2000; 2000WO-US15264.  
XX 02-JUN-1999; 99WO-US12252.  
XX 20-JUL-1999; 99US-0144732.  
XX 20-JUL-1999; 99US-0144758.  
XX 28-JUL-1999; 99US-0146222.  
XX 01-SEP-1999; 99WO-US20111.  
XX 15-SEP-1999; 99WO-US21090.  
XX 15-SEP-1999; 99WO-US21547.  
XX 29-OCT-1999; 99US-0162506.  
XX 30-NOV-1999; 99WO-US28313.  
XX 01-DEC-1999; 99WO-US28634.  
XX 09-DEC-1999; 99US-0170262.  
XX 20-DEC-1999; 99WO-US30911.  
XX 05-JAN-2000; 2000WO-US00219.  
XX 06-JAN-2000; 2000WO-US00376.  
XX 11-FEB-2000; 2000WO-US03565.  
XX 18-FEB-2000; 2000WO-US04341.  
XX 18-FEB-2000; 2000WO-US04342.  
XX 22-FEB-2000; 2000WO-US04414.  
XX 24-FEB-2000; 2000WO-US04914.  
XX 15-MAR-2000; 2000WO-US06884.  
XX 20-MAR-2000; 2000WO-US07377.  
XX 21-MAR-2000; 2000WO-US07532.  
XX 30-MAR-2000; 2000WO-US08439.  
XX 17-MAY-2000; 2000WO-US13705.  
XX 22-MAY-2000; 2000WO-US14042.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;  
PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;  
PI Wood WI;

XX WPI: 2001-025253/03.  
XX P-PSDB; AAB50910.

XX Thirty three nucleic acids encoding PRO polypeptides which are useful  
PI in the diagnosis and treatment of immune related disorders, e.g.  
PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
PT thyroiditis and diabetes mellitus -

XX Claim 48; Fig 17; 218pp; English.

XX The present sequence is one of thirty three nucleic acids encoding PRO  
CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and  
CC antagonists are useful for treating and diagnosing immune related  
CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
CC anemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central  
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic  
CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases  
CC (such as infectious, autoimmune chronic active hepatitis, primary  
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
CC food hypersensitivity and urticaria), immunological diseases of the  
CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
CC and hypersensitivity pneumonitis), transplantation associated diseases  
CC including graft rejection and graft-versus-host diseases.

XX Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;

alignment\_scores:  
Quality: 1322.50 Length: 241  
Ratio: 5.652 Gaps: 1  
Percent Similarity: 97.095 Percent Identity: 96.680  
alignment\_block:  
US-09-512-363-2 x AAC91469 ..  
Align seg 1/1 to: AAC91469 from: 1 to: 1008  
1 MetAlaGlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAl 17  
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17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34  
171 GCTGCTGTGGCGCTCAGCCTGGGTTCAGCGCCCAACCGGGGTCCCGGT 220  
34 yGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys 50  
221 CGGCGCTGGCGCTCTGCTGGGAGGGAACGGACCGCGCTGCTGC 270  
51 ArgValHisThrArgCysCysArgAspTyrProGlyGluGluCysCy 67  
271 CGGTTTACACAGCAGCGCTGCTGCCGGATTACCGGGCGAGGAGTGTCTG 320  
67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspP 84  
321 TTCCGAGTGGGACTGCATGTGTCTCCAGCCTGAATTCACATTCGGAGACC 370  
84 rOCysCysThrThrCysArgHisProCysProProGlyGlnGlyVal 100  
371 CTTCTGCACAGCTGCCGGCCACCCCTTGTCCCGAGCGAGGGGTA 420  
101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSe 117  
421 CAGTCCCGAGGGAAATTCAGTTTGGCTTCCAGTGTATCGACTGTGCCTC 470  
117 rGlyThrPheSerGlyGlyHisGlyGlyHisCysLysProTrpThrAspC 134  
471 GGGACCTTCTCCGGGGCCACGAAGGCCACTTGAACCTTTGGACAGACT 520  
134 yStrGlnPheGlyPheLeuThrValPheProGlyAspLysThrHisAsn 150  
521 GCACCAAGTTCGGGTTCCTACTGTGTTCCTGGGAACACACCCCAAC 570  
151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167  
571 GCTGTGTGCTGCCAGGGTCCCCCGCGCAGAGCGCTTGGTGGCTGAC 620  
167 rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184  
621 CGTGTCTCTCTGGCGCTGGCGGCTGGCTCTCTCTGACCTCGGCC 670  
184 lnLeuGlyLeuHisIleTrpGlnLeu.....Arg 193  
671 AGCTTGAGCTGCACATCTGGCAGCTGAGGAGTCAAGTGTGGCCCCGA 720  
194 LysThrGlnLeuLeuGluValProProSerThrGluAspAlaArgSe 210  
721 GAGACCCAGCTGCTGCTGGAGTGGCGGCTCGACCGAAGACCGCAGAG 770  
210 rCysGlnPheProGluGluGluArgGlyGluArgSerAlaGluGlySG 227  
771 CTGCCAGTCTCCCGCAGGAAGCGGGCGAGCGATCGCAGAGGAGGAGG 820  
227 lyArgLeuGlyAspLeuTrpVal 234  
821 GCGCGCTGGGAGACTGTGGGTG 843

seq\_name: /STDS8/gcgdata/geneseq/NA2001.DAT:AAC97479

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seq_documentation_block:
ID AAC97479 standard; cDNA; 1008 BP.
AC
XX AAC97479;
CC
XX
XX
XX 28-FEB-2001 (first entry)
XX
XX Human angiogenesis-associated protein PRO364 cDNA, SEQ ID NO:141.
XX
XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
KW gene therapy; transgenic animal; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200053753-A2.
XX
XX 14-SEP-2000.
XX
XX 05-JAN-2000; 2000WO-US00219.
XX
XX 08-MAR-1999; 99WO-US05028.
XX 12-MAR-1999; 99US-0123957.
XX 14-MAY-1999; 99US-0134287.
XX 02-JUN-1999; 99WO-US12252.
XX 23-JUN-1999; 99US-0141037.
XX 20-JUL-1999; 99US-0144758.
XX 26-JUL-1999; 99US-0145698.
XX 01-SEP-1999; 99WO-US20111.
XX 08-SEP-1999; 99WO-US20594.
XX 15-SEP-1999; 99WO-US21090.
XX 15-SEP-1999; 99WO-US21547.
XX 05-OCT-1999; 99WO-US23089.
XX 30-NOV-1999; 99WO-US28313.
XX 02-NOV-1999; 99WO-US28409.
XX 02-DEC-1999; 99WO-US28564.
XX 02-DEC-1999; 99WO-US28565.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
XX Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
XX Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
XX
XX WPI; 2001-090793/10.
XX P-PSDB; AAB53090.
XX
XX
XX New isolated nucleic acid for producing a PRO polypeptide, analyzing
XX genetic disorders and treating cardiovascular, endothelial or
XX angiogenic disorders, such as atherosclerosis, wounds or cancer -
XX Claim 58; Fig 53; 293pp; English.
XX
XX The invention relates to novel human angiogenesis-associated proteins
XX designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
XX PRO proteins. The invention also relates to vectors and host cells
XX comprising a PRO nucleic acid, the recombinant production of a PRO
XX protein, PRO antibodies specific for a PRO protein, fusion proteins
XX comprising a PRO protein, agonists or antagonists of a PRO protein, and
XX compounds which inhibit the expression of a PRO gene. The invention
XX additionally encompasses methods of identifying modulators of PRO
XX expression or activity; diagnosing a cardiovascular, endothelial or
XX angiogenic disorder, or a susceptibility to such a disorder by detecting
XX mutations in a PRO gene, or the expression level of a PRO gene within a
XX particular tissue; treating a cardiovascular, endothelial or angiogenic
XX disorder via the administration of a PRO protein, PRO nucleic acid, or
XX PRO agonist or antagonist; a retroviral gene therapy vector comprising a
XX PRO nucleic acid; and methods of inhibiting or stimulating endothelial

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CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
CC administration of a PRO protein, or an agonist or antagonist thereof.
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
CC agonists and PRO antagonists may be used as therapeutic agents to treat
CC cardiovascular, endothelial or angiogenic disorders, such as
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
CC disease, or stroke. PRO nucleic acids are additionally useful in the
CC recombinant production of PRO proteins, as hybridisation probes to
CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in
CC gene therapy. PRO nucleic acids can also be used to produce transgenic
CC animals useful for the development and screening of potential
CC therapeutic agents. The present sequence represents a cDNA encoding a PRO
CC protein of the invention.
XX
XX Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;
SQ

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alignment_scores:
Quality: 1322.50      Length: 241
Ratio: 5.652          Gaps: 1
Percent Similarity: 97.095 Percent Identity: 96.680

alignment_block:
US-09-512-363-2 x AAC97479 ..

Align seg 1/1 to: AAC97479 from: 1 to: 1008

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17 aleuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34
171 GCTGCTGTGGCGCTCAGCTGGTCAAGCCCGCCACCGGGGGTCCGGGT 220
34 ysGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys 50
221 GCGGCCCTGGGCGCTCTCTGCTTGGGACGGGAACGACGCGCGCTGCTGC 270
51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCy 67
271 CGGGTTCACACGACGCGCTGTGCGCGATTACCGGGCGGAGAGTGTGTG 320
67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAsp 84
321 TTCGAGTGGGACTGCATGTGTCCAGCTTCCAGCTGATCCAGTGTGCTC 370
84 roCysCysThrThrCysArgHisHisProCysProGlyGlnGlyVal 100
371 CTTGTGTCACGACCTTCGGCGCACACCTTGTCCCCAGCCAGGGGGTA 420
101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSe 117
421 CAGTCCACAGGGGAATTTCAGTTTGGCTTCCAGTGTATCCAGTGTGCTC 470
117 rGlyThrPheSerGlyGlyHisGluGlyHisCysLysProTrpThrAspC 134
471 GGGGACCTTCCTCCGGGGGCCACGAAGGCCACTGCAAACTTGGACAGACT 520
134 ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150
521 GCACCCAGTTCGGGTTCCTCACTGTGTTCCCTGGGAACAAGACCACAAAC 570
151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167
571 GCTGTGTGCTCCCGAGGTTCCTCCCGCGGAGAGCGCTTGGGTGGCTGAC 620
167 rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184
621 CGTGTCTCTCTGGCGGTGGCGCTGGTCTCTCTCTCTCTCTCTCTCTCTC 670

```

PR 20-JUL-1999; 99US-0144758.  
 PA (GETH ) GENENTECH INC.  
 XX Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;  
 XX Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK;  
 XX Wood WI;  
 XX WPI; 2001-103149/11.  
 DR P-PSDB; AAB20115.  
 XX  
 XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
 PT diagnosing and treating immune-related disorders, such as multiple  
 PT sclerosis, rheumatoid arthritis and diabetes -  
 XX  
 XX Claim 21; Fig 15; 127pp; English.  
 PS  
 CC The present sequence is that of cDNA clone DNA47365-1206 (ATCC 209436)  
 CC encoding novel human immunomodulator protein PRO364 (UNQ319) (see  
 CC AAB20115). The clone was isolated from a small intestine library.  
 CC The predicted protein (26 kDa, pI 6.34) shows homology to mouse  
 CC GTR protein and may be its human counterpart. The invention  
 CC provides polynucleotides (see AAF30050-62) encoding novel human PRO  
 CC proteins (see AAB20108-20) including PRO364. Claimed compositions  
 CC comprising these proteins or their agonists are useful for increasing  
 CC infiltration of inflammatory cells into a tissue of a mammal,  
 CC stimulating or enhancing an immune response in a mammal, or  
 CC increasing the proliferation of T-lymphocytes in a mammal in response  
 CC to an antigen. Claimed compositions comprising the PRO polypeptide  
 CC or its antagonist have the opposite effect. A claimed method for  
 CC treating an immune related disorder, such as a T cell disorder,  
 CC involves administering the PRO polypeptide, an agonist antibody or  
 CC an antagonist antibody. The disorder is selected from systemic  
 CC lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 CC juvenile chronic arthritis, spondyloarthritis, systemic  
 CC sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome,  
 CC systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia,  
 CC autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinated diseases (such as  
 CC multiple sclerosis), autoimmune chronic active hepatitis, primary  
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
 CC inflammatory bowel disease (ulcerative colitis and Crohn's disease),  
 CC gluten-sensitive enteropathy, Whipple's disease, (auto)immune-mediated  
 CC skin diseases (such as bullous skin disease, erythema multiforme and  
 CC psoriasis), allergic diseases (such as asthma, allergic rhinitis,  
 CC atopic dermatitis, food hypersensitivity and urticaria), immunologic  
 CC diseases of the lung and transplantation associated diseases (such  
 CC as graft rejection and graft-versus-host disease) (all claimed).  
 CC Claimed methods of diagnosing these disorders comprise detecting  
 CC the level of expression of the PRO gene. Also claimed are a method  
 CC of identifying a compound capable of inhibiting the expression or  
 CC activity of the PRO polypeptide, vectors, host cells, antibodies  
 CC and a method of stimulating the proliferation of T-lymphocytes  
 CC using PRO364.  
 XX  
 SQ Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;

alignment\_scores:  
 Quality: 1322.50 Length: 241  
 Ratio: 5.652 Gaps: 1  
 Percent Similarity: 97.095 Percent Identity: 96.680

alignment\_block:  
 US-09-512-363-2 x AAF30057 ..

Align seg 1/1 to: AAF30057 from: 1 to: 1008

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171 GCTGCTGTGCGCGCTCAGCCTGGGTGAGCGCCACCACCGGGGTCCCCGGT 220  
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 167 rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184  
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seq\_documentation\_block:  
 ID AAC90566 standard; cDNA; 1008 BP.

XX AAC90566;

XX 21-MAR-2001 (first entry)

XX Human PRO364 cDNA.

XX Human PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive;  
 KW vasotropic; antirheumatic; antiarthritic; antioflammatory; cytostatic;  
 KW vulnerary; antianginal; gene therapy; cardiovascular disease;  
 KW endothelial disorder; angiogenic disorder; cancer; periodontal disease;  
 XX wound healing; ss.  
 XX Homo sapiens.

XX WO200073445-A2.  
 XX 07-DEC-2000.  
 XX 17-MAY-2000; 2000WO-US13705.  
 XX 02-JUN-1999; 99WO-US12252.  
 XX 23-JUN-1999; 99US-0141037.  
 XX 20-JUL-1999; 99US-0144758.  
 XX 26-JUL-1999; 99US-0145698.  
 XX 28-JUL-1999; 99US-0146222.  
 XX 01-SEP-1999; 99WO-US20111.  
 XX 30-NOV-1999; 99WO-US28313.  
 XX 30-NOV-1999; 99WO-US28409.  
 XX 16-DEC-1999; 99WO-US28565.  
 XX 16-DEC-1999; 99WO-US30095.  
 XX 11-FEB-2000; 2000WO-US03565.  
 XX 18-FEB-2000; 2000WO-US04341.  
 XX 18-FEB-2000; 2000WO-US04342.  
 XX 24-FEB-2000; 2000WO-US05004.  
 XX 02-MAR-2000; 2000WO-US05841.  
 XX 10-MAR-2000; 2000WO-US06319.  
 XX 15-MAR-2000; 2000WO-US06884.  
 XX 21-MAR-2000; 2000WO-US07532.  
 XX 30-MAR-2000; 2000WO-US08439.  
 XX (GETH ) GENENTECH INC.  
 XX PA Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
 XX PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;  
 XX PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
 XX DR WPI: 2001-025251/03.  
 XX DR P-PSDB; AAB50954.  
 XX PT Seventeen nucleic acids encoding PRO polypeptides which are useful in  
 XX PT diagnosis and treatment of cardiovascular, endothelial or angiogenic  
 XX PT disorders in a mammal -  
 XX PS Claim 60; Fig 7; 182pp; English.  
 XX CC The present sequence is one of seventeen nucleic acids encoding PRO  
 XX CC polypeptides. The PRO nucleic acids, polypeptides, agonists and  
 XX CC antagonists are useful for treating cardiovascular, endothelial or  
 XX CC angiogenic disorders in a mammal. Examples of these disorders include  
 XX CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,  
 XX CC atherosclerosis, hypertension, arterial restenosis, Reynaud's disease,  
 XX CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis  
 XX CC and lymphangitis. The PRO polypeptides and antagonists are also used to  
 XX CC prevent tumour angiogenesis and for treating periodontal diseases. They  
 XX CC are also used to stimulate wound healing and tissue regeneration.  
 XX CC The PRO nucleic acids, polypeptides and anti-PRO antibodies are useful  
 XX CC for diagnosing a cardiovascular, endothelial or angiogenic disorder.  
 XX SQ Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;

## alignment\_scores:

Quality: 1322.50 Length: 241  
 Ratio: 5.652 Gaps: 1  
 Percent Similarity: 97.095 Percent Identity: 96.680

## alignment\_block:

US-09-512-363-2 x AAC90566 ..

Align seg 1/1 to: AAC90566 from: 1 to: 1008

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 17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34

171 GCTGCTGTGCGCGCTCAGCCTGGGTACGCCCCCACCGGGGGTCCCGGGT 220  
 34 ysglyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys 50  
 221 CGCGCCCTGGGCGCTCTGCTTGGGACGGAACGACGCGCGCTGCTGC 270  
 51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCy 67  
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 67 sserGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAsp 84  
 321 TTCGAGTGGGACTCATGTGTCCAGCCTGAATTCACCTGCGGAGACC 370  
 84 roCysCysThrThrCysArgHisHisProCysProProGlyGlnGlyVal 100  
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seq\_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2001.DAT:AAC91469

## seq\_documentation\_block:

ID AAC91469 standard; cDNA; 1008 BP.

XX AAC91469;

XX 21-MAR-2001 (first entry)

XX Human PRO364 cDNA.

XX Human; PRO; antiinflammatory; dermatological; antiarthritic;

KW antirheumatic; cardiac; antianaemic; immunosuppressive; antithyroid;  
 KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;

KW anti allergic; antiasthmatic; immune related disorder;

KW hepatobiliary disease; autoimmune disease; allergy; ss.

XX Homo sapiens.

PA (GETH ) GENENTECH INC.

PI Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;

XX WPI; 2000-412325/35.

DR P-PSDB; AAY71467.

XX New composition useful for inhibiting neoplastic cell growth and for  
PT treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or  
PT their antagonists

XX Claim 20; Fig 3; 108pp; English.

XX The present sequence is the cDNA clone, designated as DNA7365-1206,  
CC encoding the human PRO364 polypeptide. It is isolated from human small  
CC intestine tissue cDNA library, identified using probes based on the  
CC consensus sequence DNA44825, relative to the Incyte expressed sequence  
CC tag (EST) 3003460. This EST has homology to tumour necrosis factor  
CC receptor (TNFR) family of polypeptides. PRO364 sequence also shows  
CC homology to members of the TNFR family and mouse GITR protein.  
CC This clone is assigned the ATCC deposit No: 209436. PRO364 functions as  
CC a neoplastic cell growth inhibitor and is used for treating tumours,  
CC using an effective amount of PRO655, PRO364 and PRO344. This composition  
CC is especially useful for treatment of human cancers such as breast,  
CC prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.

XX Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;

alignment\_scores:

Quality: 1322.50 Length: 241  
Ratio: 5.652 Gaps: 1  
Percent Similarity: 97.095 Percent Identity: 96.680

alignment\_block:

US-09-512-363-2 x AAD01240 ..

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121 ATGGCACACACAGGGCGATGGCGCGCTTTCGGCCCTGTGGCGCTCGC 170  
17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34  
171 GCTGCTGTGCGGCTCAGCGTGGGTGAGCGCCACCGGGGGTCCGGGT 220  
34 ysGlyProGlyArgLeuLeuGlyThrGlyThrAspAlaArgCysCys 50  
221 GCGGCCCTGGGCGCTCCCTGCTGGGACGGGAACGCGCGCGCTGCTGC 270  
51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysC 67  
271 CGGGTTCACACAGCGCGCTGCTGCCCGGATACCCGGGGAGAGTGCTG 320  
67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAsp 84  
321 TTCGAGTGGGACTGCATGTGTGTCAGCCTGAATTCACCTCGCGAGACC 370  
84 roCysCysThrThrCysArgHisHisProCysProProGlyGlnGlyVal 100  
371 CTTGCTGCACGACCTCCCGGACACACCTTGTCCCGCAGCGCCAGGGGTA 420  
101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSe 117  
421 CAGTCCCGGGGAAATTCAGTTTGTGCTTCCAGTGATCGACTGTGCTC 470  
117 rGlyThrPheSerGlyHisGluGlyHisCysLysProTrpThrAspC 134  
471 GGGGACCTTCTCGGGGGCCAGGAAGCCACTGCACAACTTGGACAGACT 520  
134 ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150  
|||||

521 GCACCCAGTTCCGGTTTCTCACTGTTCCTGGGAACAACACCCACAC 570  
151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167  
|||||  
571 GCTGTGTGCTGCCAGGGTCCCGCGCGCAGAGCGCTTGGTGGCTGAC 620  
167 rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184  
|||||  
621 CGTGTCTCTCTGCGCTGGCGCTGCTGCTCTCTCTGCTGCTGCTGCGCC 670  
184 lnLeuGlyLeuHisIleTrpGlnLeu.....Arg 193  
|||||  
671 AGCTTGACGTCACATCTGGCAGCTGAGGAGTCAGTGCATCTGCCCGCA 720  
194 LysThrGlnLeuLeuGluValProProSerThrGluAspAlaArgSe 210  
:|||||  
721 GAGACCCAGCTGCTGCTGGAGTCCCGCTCGACCGAAGACGCCAGAAG 770  
210 rCysGlnPheProGluGluArgGlyGluArgSerAlaGluGluLysG 227  
|||||  
771 CTGCGAGTCCCGGAGGAAGCGGGCGGCGAGCGATCGCGAGAGGAGAG 820  
227 lyArgLeuGlyAspLeuTrpVal 234  
|||||  
821 GCGGCTGGGAGACCTGTGGGTG 843

seq\_name: /SIDS8/gcgdata/geneseq/geneseq/NA2001.DAT:AAC85433

seq\_documentation\_block:

ID AAC85433 standard; cDNA; 1008 BP.

XX AAC85433;

XX 08-MAY-2001 (first entry)

DE Clone DNA7365-1206 containing native PRO364 cDNA.

XX PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;  
KW hGTR; ligand; hGTR; PRO175; tumor necrosis factor receptor; TNFR;  
KW human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;  
KW myocardial infarction; PGF-2alpha; trauma; cancer; angiogenesis;  
KW age-related macular degeneration; antibody; periodontal disease;  
KW vascular-related drug targeting; atherosclerosis; hypertension;  
KW inflammatory vasculitides; Reynaud's disease; aneurysm;  
KW arterial restenosis; thrombophlebitis; tumor angiogenesis;  
KW lung; liver; fibrosis; neuropathy; rheumatoid arthritis; as.

OS Chimeric - Homo sapiens.

OS Chimeric - Synthetic.

XX Key Location/Qualifiers

FT CDS 121..846

FT /tag= a

FT /product= "PRO364"

FT /note= "Human cDNA fragment nucleotides 121..843"

FT primer\_bind 498..518

FT /tag= b

FT /bound\_moiety= "47365.tm.f"

FT primer\_bind 524..550

FT /tag= c

FT /bound\_moiety= "47365.tm.p"

FT /note= "probe binding site"

FT complement (555..575)

FT /tag= d

FT /bound\_moiety= "47365.tm.r"

XX WO200103720-A2.

XX 18-JAN-2001.

XX 11-JUL-2000; 2000WO-US18867.

XX 12-JUL-1999; 99US-0143304.

XX PR

XX (GETH ) GENENTECH INC.

XX PI Williams PM, Gerritsen ME;

XX WPI: 2001-138257/14.

XX P-PSDB; AAB47054.

XX Composition for diagnosing and treating cardiovascular, endothelial and  
XX angiogenic disorders, comprises a PRO364 or PRO175 polypeptide -

XX Example 1; Fig 1; 76pp; English.

XX This sequence encodes a PRO364 polypeptide, which is a human gluco-  
XX corticoid-induced tumor necrosis factor receptor (hGTR). The  
XX corresponding ligand (hGTR), PRO175, is given in AAB47056.  
XX PRO364 and PRO175 may be used in a mixture with a cardiovascular,  
XX endothelial, angiogenic or angiostatic agent for the treatment of a  
XX cardiovascular, endothelial, angiogenic or angiostatic disorder. The  
XX PRO364 sequence was isolated from an expressed sequence tag (EST)  
XX database as having homology to members of the tumour necrosis factor  
XX receptor (TNFR) family of polypeptides. The PRO175 cDNA sequence was  
XX isolated from a library of cDNA fragments derived from human umbilical  
XX vein endothelial cells (HUVEC). Administering an effective amount of  
XX PRO364 or PRO175 or their antagonists is useful for treating cardiac  
XX hypertrophy (which is initiated by myocardial infarction and  
XX characterized by the presence of an elevated level of PGF<sub>2</sub>alpha),  
XX trauma, a cancer, or age-related macular degeneration in a human.  
XX Administering a therapeutically effective amount of an antibody that  
XX binds PRO364 or PRO175 is useful for inhibiting angiogenesis induced  
XX by PRO364 or PRO175 in a human suffering from a tumor or a retinal  
XX disorder. PRO364 or PRO175, or their antagonists, are useful for  
XX vascular-related drug targeting or as therapeutic targets for the  
XX treatment or prevention of atherosclerosis, hypertension, inflammatory  
XX vasculitides, Reynaud's disease, aneurysms, arterial stenosis,  
XX thrombophlebitis, tumor angiogenesis, gut protection or regeneration  
XX and treatment of lung or liver fibrosis, periodontal diseases,  
XX attraction of bone-forming cells, central and peripheral nervous  
XX system disease and neuropathies and rheumatoid arthritis.

SQ Sequence 1008 BP; 148 A; 336 C; 353 G; 171 T; 0 other;

#### alignment\_scores:

Quality: 1322.50 Length: 241  
Ratio: 5.652 Gaps: 1  
Percent Similarity: 97.095 Percent Identity: 96.680

#### alignment\_block:

US-09-512-363-2 x AAC85433 ..

Align seg 1/1 to: AAC85433 from: 1 to: 1008

1 MetAlaGlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAl 17  
121 ATGGACACAGCAGCGGGCGATGGGCGCTTTGCGGCGCTGTGCGGCGCTGGC 170  
17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyProGlyC 34  
171 GCTGCTGTGGCGCTACGCTGGGTGACGCCGCCACCGGGGTCCCGGGT 220  
34 ySgLeuProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys 50  
221 CGGCGCTGGGCGCTCTGCTTGGGACGGAGACGACGCGCGCTGTGTC 270  
51 ArgValHisThrArgCysCysArgAspTyrProGlyGluGluCysCy 67  
271 CGGCTTCACACGACGCGCTGTGCGCGGATTACCGGCGCGAGATGCTG 320  
67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAsp 84  
321 TTCGAGTGGAGCTGCATGTGTGCCAGCTGAATCCACTGCGGAGACC 370

84 rOCysCysThrThrCysArgHisHisProCysProProGlyGlnGlyVal 100  
371 CTTGTGTGACAGCACTGCCGCGCACCACTTGTCCCCAGGCGAGGGGTA 420  
101 GlnSerGlnGlyLysSerPheGlnCysIleAspCysAla 117  
421 CAGTCCACAGGGGAAATTCAGTTTGGCTTCCAGTGTATCGACTGTGCTC 470  
117 rGlyThrPheSerGlyGlyHisGluGlyHisCysLysProThrThrAsp 134  
471 GGGGACCTTCCTCCGGGGCCACGAGAGCCACTGCCAACCTTGGACACT 520  
134 ySThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150  
521 GCACCCAGTTCGGGTTCTCACTGTGTTCCTCCCTGGGAACAAGACCCACA 570  
151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167  
571 GCTGTGTGCTGCCCTCCAGGGTCCCGCGCGGAGAGCCGCTTGGGTGGCTG 620  
167 rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAla 184  
621 CGTGTCTCTCTGGCGGCGGCGCTGCTGCTCTCTCTGACTCGGCCCC 670  
184 InLeuGlyLeuHisIleTrpGlnLeu.....Arg 193  
671 AGCTGGGACTGCACATCTGGCAGCTGAGGAGTCAGTGCATGTGGCCCCGA 720  
194 LysThrGlnLeuLeuLeuGluValProProSerThrGluAspAlaArgSe 210  
721 GAGACCCAGCTGCTGCTGGAGTGGCGCGCTGACCCGAAAGACCCAGAG 770  
210 rCysGlnPheProGluGluGluArgGlyGluArgSerAlaGluGlyLys 227  
771 CTGCGAGTTCCTCCGAGGAGAGCGGGGCGGCGAGCATCGGACGAGGAG 820  
227 lyArgLeuGlyAspLeuTrpVal 234  
821 GCGGCTGGGAGACCTGTGGGTG 843

seq\_name: /SDS8/gcgdata/geneseq/geneseq/NA2001.DAT:AAF30057

#### seq\_documentation\_block:

ID AAF30057 standard; cDNA; 1008 BP.

AC AAF30057;

DT 30-APR-2001 (first entry)

XX Human cDNA encoding PRO364.

XX PRO364; UNQ319; human; immune disease; autoimmune disease;  
XX antirheumatic; antiarthritic; antiinflammatory; antianaemic;  
XX immunosuppressive; antithyroid; antidiabetic; neuroprotective;  
XX hepatotropic; virucide; dermatological; antipsoriatic;  
XX antiasthmatic; antiallergic; immunostimulant; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 121..846

XX sig\_peptide /\*tag= a

XX mat\_peptide /\*tag= b

XX 196..843

XX /\*tag= c

XX WO200105972-A1.

XX 25-JAN-2001.

XX 15-MAR-2000; 2000WO-US06884.

XX

PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;  
 XX WPI; 2000-572271/53.  
 DR P-PSDB; AAB33431.  
 XX  
 XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
 XX  
 XX Claim 23; Fig 35; 309pp; English.  
 XX  
 CC The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are  
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, autoimmune vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
 CC autoimmune or immune-mediated skin diseases, allergic diseases,  
 CC immunological diseases of the lung, and transplantation associated  
 CC diseases including graft rejection and graft-versus-host-disease.  
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.  
 XX  
 SQ Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;

## alignment\_scores:

Quality: 1322.50 Length: 241  
 Ratio: 5.652 Gaps: 1  
 Percent Similarity: 97.095 Percent Identity: 96.680

## alignment\_block:

US-09-512-363-2 x AAC58596 ..

Align seg 1/1 to: AAC58596 from: 1 to: 1008

1 MetAlaGlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAl 17  
 121 ATGGCACACACGGGCGGATGGCGCGCTTTCGGGCGCTGTGGCGGCTGGC 170  
 17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34  
 171 GCTGCTGTGGCGCTCAGCTGGGTGAGCGCCACCGGGGGTCCGGGT 220  
 34 yGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys 50  
 221 GCGGCGCTGGGCGCTCTCTGCTTGGGACGGGAACGGACGCGCGCTGCTG 270  
 51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGlyCysC 67  
 271 CCGGTTCACACGACGCGCTGCTGCTGGCGCGATTACCGGGGAGAGTGCTG 320  
 67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAsp 84  
 321 TTCGAGTGGGACTGATGTGTCTCAGCGCTGAATTCACCTGGCGAGACC 370  
 84 rOCysCysThrThrCysArgHisHisProCysProGlyGlnGlyVal 100  
 371 CTTCGTGCACGACCTGCCGACACACCTTGTCCCGACGAGCGGGGTA 420  
 101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlase 117  
 421 CAGTCCCGAGGGAAATTCAGTTTGTGGCTTCCAGTGTATCGACTGTGCTC 470  
 117 rGlyThrPheSerGlyGlyHisGluGlyHisCysLysCysLysProTrpThrAspC 134

471 GGGGACCTTCTCCGGGGGCCACGAAGGCCACTGCAAACTTGGACAGACT 520  
 134 ySThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150  
 521 GCACCCAGTTCGGGTTTCTCACTGTGTTCCCTGGGAACAAGACCCACAAC 570  
 151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167  
 571 GCTGTGCTGCCAGGGTCCCGCGGCGAGCGCTTGGGTGGCTGAC 620  
 167 rValValLeuLeuAlaValAlaCysValLeuLeuLeuLeuThrSerAlaG 184  
 621 CGTCTCTCTCTGCGCGGCGCTGCTGCTCTCTCTGACCTCGGCCC 670  
 184 lnLeuGlyLeuHisIleTrpGlnLeu.....Arg 193  
 671 AGCTTGGACTGCACATCTGGCAGCTGAGGAGTCAGTGCATGTGGCCCCGA 720  
 194 LysThrGlnLeuLeuGluValProProSerThrGluAspAlaArgSe 210  
 721 GAGACCCAGCTGCTGTGGAGGTGCCGCGCTGACCGGAGACGCCAGAAG 770  
 210 rCysGlnPheProGluGluArgGlyGluArgSerAlaGluGlyLysG 227  
 771 CTGCCAGTTCCTCCGAGGAAGAGCGGGGCGAGCGATCGGCAGAGGAGAAG 820  
 227 lyArgLeuGlyAspLeuTrpVal 234  
 821 GCGGCTGGGAGACCTGTGGGTG 843

seq\_name: /SIDS8/gcgdata/geneseq/geneseq/NA2000.DAT:AAA77604

## seq\_documentation\_block:

ID AAA77604 standard; cDNA; 1008 BP.

XX AAA77604;  
 XX  
 XX 07-NOV-2000 (first entry)  
 XX  
 DE Human PRO364 cDNA sequence SEQ ID NO:116.  
 KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
 KW cytotstatic; gene therapy; vaccine; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200032221-A2.  
 XX  
 PD 08-JUN-2000.  
 XX  
 PF 30-NOV-1999; 99WO-US28313.  
 XX  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 16-DEC-1998; 98US-0112850.  
 PR 12-JAN-1999; 99US-0115554.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 28-APR-1999; 99US-0131445.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-OCT-1999; 99US-0162506.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;

XX Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;

XX Watanabe CK, Williams PM, Wood WT;

XX WPI; 2000-412154/35.

XX P-PSDB; AAB24409.

XX Nucleic acids encoding PRO polypeptides useful for preventing,

XX diagnosing and treating disorders in mammals

XX angiogenic disorders in mammals

XX Claim 61; Fig 43; 315pp; English.

XX The present invention describes nucleic acids encoding PRO polypeptides

XX useful for preventing, diagnosing and treating disorders in mammals

XX cardiovascular, endothelial or angiogenic disorder in mammals by

XX modulating cell proliferation, angiogenesis and cardiovascularisation,

XX and for identifying agonists and antagonists of these processes. The

XX nucleic acids and the proteins they encode may be used in the

XX prevention, treatment and diagnosis of diseases associated with

XX inappropriate PRO expression such as cardiovascular, endothelial or

XX angiogenic disorders in mammals (e.g. atherosclerosis, cancers and

XX cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors

XX containing them and the PRO polypeptide may be used to treat disorders

XX associated with decreased PRO expression. AAA77510 to AAA77721 and

XX AAB24388 to AAB24435 represent nucleotide and protein sequences used in

XX the exemplification of the present invention.

XX

SQ Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;

alignment\_scores:

Quality: 1322.50 Length: 241

Ratio: 5.632 Gaps: 1

Percent Similarity: 97.095 Percent Identity: 96.680

alignment\_block:

US-09-512-363-2 x AAA77604 ..

Align seg 1/1 to: AAA77604 from: 1 to: 1008

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17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyProGlyC 34

171 GCTGCTGTGGCGCTCAGCCYGGGTCAAGCCGCCACCGGGGGTCCCGGGT 220

34 ysGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys 50

221 CGCGCCCTGGCGGCTCTCTGTTGGAGGGAACGGACGCGCGCTGCTGCG 270

51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCy 67

271 CGGTTTCACAGCAGCGCTGTGCGCGGATTACCGCGCGAGGAGTGCTG 320

67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAsp 84

321 TTCGAGTGGGACTGCATGTGTCCAGCCCTGAATTCACCTGCGGAGACC 370

84 roCysCysThrThrCysArgHisProCysProProGlyGlnGlyVal 100

371 CTGCTGCACACCTGCGGCGCACCCCTTGTCCCGCCAGCGGGGTA 420

101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaase 117

421 CAGTCCAGGGGAATTCAGTTTGGCTTCCAGTGTATCGACTGTCCTC 470

117 rGlyThrPheSerGlyGlyHisGluGlyHisCysLysProThrThrAspC 134

471 GGGGACCTTCTCCGGGGCCACGAGGCCACTGCAACCTTGGACAGACT 520

134 ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150

521 GCACCCAGTTCGGGTTTCTCACTGTGTTCCTCGTGGGAACAAGACCCACAC 570

151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167

571 GCTGTGTCGTCCTCCAGGTCCCGCGGAGAGCGCTTGGGTGGCTGAC 620

167 rValValLeuLeuAlaValAlaAlaCysValLeuLeuThrSerAlaG 184

621 CGTCTCTCTCTGCGCGTGGCGCTGCTCTCTCTCTCTCTCTCTCTCT 670

184 InLeuGlyLeuHisIleTrpGlnLeu.....Arg 193

671 AGCTTGGACTGCACATCTGGCAGCTGAGGAGTCACTGTCATGTGGCCCGA 720

194 LysThrGlnLeuLeuGluValProProSerThrGluAspAlaArgSe 210

721 GAGACCCAGCTGCTGCTGGAGGTGCGCGCTGCGACCGAAGACCCAGAG 770

210 rCysGlnPheProGluGluArgGlyGlyGluArgSerAlaGluGluLysG 227

771 CTGCGAGTTCCTCCGAGGAGAGCGGGGCGGCGATCGCGAGAGGAGAGG 820

227 lyArgLeuGlyAspLeuTrpVal 234

821 GCGCGCTGGAGACCTGTGGTG 843

seq\_name: /SDS8/gcgdata/geneseq/geneseq/NA2000.DAT: AAD01240

seq\_documentation\_block:

ID AAD01240 standard; cDNA; 1008 BP.

XX AAD01240;

XX DT 08-NOV-2000 (first entry)

XX Human PRO364 protein encoding cDNA clone, DNA47365-1206.

XX PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;

XX neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;

XX breast; prostate; colon; lung; renal; ovarian; central nervous system;

XX CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue;

XX tumour necrosis factor receptor; GTR protein homologue; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 121..846

XX /\*tag= a

XX /product= "Human PRO364 protein"

XX /note= "Derived from clone DNA47365-1206"

XX 121..195

XX sig\_peptide

XX /\*tag= b

XX 196..843

XX mat\_peptide

XX /\*tag= c

XX /product= "Mature human PRO364 protein"

XX WO200032778-A2.

XX PN 08-JUN-2000.

XX PD 30-NOV-1999; 99WO-US28409.

XX PF 01-DEC-1998; 98WO-US25108.

XX PR 16-DEC-1998; 98US-0112850.

XX PR 22-DEC-1998; 98US-0113296.

XX PR 20-JUL-1999; 99US-0144758.

XX PR 26-JUL-1999; 99US-0145698.

XX



CC responses in mammalian cells (claimed).

XX Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;

alignment\_scores:  
Quality: 1322.50 Length: 241  
Ratio: 5.652 Gaps: 1  
Percent Similarity: 97.095 Percent Identity: 96.680

alignment\_block:  
US-09-512-363-2 x AAX87670 ..

Align seg 1/1 to: AAX87670 from: 1 to: 1008

1 MetAlaGlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAl 17  
121 ATGGCACACACGGGCGATGGCGGCTTTCGGGCCCTGTGGCGCTGGC 170

17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34  
171 GCTGCTGTGGCGCTCAGCTGGGTGAGCGCCACCGGGGTCCCGGT 220

34 yGlyProGlyArgLeuLeuGlyThrGlyThrAspAlaArgCysCys 50  
221 GCGGCCCTGGGCGCTCTCTGTGGACGGGAACGACGCGCTGCTGC 270

51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysC 67  
271 CGGGTTCACACGCGCTGTGTCGCCGATTACCCGGGCGAGGAGTGTG 320

67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAsp 84  
321 TTCGAGTGGGACTGATGTGTCCAGCCTGAATTCACCTGGGAGACC 370

84 rCysCysThrThrCysArgHisHisProCysProProGlyGlnGlyVal 100  
371 CTTGTGTGACGACCTCCCGGCGACACCTTGTCCCGCAGCGCGGGA 420

101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAla 117  
421 CAGTCCCGAGGAAATCAGTTTTTGTGCTTCCAGTGTATCGACTGCTC 470

117 rGlyThrPheSerGlyHisGlyHisCysLysProTrpThrAspC 134  
471 GGGGACCTTCTCGGGGGCCACGAGCCACTGCAAACTTGGACAGACT 520

134 yThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150  
521 GCACCCAGTTCGGGTTCTCACTGTGTTCCCTGGGAACAAGACCCACAC 570

151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167  
571 GTGTGTGCTGCCAGGGTCCCGCGGAGAGCCGCTTGGGTGGCTGAC 620

167 rValValLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184  
621 CGTGTCTCTCTGGCGCTGGCGGCTGCTGCTCTCTCTCTGACCTCGGCC 670

184 lNeuGlyLeuHisIleTrpGlnLeu.....Arg 193  
671 AGCTTGACTGCACATCTGGCAGCTGAGGAGTCAAGTGTGTGGCCCGCA 720

194 LysThrGlnLeuLeuGluValProProSerThrGluAspAlaArgSe 210  
721 GAGACCCAGCTGTGTGAGGTGCGCGCTGACCGAAGACCCGCAAG 770

210 rCysGlnPheProGluGluAlaArgGlyGluArgSerAlaGluLysG 227  
771 CTGCCAGTTCCTCCGAGAGAGCGGGGCGAGCGATCGGCAGAGGAAG 820

227 lYArgLeuGlyAspLeuTrpVal 234  
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821 GCGCGCTGGGAGACCTGTGGTG 843

seq\_name: /SID8/gcgdata/geneseq/geneseq/NA2000.DAT:AAA99903

seq\_documentation\_block:  
ID AAA99903 standard; cDNA; 1008 BP.  
XX  
AC AAA99903;  
XX  
DT 26-JAN-2001 (first entry)  
XX  
DE cDNA encoding human protein PRO364.  
XX  
KW Cardiovascular; endothelial; angiogenic disorder; PRO179;  
KW PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333;  
KW PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;  
XX gene therapy; ss.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 121..844  
FT /\*tag= a  
XX  
PN WO200053757-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 24-FEB-2000; 2000WO-US05004.  
XX  
PR 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 02-JUN-1999; 99WO-US12252.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28565.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
PI Goddard A, Gurney AL, Hillan KJ, Marsters SA, Paoni NF, Pittl RM;  
PI Watanabe CK, Williams PM, Wood WJ;  
XX  
XX WPI: 2000-611444/58.  
XX P-PSDB; AAB27651.  
XX  
XX Novel PRO polypeptides and agonists and antagonists of them, used to  
PT diagnose and treat cardiovascular, endothelial and angiogenic disorders  
PT  
XX  
XX Claim 60; Fig 5; 181pp; English.  
XX  
XX The present invention relates to methods for stimulating or inhibiting  
CC angiogenesis and cardiovascularization. The methods involve the use of  
CC pharmaceutical compositions based on the following proteins, PRO179,  
CC PRO238, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333,  
CC PRO840, PRO877, PRO878, PRO879, PRO882, PRO885 or PRO887. These  
CC proteins were identified by isolating cDNA clones encoding secreted  
CC proteins. The proteins of the invention may be used to diagnose and  
CC treat cardiovascular, endothelial or angiogenic disorders. The present  
CC sequence is a cDNA clone encoding one of the proteins of the invention.  
XX  
XX Sequence 1008 BP; 148 A; 335 C; 354 G; 171 T; 0 other;  
SQ

alignment\_scores:  
Quality: 1322.50 Length: 241

Ratio: 5.652 Gaps: 1  
Percent Similarity: 97.095 Percent Identity: 96.680  
alignment\_block:  
US-09-512-363-2 x AAA99903 ..  
Align seg 1/1 to: AAA99903 from: 1 to: 1008  
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17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyProGlyC 34  
171 GCTGCTGTGCGCTCAGCTTGGTTCAGCGGCCACCGGGGTCGCGGT 220  
34 ysGlyProGlyArgLeuLeuGlyThrGlyThrAspAlaArgCysCys 50  
221 CGGGCCCTGGGCGCTCTGCTTGGACGGGAACGACGCGCTGCTGTC 270  
51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGlyCysC 67  
271 CGGTTTCACACGACGCGCTGTGCGCGATTACCGGCGGAGGAGTGCTG 320  
67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAsp 84  
321 TTCGGAGTGGGACTGCATGTGTGTCAGCTGAATTCACCTCGGAGACC 370  
84 roCysCysThrThrCysArgHisHisProCysProProGlyGlnGlyVal 100  
371 CTGCTGTCACACCTGGCGGACCACTTGTCCCGCAGGCGAGGGGTA 420  
101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSe 117  
421 CAGTCCACAGGGGAATTCAGTTTGGCTTCAGTGTATCGACTGCGCTC 470  
117 rGlyThrPheSerGlyGlyHisGluGlyHisCysLysProTrpThrAsp 134  
471 GGGGACCTTCTCCGGGGCCAGGAAGGCACTGCAAACTTTGGACAGACT 520  
134 ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150  
521 GCACCCAGTTCGGGTTCCTCACTGTGTTCCTGGGAACAAGACCCCAAC 570  
151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167  
571 GCTGTGTGCTGCCAGGTCCTCCCGCGCAGAGCGCTTGGGTGCTGAC 620  
167 rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAla 184  
621 CGTGTCTCTCTGCGCGGCGCGCTGCTGCTCTCTCTGACCTCGGCCC 670  
184 lnLeuGlyLeuHisIleTrpGlnLeu.....Arg 193  
671 AGCTTGGACTCAGTTCGAGCTGAGGAGTCACTGATGCGCCCGCA 720  
194 LysThrGlnLeuLeuGluValProProSerThrGluAspAlaArgSe 210  
721 GAGACCCAGCTGCTGTGAGGTCGCGCGCTGACCGAAGACGCGAAG 770  
210 rCysGlnPheProGluGluArgGlyGluArgSerAlaGluGlyLysG 227  
771 CTGCCAGTTCCCGGAGGAAGCGGGGAGCGGATCGCGACAGGAGAAG 820  
227 lyArgLeuGlyAspLeuTrpVal 234  
821 GCGGCTGGGAGACCTGTGGTG 843

seq\_name: /SIDS/gcgdata/geneseq/geneseq/NA2000.DAT: AAC58596

seq\_documentation\_block:

ID AAC58596 standard; cDNA; 1008 BP.

XX

AC AAC58596;  
XX 29-JAN-2001 (first entry)  
XX Human PRO364 protein UNQ319 encoding cDNA SEQ ID NO: 91.  
XX  
XX Human; immune related disease; diagnosis; antinflammatory; cardiant;  
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;  
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;  
KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;  
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;  
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
KW autoimmune thrombocytopaenia; immune-mediated renal disease;  
KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
KW inflammatory bowel disease; gluten-sensitive enteropathy;  
KW autoimmune disease; immune-mediated skin disease; allergic disease;  
KW immunological disease; transplantation associated disease;  
KW graft rejection; graft-versus-host-disease; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200053758-A2.  
XX 14-SEP-2000.  
XX  
XX 02-MAR-2000; 2000WO-US05841.  
XX  
XX 08-MAR-1999; 99WO-US05028.  
PR 10-MAR-1999; 99US-0123618.  
PR 12-MAR-1999; 99US-0123957.  
PR 23-MAR-1999; 99US-0125775.  
PR 12-APR-1999; 99US-0128849.  
PR 20-APR-1999; 99WO-US08615.  
PR 28-APR-1999; 99US-0131445.  
PR 04-MAY-1999; 99US-0132371.  
PR 14-MAY-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 28-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 29-OCT-1999; 99US-0162506.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30999.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;

CC proliferation and cytokine production by T-cells, and potentiates T  
CC cell expansion or apoptosis. The products can be used in the  
CC treatment of conditions associated with abnormal physiology or  
CC development, including abnormal proliferation, e.g. cancerous  
CC conditions or degenerative conditions. They can be used in the  
CC regulation or development of haematopoietic cells, e.g. lymphoid cells  
CC which affect immunological responses, e.g. autoimmune disorders.  
XX  
SQ Sequence 1006 BP; 156 A; 331 C; 337 G; 182 T; 0 other;

alignment\_scores:  
Quality: 1322-50 Length: 241  
Ratio: 5.652 Gaps: 1  
Percent Similarity: 97.095 Percent Identity: 96.680

alignment\_block:

US-09-512-363-2 x AAV19153 ..

Align seg 1/1 to: AAV19153 from: 1 to: 1006

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1 ATGGCACAGCAGCGGGGATGGGCGCGTTTCGGGCGCTGTGGCGCTGGC 50  
17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyProGlyC 34  
|||||  
51 GCTGCTGTGGCGCTGACGCTGGGTTCAGCGCCACCGGGGTCCCGGT 100  
34 ysGlyProGlyArgLeuLeuGlyThrGlyThrAspAlaArgCysCys 50  
|||||  
101 CGCGCCCTGGCGCTCTGCTGGGCGGAACGGAGCGCGCTGCTGC 150  
51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysC 67  
|||||  
151 CGGGTTCACAGCAGCGCTGCTGCGCGATTACCGCGCGAGGAGTGTG 200  
67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAsp 84  
|||||  
201 TTCGAGTGGGACTGCATGTGTCCAGCCTGAATTCACCTGCGGAGACC 250  
84 roCysCysThrThrCysArgHisProCysProProGlyGlnGlyVal 100  
|||||  
251 CTTCGTCGACGACCTCGCGGACCACTCTGTCCTCCAGCGCGGGGTA 300  
101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSe 117  
|||||  
301 CAGTCCCAGGGGAAATTCAGTTTGGCTTCCAGTGTATCGACTGTGCCT 350  
117 rGlyThrPheSerGlyGlyHisGluGlyHisCysLysProThrAspC 134  
|||||  
351 GGGGACCTTCTCCGGGGGCCACGAAGGCCACTGCAAACTTTGGACAGAC 400  
134 ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150  
|||||  
401 GCACCCAGTTCGGGTCTCTACTGTGTCCCTGGGAACAACACCCACAA 450  
151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuth 167  
|||||  
451 GCTGTGTGCTCCAGAGGTCCCGCGGACAGCGCTTGGGTGGCTGAC 500  
167 rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184  
|||||  
501 CGTGTCTCTCTGCGCGCTGGCGCTGGCTCTCTCTCTGACCTCGGCC 550  
184 lnLeuGlyLeuHisIleTrpGlnLeu.....Arg 193  
|||||  
551 AGCTGGACTGCATCTGGCAGCTGGAGAGTCACTGATGTGGCCCCG 600  
194 LysThrGlnLeuLeuGluValProProSerThrGluAspAlaArgSe 210  
:|||||  
601 GAGACCCAGCTGCTGTGGAGGTGCGCGCTGCGAGCCGGAAGACGCGAG 650

210 rCysGlnPheProGluGluArgGlyGlyArgSerAlaGluGlyLysG 227  
|||||  
651 CTGCCAGTTCCTCCGAGGAGAGCGGGCGGCGATCGGAGAGAGAGG 700  
227 lyArgLeuGlyAspLeuTrpVal 234  
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701 GGCGGCTGGAGACCTGTGGGTG 723

seq\_name: /SIDS8/gcgdata/geneseq/geneseq/NA1999.DAT:AAx87670

seq\_documentation\_block:

ID AAX87670 standard; cDNA; 1008 BP.

XX

AC AAX87670;

XX

DT 26-OCT-1999 (first entry)

XX

DE Human TNF receptor homologue PRO364 cDNA clone UNQ319.

XX

KW PRO364; tumour necrosis factor receptor; human; apoptosis;

KW inflammation; antiinflammatory; NF-KB activation;

KW autoimmune disease; therapy; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 121..846

FT /\*tag= a

FT /note= "a nucleic acid comprising nucleotides

FT 121-843 is specifically claimed in

FT Claim 3"

FT sig\_peptide 121..195

FT /\*tag= b

FT mat\_peptide 196..843

FT /\*tag= c

XX

XX WO940196-A1.

XX

PD 12-AUG-1999.

XX

XX 09-FEB-1999; 99WO-US02642.

XX

XX 09-FEB-1998; 98US-0024087.

XX

XX (GETH ) GENENTECH INC.

XX

XX Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;

XX Pitti RM, Wood WI;

XX

XX WPI; 1999-494296/41.

XX P-PSDB; AAY06605.

XX

XX Tumour necrosis factor receptor homologue - useful for, e.g.

XX modulating apoptosis and NF-KB activation and proinflammatory or

XX autoimmune responses

XX

PS Claim 2; Fig 1; 104pp; English.

XX

XX This is the nucleotide sequence of a novel cDNA clone, termed  
CC UNQ319 or DNA7365-1206 (ATCC 209436), that codes for PRO364 (see  
CC AAY06605), a novel member of the tumour necrosis factor receptor  
CC family. UNQ319 was isolated from a human bone marrow tissue cDNA  
CC library by PCR amplification and probe hybridisation (see also  
CC AAX87672-75 and AAX87720-23). Nucleic acids comprising the present  
CC sequence, the PRO364 coding region, and DNA having at least 95%  
CC sequence identity to (a) DNA encoding a PRO364 polypeptide  
CC comprising amino acids 1-241, 1-X, 26-241 or 26-X of PRO364, where  
CC X is any of residues 157-167, and (b) DNA encoding mature PRO364,  
CC are claimed. PRO364 nucleic acids can be used in the recombinant  
CC production of PRO364 polypeptides, as probes, in gene and  
CC chromosome mapping, in the generation of antisense sequences, and  
CC in gene therapy. PRO364 polypeptides are useful for modulating  
CC apoptosis, NF-KB activation and proinflammatory or autoimmune

CC agonists/antagonists. The polypeptides, agonists or antagonists can be  
 CC used for treating a disease state associated with aberrant cell  
 CC survival. They can be used for treating immune deficiency disorders,  
 CC DiGeorge syndrome, HIV infection, severe combined immunodeficiency  
 CC (SCID), Wiskott-Aldrich disorder, blood coagulation disorders, blood  
 CC platelet disorders or wounds resulting from trauma or surgery. They can  
 CC also be used to treat heart attacks, strokes, Addison's disease,  
 CC haemolytic anaemia, rheumatoid arthritis, Goodpastures syndrome, Grave's  
 CC disease, multiple sclerosis, myasthenia gravis, Stiff-Man syndrome,  
 CC systemic lupus erythematosus, Guillain-Barre syndrome, insulin dependent  
 CC diabetes mellitus or autoimmune inflammatory eye disease, anaphylaxis,  
 CC hypersensitivity to an antigenic molecule, organ rejection or graft  
 CC versus host disease, inflammatory conditions, ischaemia-reperfusion  
 CC injury, complement-mediated hyperacute rejection, nephritis, cytokine or  
 CC chemokine induced lung injury, inflammatory bowel disease, Crohn's  
 CC disease, hyperproliferative disorders, or infections. They can also be  
 CC used to repair, replace, or protect tissue damaged by congenital  
 CC defects, trauma, age, disease, surgery, including cosmetic plastic  
 CC surgery, fibrosis, reperfusion injury, peripheral nerve injuries,  
 CC neuropathies, and central nervous system disease (e.g. Alzheimer's  
 CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral  
 CC sclerosis, and Shy-Drager syndrome). The products can also be used for  
 CC detection, diagnosis and prognosis.

XX  
 SQ Sequence 983 BP; 144 A; 326 C; 346 G; 167 T; 0 other;

## alignment\_scores:

Quality: 1340.00 Length: 234  
 Ratio: 5.726 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-512-363-2 x AA237762 ..

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 118 ATGGACACACAGGGGCGATGGCGGCTTTCGGGCGCTGTGGCGCTGGC 167  
 17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34  
 168 GCTGCTGTGGCGCTCAGCTGGGTGAGCGCCACCGGGGGTCCGGGT 217  
 34 ysglyProGlyArgLeuLeuGlyThrGlyThrAspAlaArgCysCys 50  
 218 GCGGCGCTGGGCGCTCTGCTTGGGACGGGAACGGACGCGCTGCTGC 267  
 51 ArgValHisThrArgCysCysArgAspTyrProGlyGluGluCysC 67  
 268 CGGGTTTCACACGACGCGCTGCTGCGCGATTACCGGGGAGAGTGCTG 317  
 67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAsp 84  
 318 TTCCGAGTGGGACTGATGTGTCTCAGCCTGAATTCACCTCGGAGACC 367  
 84 roCysCysThrThrCysArgHisHisProCysProProGlyGlnGlyVal 100  
 368 CTGTGTCACGACCTCGCGCACACCTTGTCCCGCAGCGCCAGGGGTA 417  
 101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAla 117  
 418 CAGTCCAGGGGAAATCAATTTGGCTTCCAGTGTATCGACTGTCCCTC 467  
 117 rGlyThrPheSerGlyHisGluGlyHisCysLysProTrpThrAspC 134  
 468 GGGGACCTTCTCGGGGGCCACGAGGCCACTGCAAACTTGGACGACT 517  
 134 ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150  
 518 GCACCCAGTTCGGGTTCTCACTGTGTTCCCTGGGAACAAGACCCCAAC 567

151 AlavaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167  
 568 GCTGTGTGCTGCCAGGTCCCGCGCCAGAGCGCTTGGGTGGCTGAC 617  
 167 rValValLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184  
 618 CGTGTGCTCTCTGGCGCTGGCGGCTGCTGCTCTCTGACCTCGGCC 667  
 184 InLeuGlyLeuHisIleTrpGlnLeuArgLysThrGlnLeuLeuGlu 200  
 668 AGCTTGGACTGCACATCTGCAGCTGAGGAAGACCCAGTTCGCCGAG 717  
 201 ValProSerThrGluAspAlaArgSerCysGlnPheProGluGluG 217  
 718 GTGCGCGCTCGACCGAAGACGCGCAGAAAGTCCAGTTCGCCGAGGA 767  
 217 uArgGlyGluArgSerAlaGluGlyGlyArgGlyAspLeuTrpV 234  
 768 GCGGGCGCGCATCGGCAGAGGAGAGGCGGCTGGAGACCTGTGGG 817  
 234 al 234  
 818 TG 819

seq\_name: /SID8/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV19153

## seq\_documentation\_block:

ID: AAV19153 standard; DNA; 1006 BP.

XX AC AAV19153;

XX DT 28-JUL-1998 (first entry)

XX DE Nucleotide sequence of the human 312C2 T cell gene.

KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;  
 KW antigen-specific T cell proliferation; cytokine production by T-cell;  
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell; ss;  
 KW autoimmune disorders.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..726

FT /tag- a

FT /product= "human 312C2 protein"

XX WO9806842-A1.

XX PD 19-FEB-1998.

XX PF 14-AUG-1997; 97WO-US13931.

XX PR 07-OCT-1996; 96US-0027901.

XX PR 16-AUG-1996; 96US-0689943.

XX PA (SCHE ) SCHERING CORP.

XX PI Gorman DM, Randall TD, Ziolknik A;

XX DR WPI: 1998-159534/14.

XX DR P-PSDB; AA37839.

XX Isolated 312C2 T cell gene - used to develop products for treating,  
 PT e.g. cancers, auto-immune disorders, transplantation rejection and  
 PT other T cell disorders  
 XX Claim 10; Pages 58-59; 71pp; English.

XX This is the nucleotide sequence encoding the human 312C2 T cell

CC protein. The 312C2 proteins are expressed in thymus cells and are  
 CC induced on T cells and spleen cells following activation. Engagement  
 CC of 312C2 stimulates proliferation of T cell clones, antigen-specific



CC X-linked agammaglobulinemia, severe combined immunodeficiency  
CC (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin  
CC deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2  
CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis  
CC and/or diagnose an autoimmune disease, especially rheumatoid  
CC arthritis, systemic lupus erythematosus, thrombocytopenia purpura  
CC or IgA nephropathy. The polypeptides, polynucleotides and/or  
CC antibodies can be administered to cells in vitro, ex vivo or in  
CC vivo or to a multicellular organism. Soluble forms of the  
CC polypeptides may also be used. Methods for screening for  
CC agonist/antagonist compounds are also provided.  
XX  
SQ Sequence 983 BP; 144 A; 326 C; 346 G; 167 T; 0 other;

alignment\_scores:  
Quality: 1340.00 Length: 234  
Ratio: 5.726 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-512-363-2 x AAA50304 ..

Align seg 1/1 to: AAA50304 from: 1 to: 983

1 MetAlaGlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAl 17  
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118 ATGGACACGACGCGGCGATGGCGCGTTTCGGCGCTGTGGCGCTGGC 167  
17 aLeuLeuCysAlaLeuSerLeuGlyGlnArgProThrGlyGlyProGlyC 34  
|||||  
168 GCTGTGTGGCGCTGACGCTGGGTTCACGCGCCACCGGGGTCCCGGT 217  
34 yGlyProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCys 50  
|||||  
218 CGGCGCTGGCGGCTCTCTGTGGACGGAACGACGCGCGCTGCTGC 267  
51 ArgValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysC 67  
|||||  
268 CGGTTTCACACGACGCGTGTGTGGCGGATACCGGGCGAGGAGTGCTG 317  
67 sSerGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspP 84  
|||||  
318 TTCGAGTGGGACTGCATGTGTGCCACGCTGAATTCACCTCCGAGACC 367  
84 roCysCysThrThrCysArgHisProCysProProGlyGlnGlyVal 100  
|||||  
368 CTTCGTCACACACCTCCGCGGACACACCTTGTCCCGGCGGCGGTA 417  
101 GlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSe 117  
|||||  
418 CAGTCCACAGGGAAATTCAGTTTGGCTTCAGTGTATCGACTGTGCTC 467  
117 rGlyThrPheSerGlyGlyHisGluGlyHisCysLysProThrPheAspC 134  
|||||  
468 GGGGACCTTCCTCCGGGGCCACGAGGCGACTGCAACCTTGGACAGACT 517  
134 ysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsn 150  
|||||  
518 GCACCCAGTTCGGGTTCCTACTGTGTTCCTGGGAACAGACCCCAAC 567  
151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167  
|||||  
568 GCTGTGTGGTCCCGAGGTTCCTCCCGGCGGCGGCGCTTGGGTGCTCAC 617  
167 rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184  
|||||  
618 CGTGTCTCTCTGGCGGCGGCGCTGCTCTCTCTGACCTCGGCC 667  
184 lnLeuGlyLeuHisThrPrlGlnLeuArgLysThrGlnLeuLeuGlu 200  
|||||  
668 AGCTTGGACTGCATCTGGCAGCTGAGGAAGACCCAGCTGCTGCTGGAG 717

201 ValProProSerThrGluAspAlaArgSerCysGlnPheProGluGluG1 217  
|||||  
718 GTGCGCGCGTCCACGGAAGACGCCAGAGCTGCCAGTTCCCGGAGGA 767  
217 uArgGlyGluArgSerAlaGluGluLysGlyArgLeuGlyAspLeuTrpV 234  
|||||  
768 GCGGGCGGAGCATCGCAGAGGAGGAGGCGGCTGGGAGACCTGTGGG 817  
234 al 234  
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818 TG 819

seq\_name: /SIDS8/gcgdata/geneseq/geneseq/NA2000.DAT:AAZ37762

seq\_documentation\_block:

ID AAZ37762 standard; cDNA; 983 BP.

AC AAZ37762;

XX DT 01-FEB-2000 (first entry)

XX DE Tumour necrosis factor receptor-like protein (TR11), nucleotide sequence.  
XX KW Tumour necrosis factor receptor-like protein; TR11; TR11SV1; TR11SV2;  
KW G1TR; growth; differentiation; cell death; immune deficiency disorder;  
KW Digeorge syndrome; HIV; SCID; Wiskott-Aldrich disorder; anaemia;  
KW Stiff-Man syndrome; arthritis; multiple sclerosis; diabetes;  
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; ss;  
KW inflammatory condition.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
XX CDS 118..822

XX FT /\*tag= a  
XX FT /product= TR11\_receptor  
XX FT /note= "Tumour necrosis factor receptor-like protein"  
XX FT sig\_peptide 118..192  
XX FT /\*tag= b  
XX FT /note= "Putative signal sequence"  
XX FT mat\_peptide 193..820  
XX FT /\*tag= c  
XX FT /note= "TR11"

XX WO9920758-A1.

XX PD 29-APR-1999.

XX PF 21-OCT-1998; 98WO-US22085.

XX PR 21-OCT-1997; 97US-0063212.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI NI J, Ruben SM;

XX DR WPI; 2000-061922/05.

XX PS P-PSDB; AAY52158.

XX PT New tumour necrosis factor receptor-like polypeptides used to, e.g.

XX PS treat Digeorge syndrome -

XX PS Claim 8; Fig 1; 167pp; English.

XX CC This is the nucleotide sequence of the human tumour necrosis factor  
XX CC receptor-like protein (TR11 receptor). The invention relates to TR11 and  
XX CC two splice variants TR11SV1 and TR11SV2. The nucleotide sequences were  
XX CC determined by sequencing cloned cDNAs AAZ37765-237766. The TR11 receptor  
XX CC and its splice variants show homology to the murine glucocorticoid  
XX CC induced tumour necrosis factor receptor family-related gene (G1TR).  
XX CC TR11, TR11SV1 and TR11SV2 polypeptides may be involved in the regulation  
XX CC of cell-type specific receptor-mediated cell growth, differentiation,  
XX CC and ultimately, cell death. They can be used for screening for



```

/db_xref="taxon:9606"
/clone="IMAGE:1840417"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/notes="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site.1: Not I; Site.2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI_CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Ratlma Bonaldo."
BASE COUNT      57 a      86 c      87 g      44 t
ORIGIN

```

```

alignment_scores:
  Quality: 319.50      Length: 90
  Ratio: 4.318        Gaps: 1
  Percent Similarity: 82.222      Percent Identity: 74.444

```

```
alignment_block:
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```
US-09-512-363-2 x AI214481/rev ..
```

```
Align seg 1/1 to reverse of: AI214481 from: 1 to: 274
```

```

131 TrpThrAspCysThrGlnPheGlyPheLeuThrValPheProGlyAsnLy 147
||||| ||||||| |||||||:||||||| ||||| :|||
274 TGGACAGTCTGCACCCAGTCGGGGTTCTCTCAGTGTCCCTGTGACGAA 225
||||| ||||||| ||| |||||||:||||||| |||||||
147 sThrHisAsnAlaValCysValProGlySerProAlaGluProLeuG 164
||||| ||||||| ||| |||||||:||||||| |||||||
224 GACCCACATCGCTGTGAGTCCGAGGTCFCCGCCGACAGAGCGCTTG 175
|| |||||||:|||||||:||||| |||||||:
164 lyTrpLeuThrValValLeuLeuAlaValAlaCysValLeuLeu 180
|| |||||||:|||||||:||||| |||||||:
174 GGTGACTGACCGTCGTATGTGCGCGTGTCCGCGTGAGTCCTCCTCATG 125
||||| ||||||| ||||||| ||||||| |||||||
181 ThrSerAlaGlnLeuGlyLeuHisIleTrpGlnLeu..... 192
||||| ||||||| ||||||| ||||||| |||||||
124 ACCTCGGCCAGCTTGGACTGCACATCTGGCAGCTGAGGAGTCAGTGCAT 75
193 .....ArgLysThrGlnLeuGluValProProSerThrGluA 207
||||| ||||||| ||||||| ||||||| |||||||
74 GTGCCCCGAGAGACCCAGCTGCTGGAGGTGCCCGCGTCGACCGAAG 25
207 spAlaArgSerCysGlnPhe 213
||||| |||||||
24 ACGCCAGAATGTGCCAGTTC 5

```



Ratio: 4.721 Gaps: 2  
Percent Similarity: 80.435 Percent Identity: 63.768

alignment\_block:

US-09-512-363-2 x AW483085 ..

Align seg 1/1 to: AW483085 from: 1 to: 393

25 GlyGlnArgProThrGlyGlyProGlyCysGlyProGlyArgLeuLeuLe 41  
|||||  
1 GGCCAGCGACCCCTCAGCATGTGAGCTGAGCCCTGGCCAGTTCTGCA 50  
41 uGlyThrGlyThrAspAlaArgCysCysArgValHisThrArgCysC 58  
51 TGGGACGGGACAGACGACGCTGCTGC.....CGCTGGC 85  
58 ysArgAspTyrProGlyGluGluCysCysSerGluTirpAspCysMetCys 74  
86 CC.....CCAGATGAGGGGACCTGTCTGAGCGGAGCTGCCAGTGT 126  
75 ValGlnProGluPheHisCysGlyAspProCysCysThrThrCysArgH1 91  
127 ATCCAGCCCGAGTTCACATGTGGAGACCCACACAGCTGAAGAGCTGCAAGTA 176  
91 shisProCysProProGlyGlnGlyValGlnSerGlnGlyLysPheSerP 108  
177 CTACTCTCTCCACCTGGCCAGGAGTGCAGCCTGAGGCAACTTCAAAAT 226  
108 heGlyPheGlnCysIleAspCysAlaSerGlyThrPheSerGlyGlyHis 124  
227 TGGGCTTTGAGTGTGACTGTGCCGTGGGACCTTCTCTAGGGGCCAT 276  
125 GluGlyHisCysLysProThrPheGlnPheGlyPheLeuTh 141  
277 GAGGCGCGTGCACAACTTGGCAGACTGGTCCAGCTTGGGTTCACAC 326  
141 rValPheProGlyAsnLysThrHisAsnAlaValCysValProGlySerP 158  
327 CCTGTTTCCGGAAACAGACGACACAATGCTGTGCAGCGCTGGGCTGC 376  
158 roProAlaGluPro 162  
377 CGCCCACTGAACCA 390

seq\_name: gb\_est50:AW659186

seq\_documentation\_block: 552 bp mRNA EST 14-JUL-2000

LOCUS AW659186 552 bp mRNA EST 14-JUL-2000

DEFINITION 96144 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION AW659186

VERSION AW659186.1 GI:7425013

KEYWORDS EST.

SOURCE cow.

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 552)

Smith,R.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,

Bennett,G.A., Fahrnenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid

,W.W. and Keale,J.W.

Design and use of four pooled tissue normalized cDNA libraries for

EST discovery in cattle

Unpublished (2000)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@mail.marc.usda.gov

Single pass sequencing. Bases called and alt\_trimmed with phred

PCR Primers  
FORWARD: AGGAACACCTATGACCAT  
BACKWARD: GTTTCCAGTCAGCAGC  
Plate: 83 row: A column: 19  
Seq primer: ATTTAGTGACACTATAG.

FEATURES

source

1..552  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="MARC 1BOV"  
/tissue\_type="pooled"  
/lab\_host="DH108"  
/note="Vector: pCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled tissue from lymph node, ovary,  
fat, hypothalamus, and pituitary."

BASE COUNT 95 a 179 c 175 g 103 t

ORIGIN

alignment\_scores:

Quality: 494.50 Length: 165  
Ratio: 4.263 Gaps: 1  
Percent Similarity: 70.303 Percent Identity: 56.364

alignment\_block:

US-09-512-363-2 x AW659186 ..

Align seg 1/1 to: AW659186 from: 1 to: 552

99 GlyValGlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCy 115  
|||||  
13 GGATGTCAGCTGAGGGCAACTTCAAAATTCGGCTTTCAGTGTGTGACTG 62  
115 sAlaSerGlyThrPheSerGlyGlyHisGluGlyHisCysLysProTrpT 132  
63 TGGCGTGGGACCTTCTCTAGGGGCCATGAGGGCCCTGCAACACCTTGGG 112  
132 hrAspCysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThr 148  
113 CAGACTCGTCCAGCTTGGGTTTCCACCTGTTCCCGGAAACACAGACG 162  
149 HisAsnAlaValCysValProGlySerProAlaGluProLeuGlyTr 165  
163 CACAATGCTGTGTGCAGCTGGGGCTGCCGCCACTGAACACCGACGCC 212  
165 pLeuThrValValLeuLeuAlaValAlaAlaCysValLeuLeuThrS 182  
213 AGTGACCATCGTCATCTCTCTGGGTGCTGCTGCTGCTGCTGCTGACCG 262  
182 erAlaGlnLeuGlyHisIleTrpGlnLeuArgLys..... 194  
263 TGACCCAGCTAAGCTGCACATCTGGCAGCTGAGGAGCAAGAATGTGG 312  
194 ..... 194  
313 CCCCCAGGTGAGTGTGCTCTTAGGAGGGGGGGTCCCTGCTGCTGCC 362  
195 .....ThrGlnLeuLeuLeuGluValProp 203  
363 TGCTGATTGACGCCCTCTGTCAGAGAGCCAGCTCTCTGGAGCGCCGCCAC 412  
203 roSerThrGluAspAlaArgSerCysGlnPheProGluGluGluArgGly 219  
413 CCCACCTGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 462  
220 GluArgSerAlaGluGluLysGlyArgLeuGlyAspLeuTrpVal 234  
463 GAGCGGCTGTCTCAGAGAACAGGGCGCCGAGGAGACCTGTGCGGTG 507

seq\_name: gb\_est45:AW335806

seq\_documentation\_block:

LOCUS AW335806 442 bp mRNA EST

10-JUL-2000

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DEFINITION 22020 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW335806
VERSION AW335806.1 GI:6832445
KEYWORDS EST.
SOURCE cOW.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 442)
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
W.W. and Keele,J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGACG
Plate: 15 row: F column: 18
Seq primer: ATTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source           1..442
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="MARC 1BOV"
                     /tissue_type="pooled"
                     /lab_host="DHI08"
                     /note="Vector: pCMV SP0RT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
BASE COUNT          74 a 150 c 130 g 88 t
ORIGIN
alignment_scores:
  Quality: 404.50      Length: 143
  Ratio: 4.170         Gaps: 1
  Percent Similarity: 67.832  Percent Identity: 53.147
alignment_block:
US-09-512-363-2 x AW335806 ..
Align seg 1/1 to: AW335806 from: 1 to: 442
99 GlyValGlnSerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCy 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
13 GGAGTGAGCCTGAGGCGCACTTCAAAATTCGGCTTGAGTGTGTGACTG 62
115 sAlaSerGlyThrPheSerGlyGlyHisGluGlyHisCysLysProTrpT 132
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
63 TGGCGTGGGACCTTCTCTAGGGCCATGAGGGCCGCTGCAAACTTGGG 112
132 hrAspCysThrGlnPheGlyPheLeuThrValPheProGlyAsnLysThr 148
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
113 CAGACTGGTCCACCTGGGTTTCCACCCCTGTTCCCGGAACACAGACG 162
149 HisAsnAlaValCysValProGlySerProProAlaGluProLeuGlyTr 165
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
163 CACAATGCTGTGTGACGCTGGGGCTGCGCCCACTGAACACCCAGCCG 212
165 pLeuThrValValLeuLeuAlaAlaAlaCysValLeuLeuThrS 182
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
213 AGTGACCATGTCATCTCTCTGTGGTGGCTGCTGCTGCGCCTGACCG 262

```

```

182 erAlaGlnLeuGlyLeuHisIleTrpGlnLeuArgLys..... 194
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
263 TGACCCAGCTAGCCTGCACATCTGCAGCTGCAGGAGCAAGAAATGTGG 312
194 ..... 194
313 CCCCCAGGTGAGTTGCTTGTAGGAGGGGGTCCCTGCTGCTGCTGCC 362
195 .....
363 TCCTGATTGCCAGCCCTCTGCAGAGACCCAGCTCTCTGGAGGCCGCCAC 412
203 roSerThrGluAspAlaArgSerCysGln 212
|| |||||:|||||:|||||:|||||:|||||:
413 CCCACCTGAGGATGCTGCAGTTGCCAG 441
seq_name: gb_est73:BE373185
seq_documentation_block:
LOCUS BE373185 620 bp mRNA EST 21-JUL-2000
DEFINITION 60125221F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3583589 5',
mRNA sequence.
ACCESSION BE373185
VERSION BE373185.1 GI:9318548
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 620)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-femail.nih.gov
Tissue procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8740 row: j column: 06
High quality sequence stop: 580.
FEATURES             Location/Qualifiers
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                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:3583589"
                     /clone_lib="NCI_CGAP_Mam1"
                     /tissue_type="tumor, biopsy sample"
                     /dev_stage="3 months, virgin"
                     /lab_host="DHI08"
                     /note="Organ: mammary; Vector: pCMV-SP0RT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT          143 a 145 c 200 g 132 t
ORIGIN
alignment_scores:
  Quality: 357.50      Length: 144
  Ratio: 3.405         Gaps: 5
  Percent Similarity: 72.917  Percent Identity: 45.833
alignment_block:
US-09-512-363-2 x BE373185 ..
Align seg 1/1 to: BE373185 from: 1 to: 620

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132 AAGGAGGACTGTCCAAAGAAAGGTGCATATATGTGTCCACACCTGAGTACCA 181
80 sCysGlyAspProCysThrCysArgHisHisProCysProProG 97
|||||
182 CTTGTGGAGACCTCTAGTCAAGATCTGCAAGCACTACCCCTGCCAACCCAG 231
|||||
97 lyGlnGlyValGlnSerGlnGlyLysPheSerPheGlyPheGlnCysIle 113
|||||
232 GCCAGAGGGTGGAGTCTCAAGGGGATATTGTGTTGGCTTCGGTGTGTT 281
|||||
114 AspCysAlaSerGlyThrPheSerGlyGlyHisGluGlyHisCysLysPr 130
|||||
282 GCCTGTGCCATGGCAGCCTTCTCCGAGGTCGTGACGGTCACTGCAGACT 331
|||||
130 orPthrPthrCysThrGlnPheGlyPheLeuThrValPheProGlyAsnL 147
|||||
332 TTGGACCAACTTCTCTCAGTTTGGATTCTCACCATGTTTCCCTGGGAACA 381
|||||
147 ySthrHisAsnAlaValCysValProGlySerProProAlaGluProLeu 163
|||||
382 AGACCCACAACTGCTGTGTCATCCCGGAGCCACTGCCCACTGAGCAATAC 431
|||||
164 GlyTrpLeuThrValValLeuLeuAlaValAlaCysValLeuLeuLe 180
|||||
432 GCCCATTTGACTGTCATCTCTGCTGTCATGGCTGCATGATTTCTTCCT 481
|||||
180 uThrSerAlaGlnLeuGlyLeuHisIleTrpGlnLeuArgLysThrGlnL 197
|||||
482 AACCAAGTCCAGCTCGGCTGCATATGCGAGCTGAGGAGGCAACACA 531
|||||
197 eu.LeuLeuGluValProProSerThrGluAspAlaArgSerCysGlnPh 213
|||||
532 TGTGTCCTCGAGAGACCC.....AGCCATTCGCGAGGTGCAGTTG 572
|||||
213 eProGluGluGluArg.....GlyGluArgSerAlag 624
|||||
573 TCAAGCTGAGGATGCTGCGCTCCAGTCTCGGGGGGACGGGGGCGCA 622
|||||
224 luGlu 225
|||
623 CGAA 627

seq_name: gb_est45:AW300857

seq_documentation_block:
LOCUS AW300857 340 bp mRNA EST 18-JAN-2000
DEFINITION xk07c07.x1 NCI-CGAP Co20 Homo sapiens cDNA clone IMAGE:2666028 3'
similar to TR:095851 095851 TNF RECEPTOR SUPERFAMILY
ACTIVATION-INDUCIBLE PROTEIN. ; contains MER22.b1 TARI repetitive
element ;, mRNA sequence.
ACCESSION AW300857
VERSION AW300857.1 GI:6710534
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 340)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-femail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio-llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
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FEATURES
source
Location/Qualifiers
1..340
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2666028"
/clone_lib="NCI_CGAP_Co20"
/tissue_type="moderately differentiated adenocarcinoma"
/lab_host="DH10B"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Normalized to Cot 500. Average insert size 1.11kb.
Normalized version of NCI_CGAP_Col8. Library constructed
by Life Technologies."
BASE COUNT 70 a 100 c 115 g 54 t 1 others
ORIGIN

alignment_scores:
Quality: 608.00 Length: 113
Ratio: 5.527 Gaps: 0
Percent Similarity: 97.345 Percent Identity: 94.690

alignment_block:
US-09-512-363-2 x AW300857/rev ..
Align seg 1/1 to reverse of: AW300857 from: 1 to: 340
69 GluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspProCy 85
|||||
340 GAGTGGAACTGCAATGTGTGCCACCTTGAATTCACCTCGGAAGACCCCTTG 291
|||||
85 sCysThrThrCysArgHisHisProGlyGlnGlyValGlns 102
|||||
290 CTCGACGACTGCGGGGACCACTTCTGTCCTCCAGGAGGAGTACAGT 242
|||||
102 erGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSerGly 118
|||||
241 CCCAGGGGAAATTCAGTTTGGCTTCCAGTGTATCGACTGTGCTCGGGG 192
|||||
119 ThrPheSerGlyGlyHisGluGlyHisCysLysProTrpThrAspCysTh 135
|||||
191 ACCTTCTCCGGGGGCCACGAGGCCACTTGCACAACTTGGACAGACTGCAC 142
|||||
135 rGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsnAlav 152
|||||
141 CCAGTTCGGGTTTCTCACTGTGTCTCCCTGGGAACAACACCAACGCTG 92
|||||
152 alCysValProGlySerProProAlaGluProLeuGlyTrpLeuThrVal 168
|||||
91 TGTGCGTCCCAAGGTCCTCCCGCGGACGAGCGCTTGGGTGCTGACCGTC 42
|||||
169 ValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThr 181
|||||
41 GTCTCTCTGCGCTGGCGCGCTGCTCTCTCTCTGACC 3

seq_name: gb_est83:BF117994

seq_documentation_block:
LOCUS BF117994 606 bp mRNA EST 29-DEC-2000
DEFINITION uz10e09.y1 NCI-CGAP_Mam5 Mus musculus cDNA clone IMAGE:3668680 5'
similar to TR:035714 035714 GLUCOCORTICOID INDUCED TNFR FAMILY
RELATED PROTEIN PRECURSOR. ;, mRNA sequence.
ACCESSION BF117994
VERSION BF117994.1 GI:10987470
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 606)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
```



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DEFINITION uo63d10.y1 NCI-CGAP_Maml Mus musculus cDNA clone IMAGE:2647219 5'
            similar to TR:O35714 O35714 GLUCOCORTICOID INDUCED TNFR FAMILY
            RELATED PROTEIN PRECURSOR. ;, mRNA sequence.
ACCESSION  AW230423
VERSION     AW230423.1 GI:6559719
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 644)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Other_ESTs: uo63d10.x1
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

MGI:1027671
Seq primer: -40RP from Gibco
High quality sequence stop: 425.
FEATURES    Location/Qualifiers
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                        /strain="FVB/N"
                        /db_xref="taxon:10090"
                        /clone="IMAGE:2647219"
                        /clone_lib="NCI-CGAP_Maml"
                        /tissue_type="tumor, biopsy sample"
                        /dev_stage="3 months, virgin"
                        /lab_host="DH10B"
                        /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                        Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                        Library constructed by: Life Technologies. Investigator
                        providing samples: Gilbert Smith, NIH"
BASE COUNT  141 a 173 c 183 g 145 t 2 others
ORIGIN
alignment_scores:
    Quality: 626.50      Length: 214
    Ratio: 3.867         Gaps: 3
    Percent Similarity: 75.701 Percent Identity: 52.336
alignment_block:
US-09-512-363-2 x AW230423 ..
Align seg 1/1 to: AW230423 from: 1 to: 644
3 GlnHisGlyAlaMetClyAlaPheArgAlaLeuCysGlyLeuAlaLeuLe 19
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
21 AGGAGAAGCACTATGGGCGCATGGCGCATGCTGTATGGAGTCTCGATGCT 70
19 uCysAlaLeuSerLeuGlyGln...ArgProThrGlyGlyProGlyCysG 35
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
71 CTGTGTGTCGGACCTAGGTCACCGAGTAGTGTAGGAGCGCTGGCTGTG 120
35 lYProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCysArg 51
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
121 GCCTGGCAAGGTTGACAGACGAGAGTGGCAACACACTGCTGCTCGAGC 170
52 ValHisThrThrArgCysCysArgAspTyrProGlyGluCysCysSe 68
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
171 CTGTATGCT.....CCAGGCAAGGAGGAGTCTCC 199

```

```

68 rGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspProc 85
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200 AAAAGAAAGTGCATATGTGTACACACTGAGTACCACTGTGGAGACCTC 249
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
85 yScysThrThrCysArgHisHisProCysProGlyGlnGlnValGln 101
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
250 ATGCAAGATCTGCAACACTACCCCTGCCAACCAGCCAGCGGTGGAG 299
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
102 SerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSerG 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
300 TCTCAAGGGGATATGTGTGGCTTCGGGTGTGCTGCTGTGCATGGG 349
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
118 yThrPheSerGlyClyHisGluGlyHisCysLysProThrThrAspCys 135
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
350 CACCTTCTCCGCGAGTGTGACGGTCTGACGACTGTCGACACTTTGG 399
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
135 hrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsnAla 151
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
400 CTGATTTGGATTCTCACCATGTTCCCTGNGAACAGACCCCAATGCT 449
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
152 ValCysValProGlySerProAlaGluProLeuGlyTrpLeuThrVa 168
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
450 GTGTGCATCCGGAGCCACTGCCCACTGACCAATACGCCCACTTTG 499
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
168 lValLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaGlnL 185
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
500 CATCTTCTGCTGTCATGGTGCATGCAATTTCCTTAACCACACAGTCC 549
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
185 euGlyLeuHisIleTrpGlnLeuArgLys..... 194
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
550 TCGGCTGCACATATGGCAGTGGAGGCAACACATGTGTCTCGAGAG 599
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
195 ThrGlnLeuLeuGluValProSerThrGluAspAla 208
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
600 ACCAGCAATTCGGGAGGTGCAATTGTCAGCTGAAGATGCT 641
seq_name: gb_est80:BE850742

seq_documentation_block:
LOCUS      BE850742      609 bp      mRNA      EST      26-SEP-2000
DEFINITION ux01e06.y1 Soares_thymus_2NbMT Mus musculus cDNA clone
            IMAGE:3470242 5' similar to TR:O35714 O35714 GLUCOCORTICOID INDUCED
            TNFR FAMILY RELATED PROTEIN PRECURSOR. ;, mRNA sequence.
ACCESSION  BE850742
VERSION     BE850742.1 GI:10309101
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE   1 (bases 1 to 609)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1389602
Seq primer: -40RP from Gibco
High quality sequence stop: 462.
FEATURES    Location/Qualifiers
            source          1..609
                        /organism="Mus musculus"
                        /strain="C57BL/6J"
                        /db_xref="taxon:10090"
                        /clone="IMAGE:3470242"
                        /clone_lib="Soares_thymus_2NbMT"
                        /sex="male"
                        /tissue_type="Thymus"
                        /dev_stage="4 weeks"
                        /lab_host="DH10B"

```



```
3  GlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAlaLeuLe 19
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55 AGGAGAACCACTATGGGGCATGGGCGCATGCTGTATGGAGTCTCGATGCT 104
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
19  uCysAlaLeuSerLeuGlyGln...ArgProThrGlyGlyProGlyCysG 35
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
105 CTTGTGCTGGAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 154
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
35  lProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCysArg 51
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
155 GCCTGGCAAGTTTCAGAACGGAAGTGGCAACAACACTCGCTCTGCAGC 204
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
52  ValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCys 68
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
205 CTTGTATGCT.....CCAGGCAAGGAGGAGCTGCTCC 233
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
68  rGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspPro 85
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
234 AAAGAAAGGTCGATATGTCACACTGAGTACCAGTGGAGAGCCCTC 283
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
85  yCysThrThrCysArgHisHisProCysProProGlyGlnGlyValGln 101
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
284 AGTGCAAGATCTGCAAGCACTACCTCCGCAACCAAGCCAGAGGCTGG 333
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
102 SerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSer 118
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
334 TCTCAAGGGGATATTGTTTGGCTTCCGGTGTGTTCCCTGCTGCCATGG 383
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118 yThrPheSerGlyGlyHisGluGlyHisCysLysProThrThrAspCys 135
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384 CACCTTCTCCGAGGTCGTCAGCGGTCACTGCAGACTTTGGACCAACT 433
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135 hrGlnPheGlyPheLeuThrValPheProGlyAsnLysThrHisAsnAl 151
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
434 CTCAGTTTGGATTTCTACCATGTTTCCCTGGGAACAGACCCCAATGC 483
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152 ValCysValProGlySerProProAlaGluProLeuLeuGlyTrpLeu 168
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484 GTGTGCATCCCGAGGACCACTGCCCACTGAGCAATACGCCCATTTGAC 533
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
168 lValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaGln 185
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
534 CATCTTCCTGGTCATGGCTGCAATGTTTCTTCTTCTTAACCAACAGC 583
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
185 euGlyLeuHisIleTrpGlnLeuArgLys..... 194
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584 TCGGCTGCACATATGGCAGCTGAGGAGGCAACACATGCTCTCGAGAG 633
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195 ThrGlnLeuLeuLeuGluValProProSerThrGluAspAlaArgSer 211
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
634 ACCAGCCATTCCGGAGGAGTGGATGTCAGCTGAGGATGCTTGCAGCTT 683
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
211 sGlnPheProGluGluGluArgGlyGluArgSerAlaGluGluLysGly 228
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
684 CCAGTTTCCCTGAGGAGGACGCGGGGAGGAGACA...GAAGAAAGTGC 730
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228 rGluGlyAspLeuTrp 233
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
731 ATCTGGGGGGTCTGGTGG 747
```

seq\_name: gb\_est89:BF539340

```
seq_documentation_block:
LOCUS      BF539340          953 bp      mRNA      EST      11-DEC-2000
DEFINITION 602049520F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4188724 5',
           mRNA sequence.
ACCESSION  BF539340
VERSION    BF539340.1  GI:11626721
KEYWORDS   house mouse.
SOURCE     Mus musculus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

REFERENCE  
1 (bases 1 to 953)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM9513 row: h column: 05  
High quality sequence stop: 649.

FEATURES  
Location/Qualifiers  
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/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone\_image="IMAGE:4188724"  
/clone\_lib="NCI\_CGAP\_SG2"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 212 a 235 c 274 g 232 t  
ORIGIN

alignment\_scores:  
Quality: 644.50 Length: 218  
Ratio: 3.859 Gaps: 3  
Percent Similarity: 76.606 Percent Identity: 54.587

alignment\_block:  
US-09-512-363-2 x BF539340 ..  
Align seg 1/1 to: BF539340 from: 1 to: 953

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13  LeuCysGlyLeuAlaLeuLeuCysAlaLeuSerLeuGlyGln...ArgPr 28
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
6  CTGTATGGAGTCTCGATGCTCTGTGCTGTCGACCTAGGTAGCGAGTGT 55
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28  oThrGlyGlyProGlyCysGlyProGlyArgLeuLeuLeuGlyThrGlyT 45
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
56 AGTTGAGGAGCCTGGCTGTGCCCTGCGCAAGGTTTCAGAACGGAAGTGC 105
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
45  hrAspAlaArgCysCysArgValHisThrThrArgCysCysArgAspTyr 61.
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
106 ACAACACTCGCTGCTGCAGCCTGTATGCT..... 134
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62  ProGlyGluGluCysCysSerGluTrpAspCysMetCysValGlnProGl 78
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
135 CCAGGCAAGGAGGACTGTCCAAAGAAAGAGGTGCATATGTCACACCTGA 184
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
78  uPheHisCysGlyAspProCysCysThrThrCysArgHisHisProCys 95
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
185 GTACCACTGTGGAGACCTCAGTCAAGATCTGCAAGCACTACCCCTGCC 234
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
95  roProGlyGlnGlyValGlnSerGlnGlyLysPheSerPheGlyPheGln 111
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
235 AACCAAGCCAGAGGTGGAGTCTCAAGGGGA.TATTGTGTGGCTTCGGG 283
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
112 CysTleAspCysAlaSerGlyThrPheSerGlyGlyHisGluGlyHisCy 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
284 TGTGTTGCCCTGTGCCATGGGACACCTTCTCCGAGGTCGTGAGGTCAC 333
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128 sLysProTrpThrAspCysThrGlnPheGlyPheLeuThrValPhePro 145
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334 CAGACTTTGGACCAACTCTTCTCAGTTTGGATTCTCACCATTGTTCCCTG 383
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145 lyAsnLysThrHisAsnAlaValCysValProGlySerProProAlaGlu 161  
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 384 GGAACAAGACCAATGCTGTGTCATCCCGGAGCCACTGCCACTGAG 433  
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 162 ProLeuGlyTrpLeuThrValValLeuLeuAlaAlaCysValLe 178  
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 434 CAATACGGCCATTGTCATGCTGTCATGCTGTCATGCTGCTTTT 483  
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 178 uLeuLeuThrSerAlaGlnLeuGlyLeuHisIleTrpGlnLeuArgLys. 194  
 ::::|  
 484 CTTCTAACACACATCCAGCTCGCCTGCACATATGGCAGCTGAGGAGC 533  
 |||||  
 195 .....ThrGlnLeuLeuLeuGluValProProSer 204  
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 534 AACACATGTGTCTCGAGAGACCCAGCATTCCGCGAGGTGCAGTTGCA 583  
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 205 ThrGluAspAlaArgSerCysGlnPheProGluGluGluArgGlyGluAr 221  
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 584 GCTGAGGATGCTTCAGCTTCCAGTTCCCTGAGGAGGAACCGGGAGCA 633  
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 221 gSer 222  
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 634 GACG 637

seq\_name: gb\_est44:AW230447

seq\_documentation\_block: 659 bp mRNA EST 10-DEC-1999  
 LOCUS AW230447  
 DEFINITION uc63f10.y1 NCI\_CGAP\_Mam1 Mus musculus cDNA clone IMAGE:2647243 5'  
 similar to TR:O35714 O35714 GLOCOGORTICOID INDUCED TNFR FAMILY  
 RELATED PROTEIN PRECURSOR. ;, mRNA sequence.  
 ACCESSION AW230447  
 VERSION AW230447.1 GI:6559743  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 1 (bases 1 to 659)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Other ESTs: uc63f10.x1  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-r@mail.nih.gov  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 Clone Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/dbrrp/image/image.html](http://www-bio.llnl.gov/dbrrp/image/image.html)

MGI:1027695

Seq primer: -40RP from Gibco

High quality sequence stop: 434.

#### FEATURES

source  
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 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:2647243"  
 /clone\_lib="NCI\_CGAP\_Mam1"  
 /tissue\_type="tumor, biopsy sample"  
 /dev\_stage="3 months, virgin"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: Salt;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Library constructed by Life Technologies. Investigator  
 providing samples: Gilbert Smith, NIH"  
 142 a 178 c 188 g 149 t 2 others

#### BASE COUNT

seq\_name: gb\_est44:AW230423 644 bp mRNA EST 10-DEC-1999  
 seq\_documentation\_block:  
 LOCUS AW230423

#### ORIGIN

alignment\_scores:  
 Quality: 629.50 Length: 220  
 Ratio: 3.792 Gaps: 4  
 Percent Similarity: 75.455 Percent Identity: 51.364  
 alignment\_block:  
 US-09-512-363-2 x AW230447 ..  
 Align seg 1/1 to: AW230447 from: 1 to: 659  
 3 GlnHisGlyAlaMetGlyAlaPheArgAlaLeuCysGlyLeuAlaLeu 19  
 ::::|  
 21 AGGAGAAGCACTATGGGCGCATGCTGTATGGAGTCTCGATGCT 70  
 |||||  
 19 uCysAlaLeuSerLeuGlyGln....ArgProThrGlyGlyProGlyCysG 35  
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 71 CTGTGTGCTGGACCTAGGTACGCCGAGTGTAGTTGAGGAGCCTGGCTGTG 120  
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 35 lyProGlyArgLeuLeuGlyThrGlyThrAspAlaArgCysCysArg 51  
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 121 GCCCTGGCAAGGTTGAGAACGGAAGTGGCAACACACTCCTGCTGCACG 170  
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 52 ValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCysSe 68  
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 171 CTGTATGCT.....CCAGGCAAGGAGGACTGTCTC 199  
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 68 rGluTrpAspCysMetCysValGlnProGluPheHisCysGlyAspProC 85  
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 200 AAAGAAGAGGTGTCATATGTCACACCTGAGTACCACCTGTGAGACCCCTC 249  
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 85 ysCysArgHisHisProCysProGlyGlnGlyValGln 101  
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 250 AGTCAAGATCTGCCACCTGCCAACCCAGCCAGGAGGTGGAG 299  
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 102 SerGlnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSerG 118  
 ::::|  
 300 TCTCAAGGGATATTGTGTGGCTTCGGTGTGTGCTGTCCTGCTGCTGCTG 349  
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 118 yThrPheSerGlyGlyHisGluGlyHisCysLysProThrPheAspCysT 135  
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 350 CACCTTCTCCGAGGTCGTGACGGTCACTGCAGACTTTGGACCAACTGTT 399  
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 135 hrGlnPheGlyPheLeuThrValPheProGlyValAsnLysThrHisAsnAla 151  
 ::::|  
 400 CTCAGTTTGGATTCTCACCATGTTCCCTGGGAAACAGACCCCACTGCT 449  
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 152 ValCysValProGlySerProAlaGluProLeuLeuGlyTrpLeuThrVa 168  
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 450 GTGTGCATCCCGGAGCCACTGCCCACTGAGCAATACGGCCATTGACTGT 499  
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 168 lValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaGlnL 185  
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 500 CATCTCTCTGCTGTCATGCTGTCATGCTTCTTCCTAACACAGACCTCCAG 549  
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 185 euGlyLeuHisIleTrpGlnLeuArgLysThrGlnLeuLeuLeu...Glu 200  
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 550 TCGGCTGCACATATGGCAGCTGAGGAGGCAACACATGTTGCTNCTCGAGAG 599  
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 650 TCAGTTCCCT 659

seq\_name: gb\_est44:AW230423

seq\_documentation\_block:

LOCUS AW230423



OM of: US-09-512-363-2 to: EST:\* out\_format : pfs

Date: Sep 4, 2001 3:53 PM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODE=frame+p2n.model -DEV=xip  
-Q/cgnt\_1/USPTO.spool/US09512363/runat\_04092001\_154254\_21769/app\_query.fasta\_1.293  
-DB=EST -OMT=fastap -SUFFIX=p2n.rst -GAPO=12.000 -GAPEXT=4.000  
-MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000 -QGAPO=4.500  
-QGAPEXT=0.050 -XGAPO=10.000 -XGAPEXT=0.500 -FGAPO=6.000  
-FGAPEXT=7.000 -YGAPO=10.000 -YGAPEXT=0.500 -DELOP=6.000  
-DELEXT=7.000 -START=1 -MATRIX=blomsum62 -TRANS=human40.cdi  
-LIST=45 -MODE=LOCAL -OUTMT=pfs -NORM=ext -MINLEN=0  
-ALIGN=15 -DOPE=LOCAL -OUTMT=pfs -NORM=ext -MINLEN=0  
-MAXLEN=2000000000 -USER=US09512363@cgnl\_1.2850 -NCPU=6  
-ICPU=3 -LONGLOG -NO\_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-512-363-2  
Query length: 234  
Database: EST:\*  
Database sequences: 10228115  
Database length: 431459454  
Search time (sec): 630.590000

score\_list:

Sequence	Strd	Orig	Zscore	Bscore	Len	Documentation
gb_est26:AI923712	-	853.50	1253.37	1.1e-60	650	AI923712 wn59q06.x1 NCI_CGAP_Lu
gb_est89:BF539340	+	704.00	1027.82	3.9e-48	1026	AK020762 Mus musculus 0 day ne
gb_est44:AW230447	+	644.50	940.71	2.8e-43	933	BF539340 602049520F1 NCI_CGAP_S
gb_est80:BE850742	+	629.50	922.39	2.9e-42	659	AW230447 uo63f10.y1 NCI_CGAP_Ma
gb_est73:BE374685	+	623.50	918.20	5.0e-42	644	AW230423 uo63d10.y1 NCI_CGAP_Ma
gb_est45:AW330857	+	623.50	918.20	5.0e-42	609	BE850742 uo1e06.y1 Soares.thym
gb_est83:BF117994	+	608.00	897.51	1.7e-40	669	BF374685 601224187F1 NCI_CGAP_M
gb_est47:AW483085	+	605.00	887.08	2.7e-40	606	AK300857 xk07c07.x1 NCI_CGAP_Cc
gb_est50:AW659186	+	524.00	771.94	7.0e-34	393	BF117994 u210e09.y1 NCI_CGAP_Ma
gb_est73:BE373185	+	494.50	724.84	3.0e-31	552	AW483085 u031d10.y1 NCI_CGAP_Ma
gb_est72:BE373185	+	404.50	594.22	5.6e-24	442	AW659186 96144 MARC IBOV Bos ta
gb_est17:AI236084	+	357.00	521.28	6.4e-20	620	AW330857 60122521F1 NCI_CGAP_M
gb_est17:AI214481	+	357.00	525.91	3.6e-20	370	BE373185 60122521F1 NCI_CGAP_M
gb_est86:BF318127	-	319.50	473.64	2.9e-17	274	BE244247 TCBAPE20971 Pediatric
gb_est21:AI499936	+	272.00	393.62	8.3e-13	708	AI214481 qg93d01.x1 Soares.NFL
gb_est16:AI117445	+	247.00	358.95	7.1e-11	570	AW208743 uo63d10.y1 NCI_CGAP_Ma
gb_est50:AW659189	+	238.50	352.96	1.5e-10	303	BF318127 uo1e06.y1 Soares.thym
gb_est49:AW591899	+	238.50	352.20	1.7e-10	326	AI499936 uo63a03.x1 NCI_CGAP_Ga
gb_est42:AW084829	-	238.50	351.79	1.8e-10	339	AI117445 uo88b01.r1 Soares.thym
gb_est14:AI923712	+	230.50	344.01	4.8e-10	230	BE047368 hg79h06.x1 NCI_CGAP_Ov
gb_est71:BE324427	+	219.50	320.38	1.0e-08	468	AW659189 96150 MARC IBOV Bos ta
gb_est40:AA964652	+	211.00	313.85	2.3e-08	262	AW591899 xx84g01.x1 NCI_CGAP_Ly
gb_est72:BE324427	+	200.50	288.33	6.1e-07	687	AW084829 xc63f08.x1 NCI_CGAP_Es
gb_est10:BG436824	+	200.00	276.01	3.0e-06	2092	AI236084 EST232646 Normalized r
gb_est73:BE233113	+	195.00	280.40	1.7e-06	674	AK019885 Mus musculus 11 days
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VERSION AI923712.1 GI:5659676  
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SOURCE human.  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 650)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing by: Greg Lennon, Ph.D.  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html  
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High quality sequence stop: 459.

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pooled lung tumor tissue, and was then primed with a Not I  
- oligo(dT) primer. Double-stranded cDNA was ligated to  
Eco RI adaptors (Pharmacia), digested with Not I and  
cloned into the Not I and Eco RI sites of the modified  
pT73 vector. Library went through one round of  
normalization. Library constructed by Bento Soares and M.  
Fatima Bonaldo."

BASE COUNT 112 a 218 c 216 g 102 t 2 others  
ORIGIN

alignment\_scores:  
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Ratio: 5.402 Gaps: 1  
Percent Similarity: 92.941 Percent Identity: 91.176

alignment\_block:  
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74 ...CysValGlnProGluPheHisCysGlyAsp.....ProCysCy 86
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seq\_documentation\_block:

; Sequence 1, Application US/08195967

; Patent No. 6242566

; GENERAL INFORMATION:

; APPLICANT: Godfrey, Wayne

; APPLICANT: Engleman, Edgar G.

; TITLE OF INVENTION: LIGAND (ACT-4-L) TO A RECEPTOR ON THE SURFACE OF ACTIVATED

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Hourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

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; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,967
; FILING DATE: 10-FEB-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 05490A-230
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1057 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..845
; OTHER INFORMATION: /standard_name= "ACT-4 cDNA"
; US-08-195-967-1
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Quality: 168.50 Length: 253  
Ratio: 1.518 Gaps: 8  
Percent similarity: 43.874 Percent identity: 25.692

alignment\_block:

US-09-512-363-2 x US-08-195-967-1 ..

Align seg 1/1 to: US-08-195-967-1 from: 1 to: 1057

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17 .....AlaLeuLeuCysAlaLeuSerLeuGlyG 26
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76 TGGGGCTGAGCACCGTGAAGGGGCTCCACTGTGTGGGGACACCTACCCC 125

26 lnArgProThrGlyGlyPro.GlyCysGlyProGlyArgLeuLeuG1 42
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126 AGCAAGACCGGTGCTGCCAGAGTGCAGGCCA.....GG 160

42 yThrGlyThrAspAlaArgCysCysArgValHisThrThrArgCysCysA 59
|||||
161 CAACGGGATGGTGGAGCGGTGAGCGCTCCAGAACACAGGTGTGCCGTC 210

59 rgAspTyrProGly.....GluGluCysCysSerGluTrpAspCysMet 73
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211 CGTGGCGCGCGGTCTTACAAGACAGCGTGGTCAAGTCCCAAGCGGTGCAAG 260

74 ...CysValGlnProGluPheHisCysGlyAsp.....ProCysCy 86
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261 CCCTGCACGTGTGTAACTCAAGTGGAGTGAGCGGAAGCAGGTGTG 310

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103 lnGlyLysPheSerPheGlyPheGlnCysIleAspCysAlaSerGlyThr 119
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361 TGGACAGCTACAAGCTGGAGTTGACTGTGCCCTGCCCTCCAGGGCAC 410
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461 GGCTGGGAAGCACACCTGTGAGCGCGCCAGCAATAGCTCGGACGCAATCT 510  
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; FILING DATE: 22-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE: 23-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1317 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: MOX40Fc MuteIn
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; NAME/KEY: CDS
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US-08-494-574-10

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94  .....CysProPr 96
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seq_documentation_block:
; Sequence 1, Application US/08192480A
; Patent No. 5759546
; GENERAL INFORMATION:
; APPLICANT: Andrew D. Weinberg and Arthur A.
; APPLICANT: Vandenbark
; TITLE OF INVENTION: TREATMENT OF CD4 T-CELL
; TITLE OF INVENTION: MEDIATED CONDITIONS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Polley, Esq.
; ADDRESSEE: Klarquist Sparkman Campbell
; ADDRESSEE: Leigh & Winston
; STREET: 121 S.W. Salmon Street, Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/192,480A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA: N/A
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard J. Polley, Esq.
; REGISTRATION NUMBER: 28,107
; REFERENCE/DOCKET NUMBER: 4282-38649
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 848 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA to mRNA
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168 alValLeuAlaValAlaCysValLeuLeuLeuThrSerAlaGln 184
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661 CCGCATCTGGGACTGGAGTGTGCTGCGGCGGCGGCGGCGGCGGCGG 710

185 LeuGlyLeuHisIleTrpGlnLeuArgLysThrGlnLeuLeuGluVa 201
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seq_documentation_block:
: Sequence 1, Application US/08147784
: Patent No. 5821332
: GENERAL INFORMATION:
: APPLICANT: Godfrey, Wayne
: APPLICANT: Buck, David
: APPLICANT: Engleman, Edgar G.
: TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED
: TITLE OF INVENTION: CD4+ T-CELLS: ACT-4
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourie and Crew
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/147,784
: FILING DATE: 03-NOV-1993
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 05490A-220
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1057 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHEetical: NO
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: NAME/KEY: CDS
: LOCATION: 15..845
: OTHER INFORMATION: /standard_name= "ACT-4 cDNA"
US-08-147-784-1
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  Percent Similarity: 43.874  Percent Identity: 25.692

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||||| : : : : : ||||| : : : : : |||||

17 .....AlaLeuLeuCysAlaLeuSerLeuGlyG 26
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125 GluGlyHisCysLysProThrPheGlnPheGlyPheLeuTh 141
507 CQTGGCATCTGCGACCCCTGGACAACTGTTCTTGGATGGAAGTCTGT 556
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557 GCTTGTGAATGGAGCAGAGGAGGACGTGTCTGTGGACCATCTCCAG 606
157 .....SerProProAla..... 160
607 CGGACCTCTCTCCGGGAGCATCTCTGTGACCCGCTGCCCTCGGAGA 656
161 GluProLeuGlyTrpLeuThrValVal.....LeuLeuAlaValAla 175
657 GAGCCAGGACACTCTCCGAGATCTCTCTCTTCTTCTTGGCTGACGTC 706
175 aCysValLeuLeuLeuThrSerAlaGlnLeuGlyLeuHis.....I 189
707 GACTGGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 756
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757 TTAACGGGGGAGAGAAAGAACTCTCTATATATTCACAAACACCATTTATG 806
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; Sequence 1, Application US/08816605
; Patent No. 5874240
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816.605
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PP254
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 946 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 124..780
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; NAME/KEY: sig_peptide
; LOCATION: 124..177
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 178..780
US-08-816-605-1

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68 r.....GluTrpAspCysMetCysValGlnProGluPheHisC 81
255 CACCAGCAATGCAGAGTGTACTGC.....ACTCCAGGGTTTCACT 295
81 ysGlyAspProCysCysThrThrCysArgHisHisProCysProProGly 97
296 GCCTGGGGGAGGATGCAGCATGTGT...GAACAGGATTGTAACAAGGT 342
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114 pCysAlaSerGlyThrPheSerGlyGlyHisGluGlyHisCysLysProT 131
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131 rpThrAspCysThrGlnPheGlyPheLeuThrValPheProGlyAsnLys 147
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572 AGATCATCTCTCTTCTTCTTCTGCGCTGAGTCGACTGCGTGTCTCTCTG 621
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195 rGlnLeuLeuLeuGluValProPro.....S 204
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; Sequence 10, Application US/08097827
; Patent No. 5457035
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5457035el Cytokine which is a Ligand for
; TITLE OF INVENTION: OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1317 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: MOX40Fc Mutein
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1317
; US-08-097-827-10
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seq_documentation_block:
; Sequence 10, Application US/08494574
; Patent No. 5783665
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5783665el Cytokine which is a Ligand for
; TITLE OF INVENTION: OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,574
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; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung Se
; APPLICANT: Kang, Chang-YuIl
; TITLE OF INVENTION: Monoclonal antibody against human
; TITLE OF INVENTION: receptor 4-1BB
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnard, Brown & Michaels
; STREET: 306 East State Street, Suite 220
; CITY: Ithaca
; STATE: NY
; COUNTRY: USA
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ZIP: 14850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03965
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,796
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,369
FILING DATE: 01-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/267,577
FILING DATE: 07-NOV-1988
ATTORNEY/AGENT INFORMATION:
NAME: Michaels, Christopher A
REGISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: KW05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 607-273-1711
TELEFAX: 607-273-2609
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 838 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE: H4-1BB #1
DEVELOPMENTAL STAGE: Differentiated T-cell
CELL TYPE: Lymphocyte
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NAME/KEY: CDS
LOCATION: 41..805
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NAME/KEY: mat_peptide
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678 TTAACGGGGCAGAGAAGAACTCTGTATATATCAACAACCATTTATG 727
204 .....SerThrGluAspAlaArgSerCysGlnPhePr 214
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492 GCAAAACCTGTAGCTGGGAACATTAATGACCAGAACGGTACTGCGCTC 541
128 CysLysProTrpThrAspCysThrGlnPheGlyPheLeuThrValPhePr 144
542 TCTGACACCTGCGACGAACCTGCTCTAGACGGAAGTGTGTGCTTAAGAC 591
144 oGlyAsnLysThrHisAsnAlaValCysValPro..... 155
592 CGGGACCAACGGAGAGGAGTGTGTGTGGACCCCTGTGTGAGCTTCT 641
156 .....GlySerProProAlaGlu 161
642 CTCCAGTACCACTTCTGTGTGCTCCAGAGGAGGACGAGGGGCAC 691
162 ProLeuGlyTrpLeuThrValValLeuLeuAlaValAlaAlaCysVal 178
692 TCTTTCAGGTCCTTACCTTGTCTGCGGCGTGACATCGCTTGTGCTGT 741
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742 GGCCCTGATCTTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 791
193 rGlyThrGlnLeuLeuGluValPro..... 202
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; Patent No. 5674704  
; GENERAL INFORMATION:  
; APPLICANT: Alderson, Mark R.  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple 7.5.3  
; SOFTWARE: Microsoft Word, Version #6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/236,918A  
; FILING DATE: 06-May-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/060,843  
; FILING DATE: 07-May-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Anderson, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2801-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 768 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; IMMEDIATE SOURCE:  
; CLONE: mu4-1BB  
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; LOCATION: 1..69  
US-08-236-918A-5

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Ratio: 1.883 Gaps: 10  
Percent Similarity: 49.537 Percent Identity: 28.704

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140 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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189 CTGCAGAGTG .....TGTGCAGGCTATTTCAGGTTCAGAAGT 226
66 yScysSerGluTrp .....AspCysMetCysValGlnProGluPhe 79
142 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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96 oGlyGlnGlyValGlnSerGlnGlyLysPheSerPheGlyPheGlnCysI 113
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113 leAspCysAlaSerGlyThrPheSerGlyGlyHis...GluGlyHisCys 128
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350 AAACCTGTAGCTTGGGAACATTTAATACCAAGAGCGGTACTGGCTCTGT 399
129 LysProTrpThrAspCysThrGlnPheGlyPheLeuThrValPheProG 145
400 CGACCCCTGGAGCAACTGCTCTAGACGAAGTGTGTGCTTAAGACCGG 449
145 yAsnLysThrHisAsnAlaValCysValPro ..... 155
450 GACCACGAGGAAGACGGTGTGTGGACCCCTGTGTGTGAGCTTCTCTC 499
156 .....GlySerProProAlaGluPro 162
500 CCAGTACCACCATTTCTGTGACTCCAGAGGAGGACGAGGAGGACATCC 549
163 LeuGlyTrpLeuThrValValLeuLeuAlaValAlaCysValLeuLe 179
550 TTGCAGGTTCCTTACCTTGTCTCTGCGCTGACATCGGCTTTGCTGCTG 599
179 uLeuThrSerAlaGlnLeuGlyLeuHisLe .....TrpGlnLeuArgL 194
600 CCGATCTTCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 649
194 ySthrGlnLeuLeuGluValPro .....Pro 203
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; Sequence 1, Application PC/TUS9410457
; GENERAL INFORMATION:
; APPLICANT: Byoung Se Kwon
; TITLE OF INVENTION: New Human Receptor and Related Products
; TITLE OF INVENTION: and Methods
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnard & Brown
; STREET: 306 E. State St., Suite 220
; CITY: Ithaca
; STATE: New York
; COUNTRY: United States
; ZIP: 14850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: IBM AT Compatible
; OPERATING SYSTEM: MS DOS, Version 5.0
; SOFTWARE: Special QBasic program
; CURRENT APPLICATION DATA:

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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/012,269
; APPLICATION NUMBER:
; FILING DATE: 2/1/93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/922,996
; FILING DATE: 7/30/92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/267,577
; FILING DATE: 11/7/88
; ATTORNEY/AGENT INFORMATION:
; NAME: Michaels, Christopher A.
; REGISTRATION NUMBER: 34,390
; REFERENCE/DOCKET NUMBER: kwnh41bb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 607-273-1711
; TELEFAX: 607-273-2609
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 838
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: No
; ANTI-SENSE: No
; FRAGMENT TYPE: n/a
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE: H4-1BB #1
; DEVELOPMENTAL STAGE: Differentiated T-cell
; HAPLOTYPE:
; TISSUE TYPE: Lymphocytes
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY: cDNA library
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: H4-1BB
; LOCATION:
; IDENTIFICATION METHOD: Similarity to mouse 4-1BB and other
; IDENTIFICATION METHOD: members of NGFR superfamily
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS: Kwon, B.S., and Weissman, S.M.
; TITLE: cDNA sequences of two inducible T-cell genes
; JOURNAL: Proc. Natl. Acad. Sci. USA
; VOLUME: 86
; ISSUE:
; PAGES: 1963-1967
; RELEVANT RESIDUES IN SEQ ID NO: all
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401 GYACNCARTYGGNTTYTNCACGNTWTTCNGNGNAYAAARACNCAYAY 450
151 AlaValCysValProGlySerProProAlaGluProLeuGlyTrpLeuTh 167
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167 rValValLeuLeuAlaValAlaAlaCysValLeuLeuLeuThrSerAlaG 184
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194 LysThrGlnLeuLeuLeuGluValProProSerThrGluAspAlaArgSe 210
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; Sequence 1, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1073 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 68..751
; US-08-911-423-1

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19 uCysAlaLeuSerLeuGlyGln...ArgProThrClyGlyProGlyCysG 35
106 CTGTGTCTGGACCTAGGTCTACCGAGTGTAGTTGAGGAGCCTGGCTGTG 155
35 lYProGlyArgLeuLeuLeuGlyThrGlyThrAspAlaArgCysCysArg 51
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52 ValHisThrThrArgCysCysArgAspTyrProGlyGluGluCysCysSe 68
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285 AGTCAAGATCTGCAAGCACTACCCCTGCCAACCCAGGCCAGAGGTGGAG 334
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335 TCTCAAGGGGATATTGTGTTGGCTTCGGGTGTGTTGCTGTGCCATGGG 384
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535 CATCTTCTGCTCATGCTGTCATGCAATTTCTTCTTAACACACAGTCCAGC 584
185 euGlyLeuHisIleTrpGlnLeuArgLys..... 194
585 TCGGCTGTGCACATATGGCAGCTGAGGAGGCAACACACTGTGCCCGAGAG 634
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635 ACCAGCCATTCCGGAGGTGTCAGTTGTCAGTGAGGATGCTTCAGCTT 684  
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seq\_documentation\_block:  
; Sequence 72, Application US/09188930A  
; Patent No. 6150502  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene  
; APPLICANT: Murison, James Greg  
; TITLE OF INVENTION: Compositions Isolated From Skin Cells  
; FILE OF INVENTION: and Methods For Their Use  
; FILE REFERENCE: 11000.1011c1  
; CURRENT APPLICATION NUMBER: US/09/188,930A  
; CURRENT FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 348  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 72  
; LENGTH: 267  
; TYPE: DNA  
; ORGANISM: mouse  
US-09-188-930-72

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Ratio: 3.806 Gaps: 2  
Percent Similarity: 70.526 Percent Identity: 46.316

alignment\_block:

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24 uGlyGln...ArgProThrGlyGlyProGlyCysGlyProGlyArgLeu 40  
51 AGGTCCAGCGAGTGTAGTTGAGGAGCTGGCTGTGGCCCTGGCAAGTTC 100  
40 euLeuGlyThrGlyThrAspAlaArgCysCysArgValHisThrThrArg 56  
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; Sequence 1, Application PC/TUS9603965

GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung Se  
; APPLICANT: Kang, Chang-Yuil  
; TITLE OF INVENTION: Monoclonal antibody against human  
; TITLE OF INVENTION: receptor 4-1BB  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Barnard, Brown & Michaels  
; STREET: 306 East State Street, Suite 220  
; CITY: Ithaca  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 14850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/03965  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/122,796  
; FILING DATE: 16-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/012,269  
; FILING DATE: 01-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/922,996  
; FILING DATE: 30-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/267,577  
; FILING DATE: 07-NOV-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michaels, Christopher A  
; REGISTRATION NUMBER: 34,390  
; REFERENCE/DOCKET NUMBER: KW05  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 607-273-1711  
; TELEFAX: 607-273-2609  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2347 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; ORIGINAL SOURCE:  
; ORGANISM: murine 4-1BB  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 146..916  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 146..913  
; PUBLICATION INFORMATION:  
; AUTHORS: Kwon, Byoung Se  
; AUTHORS: et al.,  
; TITLE: cDNA sequences of two inducible T-cell genes  
; JOURNAL: Proc. Natl. Acad. Sci. U.S.A.  
; VOLUME: 86  
; ISSUE: March  
; PAGES: 1963-1967  
; DATE: 1989  
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 2347  
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Date: Sep 4, 2001 3:55 PM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

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Search information block:

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; Sequence 5, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
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; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911.423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023.419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027.901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
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; TYPE: nucleic acid
; STRANDEDNESS: single
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Job time: 69 sec

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R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A:Reference number: AB2950; MUID:20437337  
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A.; Ehrlich, S.D.; Emmeron, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Kostter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Roche, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wilpat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
A.; Authors: Yoshikawa, H.F.; Zumbato, E.; Yoshikawa, H.; Danchin, A.  
A:title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
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A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
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C:Genetics:  
A:Gene: yqiI

Query Match 3.0%; Score 7; DB 2; Length 206;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ALCGLAL 18  
|||||||  
Db 9 ALCGLAL 15

---

nd with high affinity to fibronectin.

C;Genetics:  
A:Gene: GDB:GSN  
A:Cross-references: GDB:120019; OMIM:105120; OMIM:137350  
A:Map position: 9q33-q33  
A:Introns: 48/3; 117/1  
C:Superfamily: gelsolin; gelsolin repeat homology  
C;Keywords: actin binding; alternative splicing; amyloid; calcium; duplication  
F:1-27/Domain: signal sequence #status predicted <SIG>  
F:28-782/Product: gelsolin, plasma #status experimental <MAT1>  
F:51-176/Domain: actin-severing #status predicted <SEV>  
F:53-782/Product: gelsolin, cytosolic #status experimental <MAT2>  
F:66-397/Domain: gelsolin repeat homology <GEL1>  
F:123-126/Region: actin-actin interfilament contact  
F:434-782/Domain: calcium-sensitive, actin binding #status predicted <ACT>  
F:445-764/Domain: gelsolin repeat homology <GEL2>

Query Match 3.4%; Score 8; DB 1; Length 782;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ALLCALSL 24

Db 9 ALLCALSL 16

RESULT 6

I48349  
fibronectin - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 20-Aug-1999  
C:Accession: I48349; S33445  
R:Polly, P.; Nicholson, R.C.  
Gene 137, 353-354, 1993  
A:Title: Sequence of the mouse fibronectin-encoding gene promoter region.  
A:Reference number: I48349; MUID:94131313  
A:Accession: I48349  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-28 <RES>  
A:Cross-references: EMBL:222729; NID:g297911; PIDN:CAA80422.1; PID:g297912  
R:Polly, P.; Nicholson, R.C.  
submitted to the EMBL Data Library, May 1993  
A:Description: Nucleotide sequence of the murine fibronectin gene promoter region.  
A:Reference number: S33445  
A:Accession: S33445  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-27 <POL>  
A:Cross-references: EMBL:222729  
C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat

Query Match 3.0%; Score 7; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 GPGRLLL 41

Db 6 GPGRLLL 12

RESULT 7

A83044  
hypothetical protein PA4823 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: A83044  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.  
A:Reference number: A82950; MUID:20437337  
A:Accession: A83044  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-69 <STO>  
A:Cross-references: GB:AE004895; GB:AE004091; NID:g9951083; PIDN:AA080208.1; GSPDB:GN000146  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA4823

Query Match 3.0%; Score 7; DB 2; Length 69;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RALCGLA 17

Db 13 RALCGLA 19

RESULT 8

A86860  
hypothetical protein ytfA [imported] - Lactococcus lactis subsp. lactis (strain IL140)  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 23-Mar-2001  
C:Accession: A86860  
R:Boletín, A.; Winkler, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissbach, J.; Ehmann, R.  
Genome Res. in press, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium.  
A:Reference number: A86625  
A:Accession: A86860  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-92 <STO>  
A:Cross-references: GB:AE005176; NID:g12724914; PIDN:AAK05979.1; GSPDB:GN00146  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: ytfA

Query Match 3.0%; Score 7; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 VLLAVA 174

Db 80 VLLAVA 86

RESULT 9

B25429  
T-cell receptor beta chain precursor V region (SJL73) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jun-1988 #sequence\_revision 02-Jun-1988 #text\_change 30-May-1997  
C:Accession: B25429  
R:Behlke, M.A.; Chou, H.S.; Huppi, K.; Loh, D.Y.  
Proc. Natl. Acad. Sci. U.S.A. 83, 767-771, 1986  
A:Title: Murine T-cell receptor mutants with deletions of beta-chain variable region  
A:Reference number: A94132; MUID:86121021  
A:Accession: B25429  
A:Molecule type: mRNA  
A:Residues: 1-120 <BEH>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: T-cell receptor  
F:11-120/Product: T-cell receptor beta chain V region SJL73 #status predicted <MAT>

Query Match 3.0%; Score 7; DB 2; Length 120;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GPGCGPG 37

Db 5 GPCCGPG 11  
|||||||

## RESULT 10

A71173  
hypothetical protein PH0581 - Pyrococcus horikoshii  
C:Species: Pyrococcus horikoshii  
C>Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 21-Jul-2000  
C:Accession: A71173  
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hino, Y.; Yamamoto, S.; Sekin  
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yanazaki, J.; Kushida, N.; Oguchi  
DNA Res. 5, 55-76, 1998  
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a  
A:Reference number: A71000; MUID:98344137  
A:Accession: A71173  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-133 <KAW>  
A:Cross-references: GB:AP000002; NID:G3236129; PIDN:BAA29670.1; PID:G3256987  
A:Experimental source: strain OT3  
A:Note: This accession replaces an interim accession for a sequence replaced by GenBank  
C:Genetics:  
A:Gene: PH0581  
C:Superfamily: hypothetical protein MJ1081

Query Match 3.0%; Score 7; DB 2; Length 133;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 GRLLGT 43  
|||||||  
Db 103 GRLLGT 109

## RESULT 11

G75053  
hypothetical protein PAB0941 - Pyrococcus abyssi (strain Orsay)  
C:Species: Pyrococcus abyssi  
C>Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000  
C:Accession: G75053  
R:anonymous, Genoscope  
submitted to the EMBL Data Library, July 1999  
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru  
A:Reference number: A75001  
A:Accession: G75053  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-133 <KAW>  
A:Cross-references: GB:AJ248287; GB:AL096836; NID:G5458657; PIDN:CAB50324.1; PID:G545883  
A:Experimental source: strain Orsay  
C:Genetics:  
A:Gene: PAB0941  
C:Superfamily: hypothetical protein MJ1081

Query Match 3.0%; Score 7; DB 2; Length 133;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 GRLLGT 43  
|||||||  
Db 103 GRLLGT 109

## RESULT 12

UTCAB  
gonadotropin beta chain precursor - common carp  
C:Species: Cyprinus carpio (common carp)  
C>Date: 31-Aug-1979 #sequence\_revision 16-Feb-1996 #text\_change 23-Mar-2001  
C:Accession: S29677; S29678; A01504  
R:Chang, Y.S.; Huang, F.L.; Lo, T.B.

submitted to the EMBL Data Library, May 1991  
A:Reference number: S29677  
A:Accession: S29677  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-144 <CHI>  
A:Cross-references: EMBL:X59888; NID:G62619; PIDN:CAA42542.1; PID:G62620  
A:Accession: S29678  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-144 <CHI>  
A:Cross-references: EMBL:X59889; NID:G62621; PIDN:CAA42543.1; PID:G62622  
R:Chang, Y.S.; Huang, C.J.; Huang, F.L.; Lo, T.B.  
Int. J. Pept. Protein Res. 32, 556-564, 1988  
A:Title: Primary structures of carp gonadotropin subunits deduced from cDNA nucleotid  
A:Reference number: JK0024; MUID:89233593  
A:Accession: J70462  
A:Molecule type: mRNA  
A:Residues: 1-144 <CHI>  
R:Joilles, J.; Burzawa-Gerard, E.; Fontaine, Y.A.; Joilles, P.  
Biochimie 59, 893-898, 1977  
A:Title: The evolution of gonadotropins: some molecular data concerning a non-mammali  
A:Reference number: A90673; MUID:78124308  
A:Accession: A01504  
A:Molecule type: protein  
A:Residues: 28-36, 'X', 38-53; 141-142 <JOL>  
C:Genetics:  
A:Introns: 6/2; 65/3  
C:Superfamily: pituitary glycoprotein hormone beta chain  
C:Keywords: glycoprotein; pituitary  
F:1-27/Domain: signal sequence #status predicted <SIG>  
F:28-117/Product: gonadotropin beta chain #status predicted <MAT>  
F:33-58,47-81,50-112,62-134,96-124,114-117/Disulfide bonds: #status predicted  
F:37/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 3.0%; Score 7; DB 1; Length 144;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 VVLLAVA 174  
|||||||  
Db 19 VVLLAVA 25

## RESULT 13

G83342  
hypothetical protein PA2436 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: G83342  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa  
A:Reference number: A82950; MUID:20437337  
A:Accession: G83342  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-144 <STO>  
A:Cross-references: GB:AE004670; GB:AE004091; NID:G9948470; PIDN:AAG05824.1; GSPDB:GN  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA2436

Query Match 3.0%; Score 7; DB 2; Length 144;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 LCGLALL 19  
|||||||

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2001, 09:46:19 ; Search time 17.09 Seconds  
(without alignments)  
1042.999 Million cell updates/sec

Title: US-09-512-363-2  
Perfect score: 234  
Sequence: 1 MAQHGMGAFRALCGALLC.....EEERGSAAEKRLGDLWV 234

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	3.4	215	2 T33566	hypothetical prote
2	8	3.4	241	2 E70470	conserved hypothet
3	8	3.4	411	2 S61245	probable virion gl
4	8	3.4	509	2 H70597	probable membrane
5	8	3.4	782	1 FAHUP	gelosin precursor
6	7	3.0	28	2 I48349	fibronectin - mous
7	7	3.0	69	2 A83044	hypothetical prote
8	7	3.0	92	2 A86860	hypothetical prote
9	7	3.0	120	2 B25429	T-cell receptor be
10	7	3.0	133	2 A71173	hypothetical prote
11	7	3.0	133	2 G75053	hypothetical prote
12	7	3.0	144	1 UTCAB	gonadotropin beta
13	7	3.0	144	2 G83342	hypothetical prote
14	7	3.0	200	2 B83642	hypothetical prote
15	7	3.0	206	2 E69961	N-acetyluramoyl-L
16	7	3.0	213	2 G75303	conserved hypothet
17	7	3.0	232	2 S58353	CD1b protein - she
18	7	3.0	256	2 D69845	thiamin biosynthes
19	7	3.0	268	2 B42424	chitinase (EC 3.2.
20	7	3.0	272	2 C75291	guanylate kinase -
21	7	3.0	274	2 B45887	leukocyte differen
22	7	3.0	286	2 S07533	puff II/9A-2 prote
23	7	3.0	286	2 S07532	puff II/9-1 protei
24	7	3.0	288	2 G75513	thiamin biosynthes
25	7	3.0	297	2 I38517	syntaxin - human
26	7	3.0	297	2 S52726	syntaxin-4 - human
27	7	3.0	320	2 T35265	probable D-amino a
28	7	3.0	320	2 T36062	probable ABC-type
29	7	3.0	324	2 S51001	transforming prote

30 7 3.0 325 2 D83366 probable transcrip  
31 7 3.0 332 2 S63660 NADH dehydrogenase  
32 7 3.0 333 2 S47246 gene CDI protein -  
33 7 3.0 335 1 HLHUR3 T-cell surface gly  
34 7 3.0 350 2 T03485 ornithine cyclodea  
35 7 3.0 352 2 S76078 hypothetical prote  
36 7 3.0 354 2 G75548 ABC transporter, A  
37 7 3.0 359 2 A56549 cell-cell signalin  
38 7 3.0 371 2 T20093 hypothetical prote  
39 7 3.0 376 2 T35085 hypothetical prote  
40 7 3.0 377 2 G71341 conserved hypothet  
41 7 3.0 401 1 A36961 pillin biogenesis p  
42 7 3.0 407 2 E81914 probable transmem  
43 7 3.0 426 2 F81187 glucose/galactose  
44 7 3.0 440 2 A83435 ATP synthase in ty  
45 7 3.0 447 2 S37048 cysteine proteinas

#### ALIGNMENTS

##### RESULT 1

T33566  
hypothetical protein R160.6 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T33566  
R:Nelson, J.; Gattung, S.  
Submitted to the EMBL Data Library, October 1998  
A:Description: The sequence of C. elegans cosmid R160.  
A:Reference number: Z21370  
A:Accession: T33566  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-215 <NEI>  
A:Cross-references: EMBL:AF099001; PIDN:AAC68733.1; GSPDB:GN00028; CESP:R160.6  
A:Experimental source: strain Bristol N2; clone R160  
C:Genetics:  
A:Gene: CESP:R160.6  
A:Map position: X  
A:Introns: 31/2; 74/1; 96/2  
C:Superfamily: Caenorhabditis elegans hypothetical protein R160.6

Query Match 3.4%; Score 8; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 4.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 VLLAVAAC 176

Db 24 VLLAVAAC 31

##### RESULT 2

E70470  
conserved hypothetical protein aq\_1986 - Aquifex aeolicus  
C:Species: Aquifex aeolicus  
C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 18-Aug-2000  
C:Accession: E70470  
R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;

Nature 392, 353-358, 1998  
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A:Reference number: A70300; MUID:98196666  
A:Accession: E70470  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-241 <AAQ>  
A:Cross-references: GB:AF000766; NID:q2984216; PIDN:AAC07762.1; PID:q2984233; GB:AE00  
A:Experimental source: strain VF5  
C:Genetics:  
A:Gene: aq\_1986  
C:Superfamily: conserved hypothetical protein aq\_1986

Query Match 3.4%; Score 8; DB 2; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 5.2;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 ALLCALSL 24  
 |||||  
 Db 38 ALLCALSL 45

RESULT 3  
 S61245  
 probable virion glycoprotein M (gm) - bovine herpesvirus 1  
 C:Species: bovine herpesvirus 1  
 C:Date: 18-Sep-1997 #sequence\_revision 18-Sep-1997 #text\_change 26-Aug-1999  
 C:Accession: S61245  
 R:Vleck, C.; Benes, V.; Lu, Z.; Kutish, G.F.; Paces, V.; Rock, D.; Letchworth, G.J.; Sch  
 submitted to the EMBL Data Library, January 1995  
 A:Description: Nucleotide sequence analysis of a 30-kb region of the bovine herpesvirus  
 A:Reference number: S61233  
 A:Accession: S61245  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-411 <VLC>  
 A:Cross-references: EMBL:Z48053; NID:g971311; PIDN:CAA88123.1; PID:g971324  
 C:Superfamily: herpesvirus 51K protein

Query Match 3.4%; Score 8; DB 2; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 7.9;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 168 VVLLAVAA 175  
 |||||  
 Db 93 VVLLAVAA 100

RESULT 4  
 H70597  
 probable membrane protein - Mycobacterium tuberculosis (strain H37RV)  
 C:Species: Mycobacterium tuberculosis  
 C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
 C:Accession: H70597  
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
 ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
 Nature 393, 537-544, 1998  
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A:Reference number: A70500; MUID:98295987  
 A:Accession: H70597  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-509 <COL>  
 A:Cross-references: GB:Z94121; GB:ALL23456; NID:g3261736; PIDN:CAB08087.1; PID:e312290;  
 A:Experimental source: strain H37RV  
 C:Genetics:  
 A:Gene: RV3887C

Query Match 3.4%; Score 8; DB 2; Length 509;  
 Best Local Similarity 100.0%; Pred. No. 9.4;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 168 VVLLAVAA 175  
 |||||  
 Db 205 VVLLAVAA 212

RESULT 5  
 FAHUP  
 gelsolin precursor, plasma [validated] - human

N:Alternate names: actin-depolymerizing factor; brevini  
 N:Contains: amyloid protein, I2K; gelsolin, cytosolic  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 08-Dec-2000  
 C:Accession: A03011; A38797; S03073; A60849; A36029; A61263; A34137  
 R:Kwiatkowski, D.J.; Stossel, T.P.; Orkin, S.H.; Mole, J.E.; Colten, H.R.; Yin, H.L.  
 Nature 323, 455-458, 1986  
 A:Title: Plasma and cytoplasmic gelsolins are encoded by a single gene and contain a  
 A:Reference number: A93383; MUID:87014807  
 A:Accession: A03011  
 A:Molecule type: mRNA  
 A:Residues: 1-782 <KWI>  
 A:Cross-references: EMBL:X04412; NID:g35447; PIDN:CAA28000.1; PID:g736249  
 A:Accession: A38797  
 A:Molecule type: protein  
 A:Residues: 28-52; 178-194, 'XX', 197; 279-290, 'S', 292-294, 'XX', 297-303; 434-449, 'XX', 452-  
 R:Kwiatkowski, D.J.; Wehl, R.; Yin, H.L.  
 J. Cell Biol. 106, 375-384, 1988  
 A:Title: Genomic organization and biosynthesis of secreted and cytoplasmic forms of g  
 A:Reference number: S03073; MUID:88115587  
 A:Accession: S03073  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-116 <KW3>  
 A:Cross-references: EMBL:X07065  
 A:Note: 1-Met is the initiator for plasma gelsolin. 52-Met is the initiator for cyto  
 R:Bryan, J.; Hwo, S.  
 J. Cell Biol. 102, 1439-1446, 1986  
 A:Title: Definition of an N-terminal actin-binding domain and a C-terminal Ca(2+) reg  
 A:Reference number: A60849; MUID:86168493  
 A:Accession: A60849  
 A:Molecule type: protein  
 A:Residues: 'X', 52-55, 'X', 57-59, 'X', 61-62 <BRV>  
 R:Vandekerckhove, J.; Bauw, G.; Vancompernelle, K.; Honore, B.; Celis, J.  
 J. Cell Biol. 111, 95-102, 1990  
 A:Title: Comparative two-dimensional gel analysis and microsequencing identifies gels  
 A:Reference number: A36029; MUID:90307803  
 A:Accession: A36029  
 A:Molecule type: protein  
 A:Residues: 'XX', 150-153, 'X', 155, 'X', 157-159; 486-492, 'X', 494-498, 'X', 500, 'X', 628-641,  
 R:Maury, C.P.J.  
 J. Clin. Invest. 87, 1195-1199, 1991  
 A:Title: Gelsolin-related amyloidosis. Identification of the amyloid protein in Finni  
 A:Reference number: A61263; MUID:91185597  
 A:Accession: A61263  
 A:Molecule type: protein  
 A:Residues: 200-213, 'N', 215-270 <MAU>  
 A:Experimental source: familial amyloid polynuropathy (Finnish-type) heart and kidne  
 A:Note: the substitution of Asn for 214-Asp causes disease  
 R:Haltia, M.; Prelli, F.; Ghiso, J.; Kiuru, S.; Somer, H.; Palo, J.; Frangione, B.  
 Biochem. Biophys. Res. Commun. 167, 927-932, 1990  
 A:Title: Amyloid protein in familial amyloidosis (Finnish type) is homologous to gels  
 A:Reference number: A34562; MUID:90211339  
 A:Accession: A34562  
 A:Molecule type: protein  
 A:Residues: 200-214 <HAL>  
 A:Experimental source: diseased kidney, familial amyloidosis (Finnish type)  
 R:Lind, S.E.; Janney, P.A.  
 J. Biol. Chem. 259, 13262-13266, 1984  
 A:Title: Human plasma gelsolin binds to fibronectin.  
 A:Reference number: A92450; MUID:85030446  
 A:Contents: annotation; fibronectin binding  
 R:Maury, C.P.J.; Alli, K.; Baumann, M.  
 FEBS Lett. 260, 85-87, 1990  
 A:Title: Finnish hereditary amyloidosis. Amino acid sequence homology between the amy  
 A:Reference number: A34137; MUID:90127414  
 A:Accession: A34137  
 A:Molecule type: protein  
 A:Residues: 235-237; 240-252; 258-269 <MA2>  
 A:Experimental source: kidney, Finnish hereditary amyloidosis patient  
 C:Comment: Gelsolin is a calcium-regulated, actin-modulating protein that binds to th  
 can promote the assembly of monomers into filaments (nucleation) as well as sever fil  
 C:Comment: A single gene encodes two forms of gelsolin: one remains associated with t

SQ SEQUENCE 335 AA; 37717 MW; EA041C1C45A5777F CRC64;

Query Match 3.0%; Score 7; DB 1; Length 335;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 GPGRLLL 41  
| | | | |  
Db 216 GPGRLLL 222

## RESULT 15

WN5A\_AMBME  
ID WN5A\_AMBME STANDARD; PRT; 359 AA.  
AC Q06442;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE WNT-5A PROTEIN PRECURSOR.  
GN WNT-5A.  
OS Ambystoma mexicanum (Axolotl).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;  
OC Ambystoma.  
OX NCBI\_TaxID=8296;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=93183769; PubMed=8443107;

RA Busse U., Seguin C.;  
RT "Isolation of cDNAs for two closely related members of the axolotl  
Wnt family, Awnt-5A and Awnt-5B, and analysis of their expression  
during development.";

RL Mech. Dev. 40:63-72(1993).

CC -!- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING  
MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE REGIONS OF  
TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS.

CC -!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE  
EXTRACELLULAR MATRIX.

CC -!- TISSUE SPECIFICITY: NEUROECTODERMAL AND NON-NEUROECTODERMAL  
TISSUES.

CC -!- DEVELOPMENTAL STAGE: ABUNDANT IN THE BLASTULA UNTIL GASTRULATION,  
BARELY DETECTABLE DURING GASTRULATION, AND INCREASE AGAIN DURING  
NEURULATION. DETECTED THROUGHOUT THE REMAINING DEVELOPMENT AND IN  
HATCHED LARVAE.

CC -!- SIMILARITY: BELONGS TO THE WNT FAMILY.

CC -----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL: Z14047; CAA78415.1; -.

DR PIR: S24999; S24999.

DR InterPro: IPR000970; -.

DR Pfam: PF00110; wnt; 1.

DR PROSITE: PS00246; WNT1; 1.

KW Developmental protein; Glycoprotein; Signal.

FT SIGNAL 1 20 POTENTIAL.

FT CHAIN 21 359 WNT-5A PROTEIN.

FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 359 AA; 40116 MW; 533FFB0414DAAA14 CRC64;

## Query Match

Best Local Similarity 3.0%; Score 7; DB 1; Length 359;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LALLCAL 22  
| | | | |  
Db 10 LALLCAL 16

Search completed: September 5, 2001, 09:48:13  
Job time: 113 sec





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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE=95094925; PubMed=8001672;
RA Metzger R., Bader M., Ludwig T., Berberich C., Bunnemann B.,
RA Ganten D.;
RT "Expression of the mouse and rat mas proto-oncogene in the brain and
RT peripheral tissues.";
RL FEBS Lett. 357:27-32(1995).
[2]
RN SEQUENCE OF 1-25 FROM N.A.
RP STRAIN=BCBA; TISSUE=Testis;
RX MEDLINE=97422605; PubMed=9268631;
RA Schweifer N., Valk P.J., Delwel R., Cox R., Francis F.,
RA Meier-Ewert S., Lehrach H., Barlow D.P.;
RT "Characterization of the C3 YAC contig from proximal mouse chromosome
RT 17 and analysis of allelic expression of genes flanking the imprinted
RL Igf2r gene.";
RL Genomics 43:285-297(1997).
CC -1- FUNCTION: NOT KNOWN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -1- CAUTION: WAS ORIGINALLY THOUGHT TO BE A RECEPTOR FOR ANGIOTENSIN
CC II.
CC -----
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CC -----
DR EMBL: X67735; CAA47964.1; -
DR EMBL: U96273; AAB69120.1; -
DR PIR: S29619; S29619.
DR GCRDB: GCR_0660; -
DR GCRDB: GCR_2448; -
DR MGD: MGI:96918; Mas1.
DR InterPro: IPR000276; -
DR InterPro: IPR000820; -
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00533; MASONCOGENE.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS0262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Proto-oncogene.
FT DOMAIN 1 35 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 36 60 1 (POTENTIAL).
FT DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 86 2 (POTENTIAL).
FT DOMAIN 87 103 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 104 127 3 (POTENTIAL).
FT DOMAIN 128 148 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 149 171 4 (POTENTIAL).
FT DOMAIN 172 184 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 185 205 5 (POTENTIAL).
FT DOMAIN 206 223 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 224 244 6 (POTENTIAL).
FT DOMAIN 245 262 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 263 283 7 (POTENTIAL).
FT DOMAIN 284 324 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 19 19 S -> I (IN REF. 2).
SQ SEQUENCE 324 AA; 36904 MW; 24F4AB7299E6016F CRC64;
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Query Match 3.0%; Score 7; DB 1; Length 324;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 17 ALLCALLS 23
DB 153 ALLCALLS 159
[1]
[2]
RESULT 12
CIB1_SHEEP
ID CIB1_SHEEP STANDARD; PRT; 333 AA.
AC Q28565;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE T-CELL SURFACE GLYCOPROTEIN CD1B-1 PRECURSOR (CD1B-1 ANTIGEN)
DE (SCD1A25).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal thymocytes;
RX MEDLINE=96269982; PubMed=8662069;
RA Ferguson E.E., Dutia B.M., Hein W.R., Hopkins J.;
RT "The sheep CD1 gene family contains at least four CD1B homologues.";
RL Immunogenetics 44:86-96(1996).
CC -1- FUNCTION: NOT KNOWN.
CC -1- SUBUNIT: ASSOCIATES NON-COVALENTLY WITH BETA-2-MICROGLOBULIN (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z36890; CAA85359.1; -
DR HSSP: P11609; 1CD1.
DR InterPro: IPR003006; -
DR Pfam: PF00047; Ig; 1.
KW Glycoprotein; Signal; Immunoglobulin domain; Transmembrane;
KW Multigene family.
FT SIGNAL 1 18 BY SIMILARITY.
FT CHAIN 19 333 T-CELL SURFACE GLYCOPROTEIN CD1B-1.
FT DOMAIN 19 302 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 303 323 POTENTIAL.
FT DOMAIN 324 333 CYTOPLASMIC (POTENTIAL).
FT DISULFID 120 184 BY SIMILARITY.
FT DISULFID 224 279 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 333 AA; 37136 MW; 0144767E2525509 CRC64;
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Query Match 3.0%; Score 7; DB 1; Length 333;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 35 GPGRLLL 41  
DB 216 GPGRLLL 222

RESULT 13  
CIB2\_SHEEP  
ID CIB2\_SHEEP STANDARD; PRT; 333 AA.

AC 029422;  
 DT 01-OCT-2000 (Rel. 40, Created)  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DE T-CELL SURFACE GLYCOPROTEIN CD1B-2 ANTIGEN  
 DE (SCD1B-42) (ANTIGEN IAH-CC14).  
 OS Ovis aries (Sheep).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 CC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Thymus;  
 RX MEDLINE=96269982; PubMed=8662069;  
 RA Ferguson E.E., Dutia B.M., Hein W.R., Hopkins J.;  
 RT "The sheep CD1 gene family contains at least four CD1B homologues.";  
 RL Immunogenetics 44:86-96(1996).  
 RN [2]  
 RP SEQUENCE OF 21-33.  
 RX MEDLINE=99115506; PubMed=9914336;  
 RA Rhind S.M., Hopkins J., Dutia B.M.;  
 RT "Amino-terminal sequencing of sheep CD1 antigens and identification of  
 a sheep CD1B gene.";  
 RL Immunogenetics 49:225-230(1999).  
 CC -!- FUNCTION: NOT KNOWN.  
 CC -!- SUBUNIT: ASSOCIATES NON-COVALENTLY WITH BETA-2-MICROGLOBULIN (BY  
 SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; Z36891; CAA85360.1; -;  
 DR HSP; P11609; 1CD1.  
 DR InterPro; IPR003006; -;  
 KW Glycoprotein; Signal; Immunoglobulin domain; Transmembrane;  
 KW Multigene family.  
 FT SIGNAL 1 20  
 FT CHAIN 21 333 T-CELL SURFACE GLYCOPROTEIN CD1B-2.  
 FT DOMAIN 21 302 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 303 323 POTENTIAL.  
 FT DOMAIN 324 333 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 120 184 BY SIMILARITY.  
 FT DISULFID 224 279 BY SIMILARITY.  
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 333 AA; 37039 MW; 861BAE9617DB9BA1 CRC64;  
 Query Match 3.0%; Score 7; DB 1; Length 333;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 35 GPGRLLL 41  
 Db 216 GPGRLLL 222  
 RESULT 14  
 CD1D\_HUMAN  
 ID CD1D\_HUMAN STANDARD; PRT; 335 AA.  
 AC P15813; Q9Y5M4;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE T-CELL SURFACE GLYCOPROTEIN CD1D PRECURSOR (CD1D ANTIGEN) (R3G1).  
 GN CD1D.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89196496; PubMed=2467814;  
 RA Calabi F., Jarvis J.M., Martin L., Milstein C.;  
 RT "Two classes of CD1 genes.";  
 RL Eur. J. Immunol. 19:285-292(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89098892; PubMed=2463622;  
 RA Balk S.P., Bleicher P.A., Terhorst C.;  
 RT "Isolation and characterization of a cDNA and gene coding for a  
 fourth CD1 molecule.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:252-256(1989).  
 RN [3]  
 RP SEQUENCE OF 19-109 FROM N.A., AND VARIANT SER-64.  
 RX MEDLINE=99416841; PubMed=10488738;  
 RA Han M., Hannick L.I., DiBrino M., Robinson M.A.;  
 RT "Polymorphism of human CD1 genes.";  
 RL Tissue Antigens 54:122-127(1999).  
 CC -!- FUNCTION: NOT KNOWN.  
 CC -!- SUBUNIT: ASSOCIATES NON-COVALENTLY WITH BETA-2-MICROGLOBULIN.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED ON CORTICAL THYMOCYTES, ON CERTAIN  
 T-CELL LEUKEMIAS, AND IN VARIOUS OTHER TISSUES.  
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD1 entry;  
 WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd1.htm".  
 CC  
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 CC  
 DR EMBL; L38820; AAA59672.1; -;  
 DR EMBL; L38815; AAA59672.1; JOINED.  
 DR EMBL; L38817; AAA59672.1; JOINED.  
 DR EMBL; L38816; AAA59672.1; JOINED.  
 DR EMBL; L38818; AAA59672.1; JOINED.  
 DR EMBL; L38819; AAA59672.1; JOINED.  
 DR EMBL; X14974; CAA33099.1; -;  
 DR EMBL; J04142; AAA59673.1; -;  
 DR EMBL; AF142668; AAD37581.1; -;  
 DR PIR; S07715; HLHUR3.  
 DR PIR; A32217; A32217.  
 DR HSP; P11609; 1CD1.  
 DR MIM; 188410; -;  
 DR InterPro; IPR003006; -;  
 DR Pfam; PF00047; 1g; 1.  
 KW Glycoprotein; Signal; Transmembrane; Immunoglobulin domain;  
 KW Multigene family; Polymorphism.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 335 T-CELL SURFACE GLYCOPROTEIN CD1D.  
 FT DOMAIN 20 301 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 302 322 POTENTIAL.  
 FT DOMAIN 323 335 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 120 184 BY SIMILARITY.  
 FT DISULFID 224 279 BY SIMILARITY.  
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARIANT 64 64 T -> S.  
 FT /FTIG-VAR\_010211.

DR Pfam: PF00187; chitin\_binding; 1.  
 DR PROSITE; PS00026; CHITIN\_BINDING; 1.  
 DR PROSITE; PS00773; CHITINASE\_19; 1.  
 DR PROSITE; PS00774; CHITINASE\_19\_2; 1.  
 KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;  
 KW Multigene family.  
 FT SIGNAL 1  
 FT CHAIN <1 20 POTENTIAL.  
 FT DOMAIN 21 269 ENDOCHITININASE B.  
 FT DOMAIN 21 57 CHITIN-BINDING (BY SIMILARITY).  
 FT DOMAIN 58 66 HINGE REGION (GLY-RICH).  
 FT DOMAIN 67 269 CATALYTIC.  
 FT DISULFID 23 31 BY SIMILARITY.  
 FT DISULFID 25 37 BY SIMILARITY.  
 FT DISULFID 30 44 BY SIMILARITY.  
 FT DISULFID 48 53 BY SIMILARITY.  
 SQ SEQUENCE 269 AA; 28166 MW; 3D38B1BAD75DE8F CRC64;

Query Match 3.0%; Score 7; DB 1; Length 269;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 GLALLCA 21  
 Db 7 GLALLCA 13

RESULT 7  
 CDID\_SYLFL STANDARD; PRT; 275 AA.  
 AC P23043;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE T-CELL SURFACE GLYCOPROTEIN CDID (LEUCOCYTE DIFFERENTIATION-LIKE  
 DE ANTIGEN TA) (FRAGMENT).  
 GN CD1.  
 OS Sylvilagus floridanus (Cottontail rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Sylvilagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90035137; PubMed=2478462;  
 RA Calabi F., Belt K.T., Yu C.Y., Bradbury A., Mandy W.J., Milstein C.;  
 RT "The rabbit CD1 and the evolutionary conservation of the CD1 gene  
 family";  
 RL Immunogenetics 30:370-377(1989).  
 CC -1- FUNCTION: NOT KNOWN.  
 CC -1- SUBUNIT: ASSOCIATES NON-COVALENTLY WITH BETA-2-MICROGLOBULIN.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED ON CORTICAL THYMOCYTES, ON CERTAIN  
 CC T-CELL LEUKEMIAS, AND IN VARIOUS OTHER TISSUES.  
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
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 CC -----  
 CC EMBL; M26249; AAA31197.1; -  
 CC HSSP; P11609; 1CD1.  
 CC InterPro; IPR003006; -  
 CC Pfam; PF00047; ig; 1.  
 KW Glycoprotein; Immunoglobulin domain; Multigene family.  
 FT NON\_TER 1  
 FT DISULFID 99 163 BY SIMILARITY.  
 FT DISULFID 203 258 BY SIMILARITY.  
 FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT NON\_TER 275 275  
 SQ SEQUENCE 275 AA; 31047 MW; 8E7232CD5C0C31F4 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 275;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 GPGRULL 41  
 Db 195 GPGRULL 201

RESULT 8  
 PU9L\_SCICO STANDARD; PRT; 286 AA.  
 ID PU9L\_SCICO  
 AC P22311;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE PUFF II/9-1 PROTEIN PRECURSOR.  
 GN II/9-1.  
 OS Sciara coprophila (Fungus gnat).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Sciarioidea;  
 OC Scleridae; Bradysia.  
 OX NCBI\_TaxID=38358;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=6980;  
 RX MEDLINE=90133907; PubMed=2614832;  
 RA Dibratolomeis S.M., Gerbi S.A.;  
 RT "Molecular characterization of DNA puff II/9A genes in Sciara  
 RT coprophila";  
 RL J. Mol. Biol. 210:531-540(1989).  
 CC -1- MISCELLANEOUS: THE DNA PUFF II/9 PROTEINS HAVE A PROPOSED  
 CC INTERMOLECULAR COILED COIL STRUCTURE WITH POSSIBLY INTERMOLECULAR  
 CC DISULFIDE BRIDGES FORMED BY NUMEROUS CYSTEINE RESIDUES IN POSITION  
 CC D OF THE HEPTAD REPEAT.  
 CC -1- SIMILARITY: 76% IDENTICAL TO THE PUFF II/9-2 PROTEIN.  
 CC -----  
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 CC or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL; X51680; CAA35983.1; -  
 CC PIR; S07532; S07532.  
 KW Signal; Coiled coil; Glycoprotein.  
 FT SIGNAL 1 219 OR 21 (POTENTIAL).  
 FT CHAIN 720 286 PUFF II/9-1 PROTEIN.  
 FT DOMAIN 61 235 HELICAL (POTENTIAL).  
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 286 AA; 32034 MW; AAG67B55F191B1D CRC64;

Query Match 3.0%; Score 7; DB 1; Length 286;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 166 LTVVLLA 172  
 Db 7 LTVVLLA 13

RESULT 9  
 PU9L\_SCICO

ID PU92\_SCICO STANDARD; PRT; 286 AA.  
 AC P22312;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE PUFF II/9-2 PROTEIN PRECURSOR.  
 GN II/9-2.  
 OS Sclara coprophila (Fungus gnat).  
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Scleroidea;  
 CC Scleridae; Bradysia.  
 OX NCBI\_TaxID=38358;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=6980;  
 RX MEDLINE=90133907; PubMed=2614832;  
 RA Dibartolomeis S.M., Gerbi S.A.;  
 RT "Molecular characterization of DNA puff II/9A genes in Sclara  
 coprophila.";  
 RL J. Mol. Biol. 210:531-540(1989).  
 CC -!- MISCELLANEOUS: THE DNA PUFF II/9 PROTEINS HAVE A PROPOSED  
 CC INTERMOLECULAR COILED COIL STRUCTURE WITH POSSIBLY INTERMOLECULAR  
 CC DISULFIDE BRIDGES FORMED BY NUMEROUS CYSTEINE RESIDUES IN POSITION  
 CC D OF THE HEPTAD REPEAT.  
 CC -!- SIMILARITY: 76% IDENTICAL TO THE PUFF II/9-1 PROTEIN.  
 CC  
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 CC  
 DR EMBL; X51679; CAA35982.1; -;  
 DR PIR; S07533; S07533.  
 KW Signal; Coiled coil; Glycoprotein.  
 FT SIGNAL 1 219 PUFF II/9-2 (POTENTIAL).  
 FT CHAIN 220 286 PUFF II/9-2 PROTEIN.  
 FT DOMAIN 61 235 HELICAL (POTENTIAL).  
 FT CARBOHYD 156 156 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 286 AA; 32621 MW; 720AC8CC22A869C CRC64;  
  
 Query Match 3.0%; Score 7; DB 1; Length 286;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 166 LRVVLLA 172  
 Db 7 LRVVLLA 13  
  
 RESULT 10  
 STX4\_HUMAN STANDARD; PRT; 297 AA.  
 ID STX4\_HUMAN  
 AC Q12846; Q15525;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE SYNTAXIN 4.  
 GN STX4A OR STX4.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=94266173; PubMed=8206394;  
 RA Li H., Hodge D.R., Pei G.K., Seth A.;  
 RT "Isolation and sequence analysis of the human syntaxin-encoding  
 gene.";

Gene 143:303-304(1994).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=96332494; PubMed=8760387;  
 RA Jagadeish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L.,  
 RA Gough K.H., Grusovin J., Verkuylen A., Cosgrove L., Alafaci A.,  
 RA Frenkel M.J., Ward C.W.;  
 RT "Insulin-responsive tissues contain the core complex protein SNAP-25  
 RT (synaptosomal-associated protein 25) A and B isoforms in addition to  
 RT syntaxin 4 and synaptobrevins 1 and 2.";  
 RL Biochem. J. 317:945-954(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Periphereal blood neutrophils;  
 RA Nabokina S., Lazo P.A., Mollinedo F.;  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lens epithelium;  
 RA Rae J.L., Shepard A.R.;  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: POTENTIALLY INVOLVED IN DOCKING OF SYNAPTIC VESICLES  
 CC AT PRESYNAPTIC ACTIVE ZONES.  
 CC -!- SIMILARITY: BELONGS TO THE SYNTAXIN/EPIMORPHIN FAMILY.  
 CC  
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 CC  
 DR EMBL; U07158; AAA20967.1; -;  
 DR EMBL; X85784; CAA59769.1; -;  
 DR EMBL; AJ000541; CAA04174.1; -;  
 DR EMBL; AF026007; AAB88810.1; -;  
 DR HSP; P32851; LBR0.  
 DR MIM; 186591; -;  
 DR InterPro; IPR000017; -;  
 DR Pfam; PF00804; Syntaxin; 1.  
 DR PROSITE; PS00914; SYNTAXIN; 1.  
 KW Neurotransmitter transport; Coiled coil; Transmembrane.  
 FT DOMAIN 43 163 COILED COIL (POTENTIAL).  
 FT DOMAIN 199 222 COILED COIL (POTENTIAL).  
 FT TRANSMEM 276 296 POTENTIAL.  
 FT CONFLICT 174 174 E -> D (IN REF. 1).  
 FT CONFLICT 269 269 A -> V (IN REF. 1).  
 SQ SEQUENCE 297 AA; 34180 MW; 5084FD1C49A86BAA CRC64;  
  
 Query Match 3.0%; Score 7; DB 1; Length 297;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 167 TVVLLAV 173  
 Db 283 TVVLLAV 289  
  
 RESULT 11  
 MAS\_MOUSE STANDARD; PRT; 324 AA.  
 ID MAS\_MOUSE  
 AC P30554; O35944;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE MAS PROTO-ONCOGENE.  
 GN MAS1 OR MAS-1 OR MAS.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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FT REPEAT 326 334 MOTIF B.
FT REPEAT 342 358 MOTIF A.
FT REPEAT 382 393 MOTIF C.
FT DOMAIN 434 555 2A.
FT REPEAT 468 476 MOTIF B.
FT REPEAT 490 506 MOTIF A.
FT REPEAT 528 539 MOTIF C.
FT DOMAIN 556 661 2B.
FT REPEAT 588 596 MOTIF B.
FT REPEAT 602 618 MOTIF A.
FT REPEAT 634 645 MOTIF C.
FT DOMAIN 662 782 2C.
FT REPEAT 693 701 MOTIF B.
FT REPEAT 707 723 MOTIF A.
FT REPEAT 749 761 MOTIF C.
FT DOMAIN 162 169 POLYPHOSPHOINOSITIDE BINDING (BY
FT SIMILARITY)
FT DOMAIN 188 196 POLYPHOSPHOINOSITIDE BINDING (BY
FT SIMILARITY)
FT DISULFID 215 228 IN PLASMA FORM ONLY.
FT VARIANT 214 214 D -> N (IN FAF).
FT VARIANT 214 214 /FTID=VAR_007718.
FT /FTID=VAR_007719.
SQ SEQUENCE 782 AA; 85697 MW; 8CERC52257A160F7 CRC64;

Query Match 3.4%; Score 8; DB 1; Length 782;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 ALLCALS 24
Db 9 ALLCALS 16
|||||||

RESULT 3
GTH2_CYPCA STANDARD; PRT; 144 AA.
AC P01235;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GONADOTROPIN BETA-II CHAIN PRECURSOR (GTH-II-BETA) (LUTEINIZING
DE HORMONE-LIKE GTH)
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89233593; PubMed=3246480;
RA Chang Y.S., Huang C.-J., Huang F.-L., Lo T.-B.;
RT "Primary structures of carp gonadotropin subunits deduced from cDNA
RT nucleotide sequences."
RL Int. J. Pept. Protein Res. 32:556-564(1988).
RN [2]
RP SEQUENCE FROM N.A.
RA Chang Y.S., Huang F.-L., Lo T.-B.;
RL Submitted (MAY-1991) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 28-53 AND 141-142.
RX MEDLINE=78124308; PubMed=607993;
RA Jolles J., Burzawa-Gerard E., Fontaine Y.-A., Jolles P.;
RT "The evolution of gonadotropins: some molecular data concerning a
RT non-mammalian pituitary gonadotropin, the hormone from a teleost
RT fish (Cyprinus carpio L.).";
RL Biochimie 59:893-898(1977).
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.

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CC -----
CC EMBL; X59888; CAA42542.1; -
CC EMBL; X59889; CAA42543.1; -
CC PIR; S29677; S29677.
CC PIR; S29678; S29678.
CC PIR; A01504; UTCAB.
CC PIR; J0462; J0462.
CC HSP; P01233; 1HRP.
CC InterPro; IPR000359; -
CC InterPro; IPR001545; -
CC InterPro; IPR002400; -
CC Pfam; PF00007; Cys_Knot; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
CC PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
CC KW Hormone; Glycoprotein; Signal.
FT SIGNAL 1 27
FT CHAIN 28 142 GONADOTROPIN BETA-II CHAIN.
FT PROPEP 143 144
FT DISULFID 33 81 BY SIMILARITY.
FT DISULFID 47 96 BY SIMILARITY.
FT DISULFID 50 134 BY SIMILARITY.
FT DISULFID 58 112 BY SIMILARITY.
FT DISULFID 62 114 BY SIMILARITY.
FT DISULFID 117 124 BY SIMILARITY.
FT CARBOHYD 37 37 N-LINKED (GLCNAC...) (PROBABLE).
SQ SEQUENCE 144 AA; 16039 MW; 854FE80D4A39DCF8 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 144;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 VLLAVA 174
Db 19 VLLAVA 25
|||||||

RESULT 4
YQII_BACSU STANDARD; PRT; 206 AA.
AC P54525; P54526; O32017;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 22.2 KDA PROTEIN IN SPOOA-MMGA INTERGENIC REGION.
GN YQII.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / JH642;
RA Kobayashi Y., Mizuno M., Masuda S., Takemaru K., Hosono S.,
RA Sato T., Takeuchi M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE N-ACETYLMURAMOYL-L-ALANINE AMIDASE
CC FAMILY 3.
CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO

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CC -----
DR EMBL; D84432; BAA12584.1; ALT_FRAME.
DR EMBL; D84432; BAA12585.1; ALT_FRAME.
DR EMBL; Z99116; CABI4350.1; -.
DR Subtilist; BGI1717; YqII.
DR InterPro; IPR002508; -.
DR Pfam; PF01520; Amidase_3; 1.
KW Hypothetical protein; Hydrolase.
FT CONFLICT 170 170 E -> D (IN REF. 1).
SQ SEQUENCE 206 AA; 2235 MW; B0950FA7E4D12D1E CRC64;

Query Match          3.0%; Score 7; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ALCGLAL 18
   |||||
DB 9 ALCGLAL 15

RESULT 5
CIB3_SHEEP
ID CIB3_SHEEP STANDARD; PRT; 232 AA.
AC P80943;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE T-CELL SURFACE GLYCOPROTEIN CIB3-3 (CIB3-3 ANTIGEN) (SCDIT10)
DE (FRAGMENT).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal thymocytes;
RA MEDLINE=96269982; PubMed=8662069;
RT Ferguson E.E., Dutia B.M., Hein W.R., Hopkins J.;
RL "The sheep CD1 gene family contains at least four CD1B homologues.";
IMMUNOGENETICS 44:86-96(1996).
CC -|- FUNCTION: NOT KNOWN.
CC -|- SUBUNIT: ASSOCIATES NON-COVALENTLY WITH BETA-2-MICROGLOBULIN (BY
CC SIMILARITY).
CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
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CC -----
DR EMBL; X90567; CAA62187.1; -.
DR HSSP; P11609; 1CD1.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig_1.
KW Glycoprotein; Immunoglobulin domain; Transmembrane; Multigene family.
FT NON_TER 1 201
FT DOMAIN <1 201 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 202 222

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FT DOMAIN 223 232 CYTOPLASMIC (POTENTIAL).
FT DISULFID 19 83 BY SIMILARITY.
FT DISULFID 123 178 BY SIMILARITY.
FT CARBOHYD 45 45 N-LINKED (GLCNAC... (POTENTIAL).
SQ SEQUENCE 232 AA; 26023 MW; C96DB93840B56158 CRC64;

Query Match          3.0%; Score 7; DB 1; Length 232;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 GPGRLLL 41
   |||||
DB 115 GPGRLLL 121

RESULT 6
CHIB_MAIZE
ID CHIB_MAIZE STANDARD; PRT; 269 AA.
AC P29023;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ENDOCHITINASE B PRECURSOR (EC 3.2.1.14) (SEED CHITINASE B) (FRAGMENT).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae;
OC Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed;
RX MEDLINE=92202208; PubMed=1551872;
RA Huynh O.K., Hironaka C.M., Levine E.B., Smith C.E., Borgmeyer J.R.,
RA Shah D.M.;
RT "Antifungal proteins from plants. Purification, molecular cloning,
RT and antifungal properties of chitinases from maize seed.";
RL J. Biol. Chem. 267:6635-6640(1992).
RN [2]
RP SEQUENCE OF 169-184.
RC TISSUE=Seed;
RX MEDLINE=92156129; PubMed=1740436;
RA Verburg J.G., Smith C.E., Lisek C.A., Huynh O.K.;
RT "Identification of an essential tyrosine residue in the catalytic
RT site of a chitinase isolated from Zea mays that is selectively
RT modified during inactivation with
RT 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide.";
RL J. Biol. Chem. 267:3886-3893(1992).
CC -|- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC CONTAINING FUNGAL PATHOGENS.
CC -|- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -|- MISCELLANEOUS: MAIZE CHITINASE B SEEMS TO BE LESS ACTIVE THAN
CC CHITINASE A.
CC -|- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
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CC -----
DR EMBL; M84165; AAA33445.1; -.
DR HSSP; P02877; 1HEV.
DR MaizeDB; 25130; -.
DR InterPro; IPR000726; -.
DR InterPro; IPR001002; -.
DR Pfam; PF00182; Glyco_hydro_19; 1.

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OM protein - protein search, using sw model

Run on: September 5, 2001, 09:46:20 ; Search time 10.37 Seconds  
(without alignments)  
772.978 Million cell updates/sec

Title: US-09-512-363-2  
Perfect score: 234  
Sequence: 1 MAQHGAMGAFRALCGLALLC.....EEEGERSAEKGRGLDLWV 234

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size : 0

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	3.4	411	1 VGLM_HSVBC	P52370 bovine herp
2	8	3.4	782	1 GELS_HUMAN	P06396 homo sapien
3	7	3.0	144	1 QTH2_CYPCA	P01235 cyprinus ca
4	7	3.0	206	1 YQ11_BACSU	P54525 bacillus su
5	7	3.0	232	1 C1B3_SHEEP	P80943 ovis aries
6	7	3.0	269	1 CHIB_MAIZE	P29023 zea mays (m
7	7	3.0	275	1 CD1D_SVLFL	P23043 sylvilagus
8	7	3.0	286	1 PU91_SCICO	P22311 sciara copr
9	7	3.0	286	1 PU92_SCICO	P22312 sciara copr
10	7	3.0	297	1 STX4_HUMAN	Q12846 homo sapien
11	7	3.0	324	1 MAS_MOUSE	P30554 mus musculu
12	7	3.0	333	1 C1B1_SHEEP	Q28555 ovis aries
13	7	3.0	333	1 C1B2_SHEEP	Q29422 ovis aries
14	7	3.0	335	1 CD1D_HUMAN	P15813 homo sapien
15	7	3.0	359	1 WN5A_AMBME	Q06442 ambystoma m
16	7	3.0	401	1 PILC_PSEPU	P36641 pseudomonas
17	7	3.0	508	1 VGLG_IRNV	P07923 infectious
18	7	3.0	524	1 VGLG_CHRV	P13180 candidura
19	7	3.0	555	1 NUSM_CANPA	P48919 candida par
20	7	3.0	598	1 NUSM_BRALA	Q79422 branchiosto
21	7	3.0	599	1 NUSM_BRAFL	Q47430 branchiosto
22	7	3.0	600	1 NUSM_METSE	Q35099 metridium s
23	7	3.0	603	1 NUSM_GORGO	P03917 gorilla gor
24	7	3.0	603	1 NUSM_HUMAN	P03915 homo sapien
25	7	3.0	603	1 NUSM_HYLLA	P03919 hylobates l
26	7	3.0	603	1 NUSM_PANPA	P03916 pan paniscu
27	7	3.0	603	1 NUSM_PANTR	Q35648 pan troglod
28	7	3.0	603	1 NUSM_PONPA	P92699 pongo pygma
29	7	3.0	603	1 NUSM_PONPY	P03918 pongo pygma
30	7	3.0	611	1 AFAM_MOUSE	O89020 mus musculu
31	7	3.0	641	1 NUSM_ALIMA	P50365 allomyces m
32	7	3.0	653	1 CCMF_RHOCA	Q00500 rhodobacter
33	7	3.0	666	1 NUSM_CHOCR	P48920 chondrus cr

34 7 3.0 675 1 NUSM\_ACACA Q37372 acanthamoeb  
35 7 3.0 713 1 CADD\_HUMAN P55290 homo sapien  
36 7 3.0 750 1 YD33\_MYCPN P75445 mycoplasma  
37 7 3.0 757 1 COMP\_HUMAN P49747 homo sapien  
38 7 3.0 830 1 YJG2\_YEAST P40367 saccharomyc  
39 7 3.0 1248 1 SYJ2\_RAT O55207 rattus norv  
40 7 3.0 1443 1 SYJ2\_HUMAN O15056 homo sapien  
41 7 3.0 1469 1 DP27\_CAEEL P48996 caenorhabdi  
42 7 3.0 2477 1 FINC\_MOUSE P11276 mus musculu  
43 7 3.0 2477 1 FINC\_RAT P04937 rattus norv  
44 6 2.6 71 1 NXLB\_PSETE P13495 pseudonaja  
45 6 2.6 73 1 VF09\_ORFPN2 P52586 orf virus (

ALIGNMENTS

RESULT 1  
VGLM\_HSVBC  
ID VGLM\_HSVBC STANDARD: PRT: 411 AA.  
AC P52370;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE GLYCOPROTEIN M.  
GN GM OR UL10.  
OS Bovine herpesvirus type 1 (strain Cooper).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Varicellovirus.  
OX NCBI\_TaxID=10323;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95313343; PubMed=7793062;  
RA Vleck C., Benes V., Lu Z., Kutish G.F., Paces V., Rock D.,  
RA Letchworth G.J., Schwyzler M.;  
RT "Nucleotide sequence analysis of a 30-kb region of the bovine  
herpesvirus 1 genome which exhibits a collinear gene arrangement with  
the UL21 to UL4 genes of herpes simplex virus.";  
RL Virology 210:100-108(1995).  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEIN M.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL: Z48053; CAA88123.1; -.  
DR InterPro; IPR000785; -.  
DR Pfam; PF01528; Herpes\_glycop; 1.  
DR PRINTS; PR00333; HSVINTEGRIMP.  
KW Transmembrane; Glycoprotein.  
FT TRANSMEM 14 34 POTENTIAL.  
FT TRANSMEM 89 109 POTENTIAL.  
FT TRANSMEM 133 153 POTENTIAL.  
FT TRANSMEM 159 179 POTENTIAL.  
FT TRANSMEM 213 233 POTENTIAL.  
FT TRANSMEM 249 269 POTENTIAL.  
FT TRANSMEM 277 297 POTENTIAL.  
FT TRANSMEM 318 338 POTENTIAL.  
FT CARBOHYD 57 57 N-LINKED (GLCNAC... ) (POTENTIAL).  
SQ SEQUENCE 411 AA; 43029 MW; 20F156DA9F40158C CRC64;

Query Match 3.4%; Score 8; DB 1; Length 411;  
Best Local Similarity 100.0%; Pred. No. 3.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 168 VYLLAVAA 175  
|||||||

Db 93 VVLLAVAA 100

RESULT 2

GELS\_HUMAN

ID GELS\_HUMAN STANDARD; PRT; 782 AA.

AC P06396;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF)

DE (BREVIN) (AGEL).

GN GSN.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID-9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-87014807; PubMed-3020431;

RA Kwiatkowski D.J., Stossel T.P., Orkin S.H., Mole J.E., Colten H.R.,

RA Yin H.L.;

RT "Plasma and cytoplasmic gelsolins are encoded by a single gene and

RT contain a duplicated actin-binding domain.";

RL Nature 323:455-458(1986).

RN [2]

RP FIBRONECTIN BINDING.

RX MEDLINE-85030446; PubMed-6092370;

RA Lind S.E., Janmey P.A.;

RT "Human plasma gelsolin binds to fibronectin.";

RL J. Biol. Chem. 259:13262-13266(1984).

RN [3]

RP IDENTITY OF FAF AMYLOID PROTEIN WITH GELSOLIN.

RX MEDLINE-90211339; PubMed-2157434;

RA Haltia M., Prelli F., Ghiso J., Kiuru S., Sommer H., Palo J.,

RA Frangione B.;

RT "Amyloid protein in familial amyloidosis (Finnish type) is homologous

RT to gelsolin, an actin-binding protein.";

RL Biochem. Biophys. Res. Commun. 167:927-932(1990).

RN [4]

RP IDENTITY OF FAF AMYLOID PROTEIN WITH GELSOLIN.

RX MEDLINE-90127414; PubMed-2153578;

RA Maury C.P.J., Ali K., Baumann M.;

RT "Finnish hereditary amyloidosis. Amino acid sequence homology between

RT the amyloid fibril protein and human plasma gelsoline.";

RL FEBS Lett. 260:85-87(1990).

RN [5]

RP DISULFIDE BOND.

RX MEDLINE-96312883; PubMed-8703941;

RA Wen D., Corina K., Chow E.P., Miller S., Janmey P.A., Pepinsky R.B.;

RT "The plasma and cytoplasmic forms of human gelsolin differ in

RT disulfide structure.";

RL Biochemistry 35:9700-9709(1996).

RN [6]

RP DISULFIDE BOND.

RX MEDLINE-97157527; PubMed-9003812;

RA Allen P.G.;

RT "Functional consequences of disulfide bond formation in gelsolin.";

RL FEBS Lett. 401:89-94(1997).

RN [7]

RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-503.

RX MEDLINE-93361115; PubMed-8395021;

RA McLaughlin P.J., Gooch J.T., Mannherz H.-G., Weeds A.G.;

RT "Structure of gelsolin segment 1-actin complex and the mechanism of

RT filament severing.";

RL Nature 364:685-692(1993).

RN [8]

RP STRUCTURE BY NMR OF 177-196.

RX MEDLINE-96167246; PubMed-8599675;

RA Xian W., Vegners R., Janmey P.A., Braunlin W.H.;

RT "Spectroscopic studies of a phosphoinositide-binding peptide from

RT gelsolin: behavior in solutions of mixed solvent and anionic

RT micelles.";

Biophys. J. 69:2695-2702(1995).

RN [9]

RP VARIANT FAF ASN-214.

RX MEDLINE-91097517; PubMed-2176481;

RA Ghiso J., Haltia M., Prelli F., Novello J., Frangione B.;

RT "Gelsolin variant (Asn-187) in familial amyloidosis, Finnish type.";

RL Biochem. J. 272:827-830(1990).

RN [10]

RP VARIANTS FAF ASN-214 AND TYR-214.

RX MEDLINE-93265143; PubMed-1338910;

RA de la Chapelle A., Tolvanen R., Boysen G., Santavy J.,

RA Bleeker-Wagemakers L., Maury C.P.J., Kere J.;

RT "Gelsolin-derived familial amyloidosis caused by asparagine or

RT tyrosine substitution for aspartic acid at residue 187.";

RL Nat. Genet. 2:157-160(1992).

CC -!- FUNCTION: GELSOLIN IS A CALCIUM-REGULATED, ACTIN-MODULATING

CC PROTEIN THAT BINDS TO THE PLUS (OR BARBED) ENDS OF ACTIN MONOMERS

CC OR FILAMENTS, PREVENTING MONOMER EXCHANGE (END-BLOCKING OR

CC CAPPING). IT CAN PROMOTE THE ASSEMBLY OF MONOMERS INTO FILAMENTS

CC (NUCLEATION) AS WELL AS SEVER FILAMENTS ALREADY FORMED.

CC -!- SUBCELLULAR LOCATION: SECRETED (PLASMA FORM) AND CYTOPLASMIC.

CC -!- ALTERNATIVE PRODUCTS: PLASMA GELSOLIN AND CYTOPLASMIC GELSOLIN

CC ARE DERIVED FROM A SINGLE GENE BY ALTERNATE INITIATION SITES AND

CC DIFFERENTIAL SPLICING.

CC -!- TISSUE SPECIFICITY: PHAGOCYTTIC CELLS, PLATELETS, FIBROBLASTS,

CC OR MUSCLE CELLS, SMOOTH AND SKELETAL MUSCLE CELLS.

CC -!- DISEASE: DEFECTS IN GSN ARE THE CAUSE OF FAMILIAL AMYLOIDOSIS,

CC FINNISH TYPE (FAF), AN INHERITED FORM OF SYSTEMIC AMYLOIDOSIS,

CC CLINICALLY CHARACTERIZED BY CRANIAL NEUROPATHY AND LATTICE CORNEAL

CC DYSTROPHY.

CC -!- MISCELLANEOUS: IN ADDITION TO ITS ROLE IN ACTIN REGULATION, THIS

CC PROTEIN IS KNOWN TO BIND WITH HIGH AFFINITY TO FIBRONECTIN.

CC -!- SIMILARITY: BELONGS TO THE VILLIN/GELSOLIN FAMILY.

CC

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CC -----

CC EMBL; X04412; CAA28000.1; -

DR PIR; A03011; FAHUP.

DR PIR; A34137; A34137.

DR PIR; A34562; A34562.

DR PDB; 1SOL; 08-MAR-96.

DR MIM; 137350; -

DR MIM; 105120; -

DR InterPro; IPR001974; -

DR Pfam; PF00626; Gelsolin; 6.

DR PRINTS; PR00597; GELSOLIN.

DR Actin-binding; Repeat; Calcium; Alternative initiation; Signal;

KW Capping protein; Amyloid; Disease mutation; 3D-structure.

RN SIGNAL 1 27

FT CHAIN 28 782 GELSOLIN, PLASMA ISOFORM.

FT CHAIN 53 782 GELSOLIN, CYTOPLASMIC ISOFORM.

FT INIT\_MET 52 52 FOR CYTOPLASMIC ISOFORM.

FT DOMAIN 53 176 ACTIN-SEVERING (POTENTIAL).

FT DOMAIN 434 782 ACTIN-BINDING, CA-SENSITIVE (POTENTIAL).

FT SITE 123 126 ACTIN-ACTIN INTERFILAMENT CONTACT POINT.

FT REPEAT 57 416 1ST HALF.

FT DOMAIN 417 433 HINGE REGION.

FT REPEAT 434 782 2ND HALF.

FT DOMAIN 57 176 1A.

FT REPEAT 89 97 MOTIF B.

FT REPEAT 112 128 MOTIF A.

FT REPEAT 150 161 MOTIF C.

FT REPEAT 177 233 1B.

FT DOMAIN 210 218 MOTIF B.

FT REPEAT 224 240 MOTIF A.

FT REPEAT 263 274 MOTIF C.

FT DOMAIN 294 416 1C.



Search completed: September 4, 2001, 16:12:11  
Job time: 1108 sec

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-461 <SMI>  
A:Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186  
R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990  
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occurring  
A:Reference number: A36475; MUID:91045991  
A:Accession: A36475  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-195, 'R', 197-461 <KOH>  
A:Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758  
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M. Cytokine 2, 231-237, 1990  
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular, A:Reference number: A48416; MUID:91370690  
A:Accession: A48416  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 23-461 <DEM>  
A:Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649  
A:Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIP:63371)  
R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990  
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration  
A:Reference number: A36007; MUID:90349572  
A:Accession: A36007  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>  
A:Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752  
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M. J. Biol. Chem. 265, 20131-20138, 1990  
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors  
A:Reference number: A23666; MUID:91056048  
A:Accession: A23666  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 23-40; 65-69; 136-141; 300-306 <LOE>  
R:Engelmann, H.; Novick, D.; Wallach, D. J. Biol. Chem. 265, 1531-1536, 1990  
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence  
A:Reference number: A35010; MUID:90110215  
A:Accession: B35010  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 27-31 <ENG>  
R:Kuhnert, P.; Kemper, O.; Wallach, D. Gene 150, 381-386, 1994  
A:Title: Cloning, sequencing and partial functional characterization of the 5' region of  
A:Reference number: I38094; MUID:95121934  
A:Accession: I38094  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-37 <RES>  
A:Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701  
C:Genetics:  
A:Gene: GDB:TNFR2  
A:Cross-references: GDB:I25914; OMIM:191191  
A:Map position: lp36.2-lp36.2  
A:Introns: 26/3  
A:Note: the list of introns is incomplete  
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>  
F:40-76/Domain: NGF receptor repeat homology <NG1>  
F:78-119/Domain: NGF receptor repeat homology <NG2>  
F:120-162/Domain: NGF receptor repeat homology <NG3>  
F:164-201/Domain: NGF receptor repeat homology <NG4>  
F:262-279/Domain: transmembrane #status predicted <TMN>  
F:280-461/Domain: intracellular #status predicted <INT>

F:171.193/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 12.3%; Score 119; DB 1; Length 461;  
Best Local Similarity 26.3%; Pred. No. 0.022;  
Matches 41; Conservative 14; Mismatches 63; Indels 38; Gaps 8;  
QY 34 CGPG---RLLLGGTGTDARC-----CRVHTTRCCRDYPGEGCCSEMD-- 71  
Db 57 CSPGQHAQVCTKTSDIVDCDESDTYTLWNWVPECLSCGSRSSDOVEFQAQREQNR 116  
QY 72 -CMCVQPEFHC-----GDPCCTCRHHPCPPGQGVQSQKFSFGFCIDCASGTFSG-- 122  
Db 117 ICTC-RPGWYCALSKQEGRCALPLR--KCRPGFVARPGTETSDVVCVKPCAPGTFSTNT 173  
QY 123 GREGHCKPWTDCTQFGFLTVFPNGKTHNAVCPGSP 158  
Db 174 SSTDICRPHOICN----VVAIPGNASMDAVCTSTSP 205  
RESULT 12  
B38634  
tumor necrosis factor receptor type 2 precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Jul-1999  
C:Accession: B38634; A40254; S54816  
R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor  
A:Reference number: A38634; MUID:91187885  
A:Accession: B38634  
A:Molecule type: mRNA  
A:Residues: 1-474 <LEW>  
A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828  
R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J Mol. Cell. Biol. 11, 3020-3026, 1991  
A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f  
A:Reference number: A40254; MUID:91246168  
A:Accession: A40254  
A:Molecule type: mRNA  
A:Residues: 1-474 <GOO>  
A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828  
R:Kissonerghis, M.; Followes, R.; Feldmann, M.; Chernajovsky, Y. submitted to the EMBL Data Library, May 1995  
A:Description: Characterization of the promoter region of the murine p75-TNF receptor  
A:Reference number: S54816  
A:Accession: S54816  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-22 <KTS>  
A:Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044  
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
C:Keywords: cytokine receptor; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>  
F:40-77/Domain: NGF receptor repeat homology <NG1>  
F:79-120/Domain: NGF receptor repeat homology <NG2>  
F:166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 12.3%; Score 119; DB 2; Length 474;  
Best Local Similarity 31.0%; Pred. No. 0.023;  
Matches 36; Conservative 8; Mismatches 54; Indels 18; Gaps 5;  
QY 46 DARCCRVHTTRCCRDYPGEGCCSEMDCMQVPEFHCGDPCCTTC-RHHPCPPGQGVQSQG 104  
Db 107 EIRACTKQKNRVCAACEAGRYCAL-----KTHSGS--CROCRLSKCGPGFGVASSR 155  
QY 105 KFSFGFCIDCASGTFSG--GHEGHCAKPTWTDCTQFGFLTVFPNGKTHNAVCPGSP 158  
Db 156 APNGNVLCACAPGTFSDTTSSTDVCRPHRICS-----ILAIPGNASTDAVCAPESP 207

**RESULT 13**

A60771  
B-cell activation protein CD40 precursor - human  
N:Alternate names: B-cell surface antigen Bp50  
C:Species: Homo sapiens (man)  
C>Date: 03-Jun-1993 #sequence\_revision 03-Feb-1994 #text\_change 21-Jul-2000  
C:Accession: S04460; A60771  
R:Stamenkovic, I.; Clark, E.A.; Seed, B.  
EMBO J. 8, 1403-1410, 1989  
A>Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor  
A:Reference number: S04460; MUID:89356608  
A:Accession: S04460  
A:Molecule type: mRNA  
A:Residues: 1-277 <STA>  
A:CROSS-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851  
R:Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.  
J. Immunol. 142, 562-567, 1989  
A>Title: Biochemical characteristics and partial amino acid sequence of the receptor-like  
A:Reference number: A60771; MUID:89093941  
A:Accession: A60771  
A:Molecule type: protein  
A:Residues: 21-50 <BRA>  
A:Experimental source: Burkitt lymphoma cell line Raji  
C:Genetics:  
A:Gene: GDB:CD40  
A:CROSS-references: GDB:215268; OMIM:109535  
A:Map position: 20q12-20q13.2  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>  
F:21-193/Domain: extracellular #status predicted <EXT>  
F:194-215/Domain: transmembrane #status predicted <TM>  
F:216-277/Domain: intracellular #status predicted <CYT>  
F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	12.2%;	Score 118.5;	DB 2;	Length 277;
Best Local Similarity	27.7%;	Pred. No. 0.017;		
Matches	36;	Conservative	10;	Mismatches 73; Indels 11; Gaps 5;

QY 34 CGPGRLLLTGTDARCRVHTTRCCRYDPG-----EECCSEWDCMCVOPE-FHCGDPCCTT 88  
|| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 62 CGSEFLDTWNREPHC----HQHKYCDPNGLRLVQOKGTSETDTICTCEGMHCTSEACES 118  
  
QY 89 C-RHHCPPGGVQSOGKSEFGFCIDCASFTSGSHEG--HCKPWTDCTQFGPLTVFP 145  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 119 CVLHRSCSPGFVGKQIATGVSDTICEPCPVFFSNSSAFEKHPWTSCETKDILVVQQAG 178  
  
QY 146 NKTHNAVCP 155  
: | | | |  
Db 179 TNKTDDVCGP 188

**RESULT 14**

I54182  
tumor necrosis factor receptor 2-related protein - human  
C:Species: Homo sapiens (man)  
C>Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 17-Mar-2000  
R:Baens, M.; Chafiniet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.  
Genomics 16, 214-218, 1993  
A>Title: Construction and evaluation of a hncDNA library of human l2p transcribed sequer  
A:Reference number: I54182; MUID:93252381  
A:Accession: I54182  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-435 <RES>  
A:CROSS-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762  
C:Genetics:  
A:Gene: GDB:LTBR  
A:CROSS-references: GDB:1230195; OMIM:600979  
A:Map position: 12p13.3-12p13.1

C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match	12.1%;	Score 117;	DB 2;	Length 435;
Best Local Similarity	25.6%;	Pred. No. 0.031;		
Matches	42;	Conservative	12;	Mismatches 66; Indels 44; Gaps 10;

  

Qy	34	CGPGRLLGGTGDARCCRVHTTRC-----CRDPYGBE---C 66
Db	62	CPP-----GTVSAKCSKRIDTCATCAENSYNHWNLYTICQLCRCPDPMVGLLEIAPC 116
Qy	67	CS--EWDCMCVPFFHGCDPC--CTTCR-HUPCPPGGVQSOGKFSG-FQCIDCASGTF 120
Db	117	TSKRKTQRC-QPGMFAAWALETHCELLSDCPGTGAELKDVEVGKNHCVPCKAGHF 175
Qy	121	--SGHEGHGKPWTDCTQCFGLTVFPGNKTNHAVCVFGSPPAEP 162
Db	176	QNTSSPSARCOPHTRCNENQGLVEAAPTASDDTYC---KNPLEP 216

  

RESULT 15  
A33837

insulin-like growth factor I receptor precursor - rat  
N:Contains: insulin-like growth factor I alpha chain; insulin-like growth factor I beta chain;  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 16-Mar-1990 #sequence\_revision 03-Nov-1995 #text\_change 21-Jul-2000  
C:Accession: JC2461; A33837; PC1131  
R:Pedrini, M.T.; Giorgino, F.; Smith, R.J.  
Biochem. Biophys. Res. Commun. 202, 1038-1046, 1994  
A>Title: cDNA cloning of the rat IGF I receptor: Structural analysis of rat and human

A;Reference number: JC2461; MUID:94324926  
A:Accession: JC2461  
A:Molecule type: mRNA  
A:Residues: 1-1371 <PE>  
R:Werner, H.; Woloschak, M.; Adamo, M.; Shen-Orr, Z.; Roberts Jr., C.T.; LeRoith, D.  
Proc. Natl. Acad. Sci. U.S.A. 86, 7451-7455, 1989  
A>Title: Developmental regulation of the rat insulin-like growth factor I receptor gene  
A:Reference number: A33837; MUID:90017496  
A:Accession: A33837  
A:Molecule type: mRNA  
A:Residues: 1-364 <WER>  
A:Cross-references: GB:M27293  
R:Kurachi, H.; Jobo, K.; Ohta, M.; Kawasaki, T.; Itoh, N.  
Biochem. Biophys. Res. Commun. 187, 934-939, 1992  
A>Title: A new member of the insulin receptor family, insulin receptor-related receptor  
A:Reference number: PC1130; MUID:92412145  
A:Accession: PC1131  
A:Molecule type: mRNA  
A:Residues: 913-984/'PY',987-1017 <KUR>  
A:Cross-references: GB:D12679; NID:g220918; PIDN:BAA20983.1; PID:g4433359  
C:Superfamily: Insulin receptor; protein kinase homologous  
C:Keywords: ATP; growth factor receptor; kinase-related transforming protein; transmembrane  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-741/Product: insulin-like growth factor I alpha chain #status predicted <IGA>  
F:742-1371/Product: insulin-like growth factor I beta chain #status predicted <IGB>  
F:937-959/Domain: transmembrane #status predicted <TMN>  
F:971-974/Region: GPXY motif  
F:978-981/Region: NPXY motif  
F:998-1275/Domain: protein kinase homologous <KIN>  
F:1006-1014/Region: protein kinase ATP-binding motif

  

Query Match	11.9%;	Score 115.5;	DB 2;	Length 1371;
Best Local Similarity	27.1%;	Pred. No. 0.085;		
Matches	57;	Conservative	22;	Mismatches 52; Indels 79; Gaps 20;

  

Qy	8	GAFRA-----LCGLA-----LICALS-----LGORPTGGPGCG---PGRLL-----L 40
Db	139	GAIPIEKADLCYLSTIDWSLIIDAVSNIVGNKKPP--KECGDLCPGLEEKPMCEKTT 196
Qy	41	LGTGTDAACRRVHTTRC---CRDPYGECCSEWDCMCVQPFHCGDPC-----CTTC 89

C:Keywords: growth factor receptor; transmembrane protein  
F:1-19/Domain: signal sequence #status predicted <Sig>  
F:20-271/Product: OX40 antigen #status predicted <MAT>  
F:211-235/Domain: transmembrane #status predicted <TMM>

Query Match 15.6%; Score 151; DB 2; Length 271;  
Best Local Similarity 28.5%; Pred. No. 5.1e-05;  
Matches 47; Conservative 12; Mismatches 62; Indels 44; Gaps 8;  
Qy 26 ORPTGCGCGPGRLLG--TGTDAKCCRVHTT-----RCRD-YPEEECCSEWD----- 71  
Db 6 QOPT-----AFLGLGLSVTVKLVNCKDTPSGHKCCRCQCPGHHVMVSCDHTTRDTV 58  
Qy 72 CMCVQPEFHCG----DPC--CTTCRHH-----PCPPQGGVQSQGKF 108  
Db 59 CHPCEPGFYNEAVNYDTCKQCTQCNHRSGSELKQNCPTPTDVCQCRPTQPRQDSSHL 118  
Qy 109 GFQCIDCASGTFSGGHEGCHKPWTCTQFGFTVTPGNKTHNAV 153  
Db 119 GVDCVPCPPGHFSPGSNQACKPWTNCTLSGKQIRHPASNSLDTVC 163

RESULT 6  
JC5559  
lectin-B - Virginian pokeweed  
C:Species: Phytolacca americana (Virginian pokeweed)  
C:Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 17-Mar-2000  
C:Accession: JC5559  
R:Yamaguchi, K.; Yurino, N.; Kino, M.; Ishiguro, M.; Funatsu, G.  
Biosci. Biotechnol. Biochem. 61, 690-698, 1997  
A:Title: The amino acid sequence of mitogenic lectin-B from the roots of pokeweed (Phytolacca americana)  
A:Reference number: JC5559; MUID:97290889  
A:Accession: JC5559  
A:Molecule type: protein  
A:Residues: 1-295 <YAM>  
A:Experimental source: root  
C:Comment: This protein is a lectin specific for N-acetylglucosamine-containing saccharides  
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; plant lectin  
C:Keywords: glycoprotein  
F:96,139/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.3%; Score 139; DB 2; Length 295;  
Best Local Similarity 28.8%; Pred. No. 0.00046;  
Matches 36; Conservative 18; Mismatches 41; Indels 30; Gaps 8;  
Qy 20 CALSLGQRPTGCP-----GCGPGRLLLTGTDACRCRVHTTRCCRDYPG-----EECC 67  
Db 133 CGVDFGNRTCPNDLCCSEWGMCGITEGYCGECQSQC---NHQRCGKDFAGRTLNDLCC 189  
Qy 68 SEWDCMCVQPEPHCGDPCCTTCRHHPCPPGQVQSQGKFSGFQ-C---IDCASGTFSGG 123  
Db 130 SEWGC-WCSSEAHCGGCGQSNYNRC-----GR-NFGFRTCPNELCCSSGWC 238  
Qy 124 HEGHC 128  
Db 239 NDAHC 243

RESULT 7  
A46476  
B cell-associated surface molecule CD40, long splice form - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Nov-2000  
C:Accession: A46476; A46515  
R:Torres, R.M.; Clark, E.A.  
J. Immunol. 146, 620-626, 1992  
A:Title: Differential increase of an alternatively polyadenylated mRNA species of murine CD40  
A:Reference number: A46476; MUID:92105763  
A:Accession: A46476  
A:Status: preliminary  
A:Molecule type: mRNA

A:Residues: 1-305 <TOR>  
A:Cross-references: GB:M83312; NID:gl553058  
A:Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:75207)  
R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockay  
J. Immunol. 149, 3921-3926, 1992  
A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.  
A:Reference number: A46515; MUID:93094586  
A:Accession: A46515  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-287, LV' <GRI>  
A:Cross-references: GB:M83312; NID:gl553058; PIDN:AAB08705.1; PID:gl553059; GB:M94126  
A:Experimental source: BALB/c, liver  
A:Note: sequence extracted from NCBI backbone (NCBI:120357)  
C:Comment: For an alternative splice form, see PIR:A46515.  
C:Comment: For an alternative splice form, see PIR:A46476.  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: alternative splicing; transmembrane protein  
F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 14.0%; Score 135.5; DB 2; Length 305;  
Best Local Similarity 26.1%; Pred. No. 0.00089;  
Matches 49; Conservative 10; Mismatches 74; Indels 55; Gaps 8;  
Qy 13 LCGL--ALLCALSLGSRPTGPGCGPGRLLLTGCTDARCC----- 50  
Db 7 LCALMGCLLTAVHLGQCVT----CSDKQYL-----HDGQCCLDLPQPSRLTSHCTALEKTQ 58  
Qy 51 -----RVHTTRCCRDYPG-----EECCSEWDCMCVQPE-FHCGDPCCTT 88  
Db 59 CHPDCSGEFAQNNREIRCHQHRCEPNQGLRVKKEGTASDVTCTCKEGOHCSTKCEA 118  
Qy 89 C-RHHPGPPGQVQSQGKFSFGFCIDCASGTFSGGHE--GHCKPWTCTQFGFLTVP 145  
Db 119 CAQHTPCIPGFGVEMATETTDVCHPCVPVGFSSQSLFEKCYPMWTSCEKDNLEVLQKG 178  
Qy 146 NKTHNAV 153  
Db 179 TSQTNVIC 186

RESULT 8  
MMRTS  
laminin beta-2 chain precursor - rat  
N:Alternate names: laminin chain B3; S-laminin  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 10-Dec-1999  
C:Accession: S03539  
R:Hunter, D.D.; Shah, V.; Merille, J.P.; Sanes, J.R.  
Nature 338, 229-234, 1989  
A:Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neocortex  
A:Reference number: S03539; MUID:89159410  
A:Accession: S03539  
A:Molecule type: mRNA  
A:Residues: 1-1801 <HUN>  
A:Cross-references: EMBL:X16563; NID:g57250; PIDN:CAA34561.1; PID:g57251  
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C:Function:  
A:Description: interact with cells and with other basement membrane proteins to promote cell adhesion  
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular matrix  
F:1-35/Domain: signal sequence #status predicted <SIG>  
F:36-1801/Product: laminin beta-2 chain #status predicted <MAT>  
F:36-285/Domain: VI <DOM6>  
F:286-555/Domain: V <DOM5>  
F:286-347/Domain: laminin-type EGF-like homology <LE01>  
F:350-410/Domain: laminin-type EGF-like homology <LE02>  
F:413-470/Domain: laminin-type EGF-like homology <LE03>  
F:473-522/Domain: laminin-type EGF-like homology <LE04>  
F:525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F:556-784/Domain: IV <DOM4>

F;786-831/Domain: laminin-type EGF-like homology <LE06>  
F;788-1196/Domain: III <DOM3>  
F;834-877/Domain: laminin-type EGF-like homology <LE07>  
F;880-927/Domain: laminin-type EGF-like homology <LE08>  
F;930-986/Domain: laminin-type EGF-like homology <LE09>  
F;989-1038/Domain: laminin-type EGF-like homology <LE10>  
F;1041-1095/Domain: laminin-type EGF-like homology <LE11>  
F;1098-1143/Domain: laminin-type EGF-like homology <LE12>  
F;1146-1190/Domain: laminin-type EGF-like homology <LE13>  
F;1197-1412/Domain: II <DOM2>  
F;1197-1412/Region: heptad repeats  
F;1413-1445/Domain: alpha <ALP>  
F;1446-1801/Region: heptad repeats  
F;1446-1801/Domain: I <DOM1>  
F;145-50/Disulfide bonds: #status predicted  
F;251.371.1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status p  
F;1193,1196,1800/Disulfide bonds: interchain #status predicted

Query Match 13.9%; Score 134.5; DB 1; Length 1801;  
Best Local Similarity 26.9%; Pred. No. 0.0034;  
Matches 63; Conservative 6; Mismatches 60; Indels 105; Gaps 15;

QY 8 GAFRALC-GLALLCALSLG-----QRTGG-PCGCP-----GRLLLTGTGDARCCRV 52  
DB 840 GALSALCEGTSGQCLCRTGAFGLRCDHCQGWGFPNCRPCVNGR-----ADEEDA 891  
QY 53 HTTRC--CRDYPGECCSEWDCMCVQPEFHCDCPCCT---TCRHHPGPPGQVQSGQKFS 107  
DB 892 HTGACLCGRDVTGHECER---CI-AGFH-GDRLPYGGQCRPCPCPEGG--SORHEA 943  
QY 108 -----FGQCIDCASGTF----- 120  
DB 944 TSCHRDGYSQIVCHCRAGYTGRLRCEACAPGDFGPKGGRCLCECSGNIDPTDPGAC 1003  
QY 121 -----SGHEGHCXPTWDTCTQFGFLTFVPGNKNHNAV-VPGSP 159  
DB 1004 DPHGTGCLRLHHTGPHGCHKP-----GFHQAAAROSCHRCTNLLGTDP 1050

RESULT 9  
I48854  
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 23-Jul-1999  
C:Accession: I48854  
R:Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.  
Mamm. Genome 5, 726-727, 1994  
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.  
A;Reference number: I48854; MUID:95178848  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A;Residues: 1-459 <RES>  
A:Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831  
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
F;151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 12.4%; Score 120.5; DB 2; Length 459;  
Best Local Similarity 30.3%; Pred. No. 0.017;  
Matches 37; Conservative 11; Mismatches 57; Indels 17; Gaps 6;

QY 48 RCRRVHTTCRDYPGEECCSEWD---CMCVQPEF-----HCGDPCCTTC-RHHPCPPGQ 98  
DB 77 RTCLSCSSSSTQVETRACTKQNRVCAACEAGRYCALKTHSGS--CRQCMRLSKCGPGF 134  
QY 99 GVOGQKFSFGQCIDCASGTFSG--GHEGHCXPTWDTCTQFGFLTFVPGNKNHNAVCPVG 156  
DB 135 GVASSRAPNGVNLKACAPGTFSDTTSSTVDCRPHRCS----ILAIPGNASTDAVCAPE 190  
QY 157 SP 158  
II

Db 191 SP 192

RESULT 10  
S53869  
laminin beta-2 chain precursor (version 2) - human  
N;Alternate names: s-laminin  
C:Species: Homo sapiens (man)  
C:Date: 27-Oct-1995 #sequence\_revision 23-Feb-1996 #text\_change 24-Sep-1998  
C:Accession: S53869  
R:Ilvanainen, A.; Vuolteenaho, R.; Sainio, K.; Eddy, R.; Shows, T.B.; Sariola, H.; Tr  
Matrix Biol. 14, 489-497, 1994  
A;Title: The human laminin beta-2 chain (S-laminin): structure, expression in fetal t  
A;Reference number: S53869  
A;Accession: S53869  
A:Molecule type: mRNA  
A;Residues: 1-1798 <IIV>  
C:Genetics:  
A;Gene: GDB:LAMB2  
A:Cross-references: GDB:132363; OMIM:150325  
A;Map position: 3p21.3-3p21.2  
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C:Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer  
F;1-32/Domain: signal sequence #status predicted <SIG>  
F;33-1798/Product: laminin beta-2 chain #status predicted <MAT>  
F;283-344/Domain: laminin-type EGF-like homology <LE01>  
F;347-407/Domain: laminin-type EGF-like homology <LE02>  
F;410-467/Domain: laminin-type EGF-like homology <LE03>  
F;470-519/Domain: laminin-type EGF-like homology <LE04>  
F;522-552/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F;783-828/Domain: laminin-type EGF-like homology <LE06>  
F;831-874/Domain: laminin-type EGF-like homology <LE07>  
F;877-924/Domain: laminin-type EGF-like homology <LE08>  
F;927-983/Domain: laminin-type EGF-like homology <LE09>  
F;986-1035/Domain: laminin-type EGF-like homology <LE10>  
F;1038-1092/Domain: laminin-type EGF-like homology <LE11>  
F;1095-1140/Domain: laminin-type EGF-like homology <LE12>  
F;1143-1187/Domain: laminin-type EGF-like homology <LE13>

Query Match 12.3%; Score 119.5; DB 2; Length 1798;  
Best Local Similarity 23.9%; Pred. No. 0.05;  
Matches 57; Conservative 10; Mismatches 62; Indels 109; Gaps 14;

QY 8 GAFRALC---GLALLCALSLGQR-----PTGPGGCGPGRLLLTGTCTDARC----- 49  
DB 837 GALSLECEKTSQCLCRTGAFGLRCDRCQGWGFPFSCR-----CVCNGHAD 884  
QY 50 -CRVHTTRC--CRDYPGECCSEWDCMCVQPEFHCDCPCCT---TCRHHPGPPGQVQ--- 101  
DB 885 ECNHTGACLCGRDHTGHECER---CI-AGFH-GDRLPYGGQCRPCPCPEGSGQRH 938  
QY 102 -----SOGKFS-----FGQCIDCASGTF----- 120  
DB 939 PATSCHODEYSQQIVCHCRAGYTGRLRCEACAPGDFGSPRGGRCQCLCECSGNIDPMPDD 998  
QY 121 -----SGHEGHCXPTWDTCTQFGFLTFVPGNKNHNAV-VPGSPPAE 161  
DB 999 ACDPHGTGCLRLHHTGPHGCHKP-----GFHQAAAROSCHRCTNLLGTNPQQ 1049

RESULT 11  
A35356  
tumor necrosis factor receptor 2 precursor [validated] - human  
N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2  
C:Species: Homo sapiens (man)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 08-Dec-2000  
C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094  
R:Smith, C.A.; Davis, T.; Anderson, D.; Solan, L.; Beckmann, M.P.; Jerzy, R.; Dower,  
Science 248, 1019-1023, 1990  
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular a  
A;Reference number: A35356; MUID:90260639  
A;Accession: A35356

I37552  
OX40 homolog - human  
C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000  
C;Accession: I37552  
R;Latza, U.; Durrkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat  
Eur. J. Immunol. 24, 677-683, 1994  
A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment  
A;Reference number: I37552; MUID:94170844  
A;Accession: I37552  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-277 <RES>  
A;Cross-references: EMBL:X75962; NID:g472957; PIDN:CRA53576.1; PID:g472958  
C;Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match            16.7%; Score 162; DB 2; Length 277;  
Best Local Similarity 29.7%; Pred.No. 7.2e+06;  
Matches 51; Conservative 11; Mismatches 92; Indels 18; Gaps 5;

QY 5 GAMGAFRALCGALLCALSLG-----QRPTGGPGCGPGRLLLTGTDTARCCRVHT 54  
|| | | | | | | | | | | | | | | | | | | | | | | | |  
Db 4 GARLRGPCAALLLLGLGLSTVTGLHCVGDTVPNSDRNCHECR--PGNGMWSCRSSQN 61  
| | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 55 TRCRDYPG--EECCSEWDCM-CVQPEFHGCD---PCITTCRRHHPPCPGGGVSGKQFSF 108  
| | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 62 TVCRPCGPGFYNDVVSKPKPCCTWCNLRSGERKKQLCTATQDTVRCRAGTQLDSYKP 121  
| | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 109 GFQCIDCASGTFSGHGEGHKPWTDCTQFGFLTVFPGNKTHNAVCPGPSPPA 160  
| | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 122 GVDCAPCPGHFSPGDNQACKPWNTCTLAGKHILQPASNSSDAICEDRDPPA 173  
| | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3  
I38426  
lymphocyte activation-induced receptor ILA precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 01-Dec-2000  
C;Accession: I38426; JT0752  
R;Allderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; F  
Eur. J. Immunol. 24, 2219-2227, 1994  
A;Title: Molecular and biological characterization of human 4-1BB and its ligand.  
A;Reference number: I38426; MUID:94374434  
A;Accession: I38426  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-255 <RES>  
A;Cross-references: EMBL:U003397; NID:g571320; PIDN:AAA53133.1; PID:g571321  
R;Schwarz, H.; Tuckwell, J.; Lotz, M.  
Gene 134, 295-298, 1993  
A;Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne  
A;Reference number: JT0752; MUID:94085794  
A;Accession: JT0752  
A;Molecule type: mRNA  
A;Residues: 1-106,'R',108-255 <SCH>  
C;Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necro  
C;Comment: This receptor recognizes soluble, cell-surface bound or extracellular matrix  
C;Superfamily: CD27 antigen; NGF receptor repeat homology  
C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein  
F;1-17/Domain: signal sequence #status predicted <SIG>  
F;18-235/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT>  
F;187-213/Domain: transmembrane #status predicted <TMW>  
F;138,149/Binding site: carbohydurate (Asn) (covalent) #status predicted  
F;234,235/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predict  
F;242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match            16.6%; Score 160.5; DB 2; Length 255;  
Best Local Similarity 30.9%; Pred.No. 9e+06;  
Matches 47; Conservative 12; Mismatches 52; Indels 41; Gaps 9;

QY 34 CGPGRLLLTGTDAACRCRVHTTRCCRDYPG-----EBCCS----EWDCMCVQPFHCGBP 84  
| | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 48 CPPNSSFSAAG--QRTCDI-----CRCKGVFRTRKCSSTSNAECDC---TPGFHCLGA 97  
| | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 85 CCTCTCHHPCPPGQVQSQQKFSFGFCIDCASTFSGHGHCCKPWTDTCTQFGFLTVFP 144  
| | | | : | : | : | : | : | : | : | : | : | :  
Db 98 GCSMC-EQDCKQGQLTKG-----CKDCCFTEFNQKRIGICRPWTNCSLDGKSALVN 149

Qy 145 GNKTINAVCPG-----SPPA---EP 162  
| | | | : | : | : | : | : | : | : | : | : | :  
Db 150 GTKERDVCGPSPADLSPGASSVTTPAPAREP 181

RESULT 4  
B3293  
T-cell antigen 4-LBB precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 21-Jul-2000  
C:Accession: B32393; I48879  
R:Kwon, B.S.; Weissman, S.M.  
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989  
A:Title: cDNA sequence of two inducible T-cell genes.  
A:Reference number: A33293; MUID:89184547  
A:Accession: B32393  
A:Molecule type: mRNA  
A:Residues: 1-256 <KWQ>  
A:Cross-references: GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122  
R:Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.  
J. Immunol. 152, 2256-2262, 1994  
A:Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-LBB  
A:Reference number: I48879; MUID:94179805  
A:Accession: I48879  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-256 <RES>  
A:Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178  
C:Genetics:  
A:Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: transmembrane protein  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-256/Product: 4-LBB protein #status predicted <MAT>

Query Match 15.8%; Score 153; DB 2; Length 256;  
Best Local Similarity 31.5%; Pred. No. 3.4e-05;  
Matches 40; Conservative 17; Mismatches 52; Indels 18; Gaps 7;

Qy 34 CGPGRL-LLGTGDARCCRVHTTRCCRDYEGEECCSEW---DCMGVQPEFHCGDPCCPTC 89  
| | | | : | : | : | : | : | : | : | : | : | :  
Db 47 CPPSTFSSITGGPNCNICRV---CAGYFRFKFCSTTHNAECIE-GFHCLGFQCPCR 101

Qy 90 RHHPCPPGQVQSQQKFSFGFCIDCASTFSGGH-BGHCKPWTDTCTQFGFLTVFPGNKT 148  
| | | | : | : | : | : | : | : | : | : | : | :  
Db 102 -EKDCRPQGELTKQ-----CKTCSLGTFNDQNGTGVCPRWTNCSLDGRSVLKTGTTE 153

Qy 149 HNACVP 155  
: | | |  
Db 154 KDVGCP 160

RESULT 5  
SI2783  
OX40 antigen precursor - rat  
N:Alternate names: nerve growth factor receptor homolog  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 05-Nov-1999  
C:Accession: SI2783; S08036  
R:Mallett, S.; Fossum, S.; Barclay, A.N.  
EMBO J. 9, 1063-1068, 1990  
A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes  
A:Reference number: SI2783; MUID:90214614  
A:Accession: SI2783  
A:Molecule type: mRNA  
A:Residues: 1-271 <MAL>  
A:Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831  
C:Superfamily: CD27 antigen; NGF receptor repeat homology

---



```
FT DOMAIN 831 876 LAMININ EGF-LIKE 7.
FT DOMAIN 877 926 LAMININ EGF-LIKE 8.
FT DOMAIN 927 985 LAMININ EGF-LIKE 9.
FT DOMAIN 986 1037 LAMININ EGF-LIKE 10.
FT DOMAIN 1038 1094 LAMININ EGF-LIKE 11.
FT DOMAIN 1095 1142 LAMININ EGF-LIKE 12.
FT DOMAIN 1143 1189 LAMININ EGF-LIKE 13.
FT DOMAIN 1190 1409 DOMAIN II.
FT DOMAIN 1410 1442 DOMAIN ALPHA.
FT DOMAIN 1443 1798 COILED COIL (POTENTIAL).
FT DOMAIN 1799 1839 COILED COIL (POTENTIAL).
FT DISULFID 283 292 BY SIMILARITY.
FT DISULFID 285 310 BY SIMILARITY.
FT DISULFID 312 321 BY SIMILARITY.
FT DISULFID 324 344 BY SIMILARITY.
FT DISULFID 347 356 BY SIMILARITY.
FT DISULFID 349 374 BY SIMILARITY.
FT DISULFID 377 386 BY SIMILARITY.
FT DISULFID 389 407 BY SIMILARITY.
FT DISULFID 410 423 BY SIMILARITY.
FT DISULFID 412 438 BY SIMILARITY.
FT DISULFID 440 449 BY SIMILARITY.
FT DISULFID 452 467 BY SIMILARITY.
FT DISULFID 470 484 BY SIMILARITY.
FT DISULFID 472 491 BY SIMILARITY.
FT DISULFID 493 502 BY SIMILARITY.
FT DISULFID 505 519 BY SIMILARITY.
FT DISULFID 783 795 BY SIMILARITY.
FT DISULFID 785 802 BY SIMILARITY.
FT DISULFID 804 813 BY SIMILARITY.
FT DISULFID 816 828 BY SIMILARITY.
FT DISULFID 831 843 BY SIMILARITY.
FT DISULFID 833 850 BY SIMILARITY.
FT DISULFID 852 861 BY SIMILARITY.
FT DISULFID 864 874 BY SIMILARITY.
FT DISULFID 877 886 BY SIMILARITY.
FT DISULFID 879 893 BY SIMILARITY.
FT DISULFID 896 905 BY SIMILARITY.
FT DISULFID 908 924 BY SIMILARITY.
FT DISULFID 927 943 BY SIMILARITY.
FT DISULFID 929 954 BY SIMILARITY.
FT DISULFID 956 965 BY SIMILARITY.
FT DISULFID 968 983 BY SIMILARITY.
FT DISULFID 986 1000 BY SIMILARITY.
FT DISULFID 988 1007 BY SIMILARITY.
FT DISULFID 1010 1019 BY SIMILARITY.
FT DISULFID 1022 1035 BY SIMILARITY.
FT DISULFID 1095 1107 BY SIMILARITY.
FT DISULFID 1097 1114 BY SIMILARITY.
FT DISULFID 1116 1125 BY SIMILARITY.
FT DISULFID 1128 1140 BY SIMILARITY.
FT DISULFID 1143 1155 BY SIMILARITY.
FT DISULFID 1145 1162 BY SIMILARITY.
FT DISULFID 1164 1173 BY SIMILARITY.
FT DISULFID 1176 1187 BY SIMILARITY.
FT DISULFID 1190 1190 INTERCHAIN (PROBABLE).
FT DISULFID 1193 1193 INTERCHAIN (PROBABLE).
FT DISULFID 1797 1797 INTERCHAIN (PROBABLE).
FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1085 1085 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1249 1249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1308 1308 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1348 1348 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1499 1499 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 914 914 R -> G (IN REF. 2).
FT CONFLICT 1179 1179 G -> A (IN REF. 2).
SQ SEQUENCE 1798 AA; 196079 MW; 9555CF5B24850CB7 CRC64;
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Query Match

11.58; Score 111.5; DB 1; Length 1798;

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Best Local Similarity 23.28; Pred. No. 0.017;
Matches 55; Conservative 10; Mismatches 65; Indels 107; Gaps 13;
QY 8 GAFRALC---GLALLCALSLGOR-----PTGGPCGCGPGRLLLTGTGTDARC----- 49
Db 837 GALSSLCCKTSQGLCTGTGAFGLRCDRCQRGQMGFPSCR-----CVCNGHAD 884
QY 50 -CRVHTTRC--CRDYPGEECCSEWDCMCVQPEPHCGD--PCCTTCRHHPCPPGQGVQ--- 101
Db 885 ECNTHTGACILGCHRDHTTGEHCEH---CI-AGPHRDRPLPYGGQCRPCPCPEGPSQRHF 939
QY 102 -----SOGKFS-----FGQCIDCASGTF----- 120
Db 940 ATSCHQDEYSQIIVCHCRAGYTLGRCEACAPGHGDPSPRPGRCQLCECSGNIDPMDPDA 999
QY 121 -----SGGHEGHCKPWTDCDTQFGFLTVPGNKTHNAV---VPGSPPAE 161
Db 1000 CDPHTGQCLRLHHTTEGPHCAHCKP-----GFHGQAARQSCHRCTNLLGTNPQQ 1049
```

Search completed: September 4, 2001, 16:15:21  
Job time: 1133 sec



KW Glycoprotein; ATP-binding; Phosphorylation; Repeat; Signal.  
FT SIGNAL 1 30 POTENTIAL.  
FT CHAIN 31 741 INSULIN-LIKE GROWTH FACTOR I RECEPTOR,  
FT ALPHA-CHAIN.  
FT CHAIN 742 1370 INSULIN-LIKE GROWTH FACTOR I RECEPTOR,  
FT BETA-CHAIN.  
FT DOMAIN 742 936 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 937 960 POTENTIAL.  
FT DOMAIN 961 1370 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 608 829 FIBRONECTIN TYPE-III.  
FT DOMAIN 830 929 FIBRONECTIN TYPE-III.  
FT DOMAIN 1000 1275 PROTEIN KINASE.  
FT NP\_BIND 1006 1014 ATP (BY SIMILARITY).  
FT BINDING 1034 1034 ATP (BY SIMILARITY).  
FT ACT\_SITE 1136 1136 BY SIMILARITY.  
FT MOD\_RES 1166 1166 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
FT CARBOHYD 51 51 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 245 245 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 314 314 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 418 418 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 439 439 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 535 535 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 608 608 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 623 623 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 641 641 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 748 748 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 757 757 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 765 765 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 901 901 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 914 914 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CONFLICT 985 986 AD -> PY (IN REF. 3).  
SQ SEQUENCE 1370 AA; 155395 MW; A5946897A41CB145 CRC64;

Query Match 11.9%; Score 115.5; DB 1; Length 1370;  
Best Local Similarity 27.1%; Pred. No. 0.0064;  
Matches 57; Conservative 22; Mismatches 52; Indels 79; Gaps 20;

QY 8 GAFRA-----LCGLA-----LICALS-----LGORPTGGPGCG--PGRLL-----L 40  
DB 139 GATRIEKADLCYLSTIDSLIDAVSNVIVGNKPP--KECGDLCPGTLEKPMCKRTT 196  
QY 41 LGTGTDAKCCRVHTTRC---CRDYPGECCSEWDCMCVQPEFHCGDPC-----CTTC 89  
DB 197 INNEYNYRCWT--TNRCQKWCPSVCGKRACTE--NNECCHPE--CLGSCHTPDDNTTCVAC 251  
QY 90 RHH-----PCPPGGVGSQGFSP-GRQCID--CAS-----GTFSGG--HEGHCK 129  
DB 252 RHYYYKGVCPVCPACPP-----GTYREGWRVDRDFCANIPNAESDSGDFVIHDEC- 303  
QY 130 PWTDCQTFGLTFPPGNKTNVAVCPGSP 159  
DB 304 -MECPSP-GFIR-----NSTOSMYCIPCEGP 327

RESULT 15  
ID\_LMB2\_HUMAN STANDARD; PRT; 1798 AA.  
AC P55268; Q16321;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ).  
GN LAMB2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95213013; PubMed=7698745;

RA Wever U.M., Gerecke D.R., Durkin M.E., Kurtz K.S., Mattei M.-G.,  
RA Champlaud M.F., Burgeson R.E., Albrechtsen R.;  
RT "Human beta 2 chain of laminin (formerly S chain): cDNA cloning,  
RT chromosomal localization, and expression in carcinomas.";  
RL Genomics 24:243-252(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95316263; PubMed=7795887;  
RA Iivainen A., Vuolteenaho R., Sainio K., Eddy R., Shows T.B.,  
RA Sariola H., Tryggvason K.;  
RT "The human laminin beta 2 chain (S-laminin): structure, expression in  
RT fetal tissues and chromosomal assignment of the LAMB2 gene.";  
RL Matrix Biol. 14:489-497(1995).  
CC -1- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ  
CC IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF  
CC CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING  
CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.  
CC -1- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE  
CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND  
CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE  
CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.  
CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4  
CC (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).  
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
CC -1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR  
CC COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC  
CC CLEFT OF THE NEUROMUSCULAR JUNCTION.  
CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT  
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.  
CC -1- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.  
CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).  
CC -1- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.  
CC -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.  
CC -----  
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CC -----  
DR EMBL; Z68155; CA92279.1; -;  
DR EMBL; Z68156; CA92279.1; JOINED.  
DR EMBL; X79683; CA56130.1; -;  
DR EMBL; S77512; AAB34682.2; -;  
DR HSSP; P02468; 1KLO.  
DR MIM; 150325; -;  
DR InterPro; IPR000561; -;  
DR InterPro; IPR001886; -;  
DR InterPro; IPR002049; -;  
DR Pfam; PF00053; laminin\_EGF; 13.  
DR Pfam; PF00055; laminin\_Nterm; 1.  
DR PRINTS; PR00011; EGF\_LAMININ.  
DR PROSITE; PS00022; EGF\_1; 10.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 12.  
DR KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
FT SIGNAL 1 32 POTENTIAL.  
FT CHAIN 33 1798 LAMININ BETA-2 CHAIN.  
FT DOMAIN 33 280 LAMININ N-TERMINAL (DOMAIN VI).  
FT DOMAIN 281 552 4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN  
FT V).  
FT DOMAIN 283 346 LAMININ EGF-LIKE 1.  
FT DOMAIN 347 409 LAMININ EGF-LIKE 2.  
FT DOMAIN 410 469 LAMININ EGF-LIKE 3.  
FT DOMAIN 470 521 LAMININ EGF-LIKE 4.  
FT DOMAIN 522 552 LAMININ EGF-LIKE 5 (INCOMPLETE).  
FT DOMAIN 553 781 LAMININ DOMAIN IV.  
FT DOMAIN 782 1190 8 X LAMININ EGF-LIKE REPEATS (DOMAIN  
FT III).  
FT DOMAIN 783 830 LAMININ EGF-LIKE 6.

```

DR EMBL; U52160; AAC50622.1; JOINED.
DR EMBL; U52161; AAC50622.1; JOINED.
DR EMBL; U52162; AAC50622.1; JOINED.
DR EMBL; U52163; AAC50622.1; JOINED.
DR EMBL; U52164; AAC50622.1; JOINED.
DR EMBL; M55994; AAA36755.1; -.
DR PIR; A35356; A35356.
DR PIR; A36007; A36007.
DR PIR; A36475; A36475.
DR PIR; B35010; B35010.
DR PIR; A23666; A23666.
DR PDB; 1CA9; 12-APR-99.
DR MIN; 191191; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 4.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
KW Phosphorylation; Pharmaceutical; 3D-structure.
FT SIGNAL 1 22
FT CHAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT DOMAIN 23 257 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 258 287 POTENTIAL.
FT DOMAIN 288 461 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 39 201 4 X TNFR-CYS.
FT REPEAT 39 76 TNFR-CYS 1.
FT REPEAT 77 118 TNFR-CYS 2.
FT REPEAT 119 162 TNFR-CYS 3.
FT REPEAT 163 201 TNFR-CYS 4.
FT DISULFID 40 53 BY SIMILARITY.
FT DISULFID 54 67 BY SIMILARITY.
FT DISULFID 57 75 BY SIMILARITY.
FT DISULFID 78 93 BY SIMILARITY.
FT DISULFID 96 110 BY SIMILARITY.
FT DISULFID 100 118 BY SIMILARITY.
FT DISULFID 120 126 BY SIMILARITY.
FT DISULFID 134 143 BY SIMILARITY.
FT DISULFID 137 161 BY SIMILARITY.
FT DISULFID 164 179 BY SIMILARITY.
FT CARBOHYD 171 171 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 193 193 R -> P (IN REF. 4).
FT CONFLICT 141 141 R -> M (IN REF. 1 AND 3).
FT CONFLICT 196 196 A -> T (IN REF. 4).
FT CONFLICT 363 363
SQ SEQUENCE 461 AA; 48316 MW; 603B580ECD67636F CRC64;

Query Match 12.5%; Score 121; DB 1; Length 461;
Best Local Similarity 26.3%; Pred. No. 0.00096;
Matches 41; Conservative 14; Mismatches 63; Indels 38; Gaps 8;

QY 34 CGPG---RLLLGTGTDCR-----GDPCTCTTCHHPGCPGQVSGQKFSFGFCIDCASGTFSG-- 71
Db 57 CSPGQAKVFTKTSDDTVCDSCEDSTYTLQNNWPECLSCGRSCSDQVETQACTREQNR 116
QY 72 -CMCVQPEFHC-----GDPCTCTTCHHPGCPGQVSGQKFSFGFCIDCASGTFSG-- 122
Db 117 ICTC-RPGWYCALSKQECRCAPLR--KCRFGFGVARGPTETSDVCKPCAPGFSNIT 173
QY 123 GHEGHCKPWTDCTQFGTLTVFPGKNKTHNACVPGSP 158
Db 174 SSTDCRPHQICN----VVAIPGNASRDVACTSTSP 205

RESULT 11
TNR2_MOUSE
ID TNR2_MOUSE STANDARD; PRT; 474 AA.
AC P25119; P97893;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).
GN TNFRSF1B OR TNFR2 OR TNFR-2.

```

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

[1]

SEQUENCE FROM N.A.

RX MEDLINE=91167885; PubMed=1849278;

RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H., Chen E.Y., Goeddel D.V.;

RT "Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.";

RT Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).

RN [2]

SEQUENCE FROM N.A.

RX MEDLINE=91246168; PubMed=1645445;

RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.;

RT "Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor.";

RT Mol. Cell. Biol. 11:3020-3026(1991).

RN [3]

SEQUENCE OF 1-26 FROM N.A.

RP STRAIN=NOD;

RC Jacob C.O., Liu J.;

RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.

RN [4]

SEQUENCE OF 1-22 FROM N.A.

RC Tissue=Liver;

RA Kissinger M., Fellowes R., Feldmann M., Chernajovsky Y.;

RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

CC

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CC

EMBL; M60469; AAA39752.1; -.

DR EMBL; M59378; AAA40463.1; -.

DR EMBL; U39488; AAA85021.1; -.

DR EMBL; X87128; CAA60618.1; -.

DR PIR; B38634; B38634.

DR HSP; P19438; INCF.

DR MGD; MGI:1314883; Tnfrsf1b.

DR InterPro; IPR001368; -.

DR Pfam; PF00020; TNFR\_C6; 4.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.

DR PROSITE; PS00500; TNFR\_NGFR\_2; 3.

KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 22

FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.

FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 259 288 POTENTIAL.

FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 39 203 4 X TNFR-CYS.

FT REPEAT 39 77 TNFR-CYS 1.

FT REPEAT 78 119 TNFR-CYS 2.

FT REPEAT 120 164 TNFR-CYS 3.

FT REPEAT 165 203 TNFR-CYS 4.

FT DISULFID 40 54 BY SIMILARITY.

FT DISULFID 55 68 BY SIMILARITY.

FT DISULFID 58 76 BY SIMILARITY.

FT DISULFID 79 94 BY SIMILARITY.

FT DISULFID 97 111 BY SIMILARITY.

FT DISULFID 101 119 BY SIMILARITY.

FT DISULFID 121 127 BY SIMILARITY.

FT DISULFID 136 145 BY SIMILARITY.

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FT DISULFID 139 163 BY SIMILARITY.
FT DISULFID 166 181 BY SIMILARITY.
FT CARBOHYD 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Query Match 12.3%; Score 119; DB 1; Length 474;
Best Local Similarity 31.0%; Pred. No. 0.0015;
Matches 36; Conservative 8; Mismatches 54; Indels 18; Gaps 5;

QY 46 DARCCRVHTRCCRDYGECCSWDCMCVQPEHCHGDPCCCTTC-RHPPCPGOGVQSOG 104
DB 107 EIRACTKQQRVACAGRYCAL-----KTHSGS--CRQCMRLSKGPGGVASSR 155
QY 105 KFSFGFCIDCASGTFSG--GHECHGCPWTDCTQFGELTVPFGKNTNNAVCVPGSP 158
DB 156 APNGVNLKACACGTFTSDTSSDVCPRHICS-----ILAIPGNASTDAVCAPEP 207

RESULT 12
CD40_HUMAN
ID CD40_HUMAN STANDARD; PRT; 277 AA.
AC P25942;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)
DE (TUMOR NECROSIS FACTOR RECEPTOR 5).
GN TNFRSF5 OR CD40.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89356608; PubMed=2475341;
RA Stamenkovic I., Clark E.A., Seed B.;
RT "A B-lymphocyte activation molecule related to the nerve growth
RT factor receptor and induced by cytokines in carcinomas.";
RL EMBO J. 8:1403-1410(1989).
RN [2]
RP 3D-STRUCTURE MODELING OF 24-144.
RX MEDLINE=97189482; PubMed=9037712;
RA Bajorath J., Aruffo A.;
RT "Construction and analysis of a detailed three-dimensional model of
RT the ligand binding domain of the human B cell receptor CD40.";
RL Proteins 27:59-70(1997).
RN [3]
RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
RX MEDLINE=98266353; PubMed=9605317;
RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
RA Zheng Z., Naismith J.H., Thomas D.;
RT "The role of polar interactions in the molecular recognition of CD40L
RT with its receptor CD40.";
RL Protein Sci. 7:1124-1135(1998).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X60592; CAA43045.1;
DR PIR; S04460; S04460.
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DR PDB; 1CDF; 01-APR-97.
DR MIM; 109535;
DR InterPro; IPR001368;
DR Pfam; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 4.
KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
KW 3D-structure.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 277 CD40L RECEPTOR.
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 194 215 POTENTIAL.
FT DOMAIN 216 277 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 187 4 X TNFR-CYS.
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
FT DISULFID 26 37
FT DISULFID 38 51
FT DISULFID 41 59
FT DISULFID 62 77
FT DISULFID 83 103
FT DISULFID 105 119
FT DISULFID 111 116
FT DISULFID 125 143
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 277 AA; 30619 MW; BC8776EC2C4A5680 CRC64;

Query Match 12.2%; Score 118.5; DB 1; Length 277;
Best Local Similarity 27.7%; Pred. No. 0.0011;
Matches 36; Conservative 10; Mismatches 73; Indels 11; Gaps 5;

QY 34 CGPGRLLLTGTGDARCCRVHTRCCRDYPG-----EECCSEWDCMCVQPE-FHCGDPCCCTT 88
DB 62 CGSEFLDTWNRETHC---HQHKYCDPNLGRVQKGTSETDTICTCEGHWHTSEACES 118
QY 89 C-RHPPCPGOGVQSOGKFSFGFCIDCASGTFSGHEG--HCKPWTDCTQFGELTVPFG 145
DB 119 CVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVSAFEKCHPWTSCETKDLVVQAG 178
QY 146 NKTINAVCV 155
DB 179 TNKTDVVC 188

RESULT 13
TNRC_HUMAN
ID TNRC_HUMAN STANDARD; PRT; 435 AA.
AC P36941;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
DE 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
GN LTBR OR TNFR OR TNFRSF3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93252381; PubMed=8486360;
RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT "Construction and evaluation of a hncDNA library of human 12p
RT transcribed sequences derived from a somatic cell hybrid.";
RL Genomics 16:214-218(1993).
RN [2]
RP FUNCTION.
RX MEDLINE=94225209; PubMed=8171323;
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FT	SIGNAL	1	35	POTENTIAL.	FT	DISULFID	1798	1798	INTERCHAIN (PROBABLE).
FT	CHAIN	36	1799	LAMININ BETA-2 CHAIN.	FT	CARBOHYD	251	251	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	36	283	LAMININ N-TERMINAL (DOMAIN VI).	FT	CARBOHYD	371	371	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	284	555	4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN V).	FT	CARBOHYD	1086	1086	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	286	349	LAMININ EGF-LIKE 1.	FT	CARBOHYD	1250	1250	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	350	412	LAMININ EGF-LIKE 2.	FT	CARBOHYD	1309	1309	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	413	472	LAMININ EGF-LIKE 3.	FT	CARBOHYD	1349	1349	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	473	524	LAMININ EGF-LIKE 4.	FT	CARBOHYD	1500	1500	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	525	555	LAMININ EGF-LIKE 5 (INCOMPLETE).	SQ	SEQUENCE	1799 AA;	196352 MW; 1f28967a67aede33 CRC64;	
FT	DOMAIN	556	782	LAMININ DOMAIN IV.					
FT	DOMAIN	783	1191	8 X LAMININ EGF-LIKE REPEATS (DOMAIN III).					
FT	DOMAIN	784	831	LAMININ EGF-LIKE 6.					
FT	DOMAIN	832	877	LAMININ EGF-LIKE 7.					
FT	DOMAIN	878	927	LAMININ EGF-LIKE 8.	QY	5	GAMGAFRALC---	GLALLCALISLGORPT-----GGPGCGP-----GRL 39	
FT	DOMAIN	928	986	LAMININ EGF-LIKE 9.	Db	825	GPAGCQCQSPGALSALCEGTSGQCP	RPGAFLKCDHCQRCQWGFPPNCRPCVNGR- 883	
FT	DOMAIN	987	1038	LAMININ EGF-LIKE 10.					
FT	DOMAIN	1039	1095	LAMININ EGF-LIKE 11.					
FT	DOMAIN	1096	1143	LAMININ EGF-LIKE 12.	QY	40	LLGTGTDAARCCRVHTTRC--	CRDYPGEECCSEWDCMCVQPEFHCGDPCCCT---TCRIHPC 94	
FT	DOMAIN	1144	1190	LAMININ EGF-LIKE 13.	Db	884	-----ADECDTHTGACLCGRD	YTGGEHCEH-----CI-AGFH-GDRLPYGGQCRPCPC 930	
FT	DOMAIN	1191	1410	DOMAIN II.					
FT	DOMAIN	1411	1443	DOMAIN ALPHA.					
FT	DOMAIN	1444	1799	DOMAIN I.	QY	95	PPGQGVQSQGKFS-----	FGQCIDCAGTF----- 120	
FT	DOMAIN	1257	1304	COILED COIL (POTENTIAL).					
FT	DOMAIN	1473	1527	COILED COIL (POTENTIAL).	Db	931	PEGPG--SORHFATSCHRDGY	SSQIVCHCRAGYTLGRCEACAPGPGDPSKPGRCOLCE 988	
FT	DOMAIN	1577	1791	COILED COIL (POTENTIAL).					
FT	DISULFID	286	295	BY SIMILARITY.	QY	121	-----	SGGHEGCHKPWTCTQGFPLTVFGNKNTHNAV 153	
FT	DISULFID	288	313	BY SIMILARITY.	Db	989	CSGNIDPMDPADCPHTGQCL	RCLHNTGPHGCKP-----GFHQGAAROSCHIRCTC 1041	
FT	DISULFID	315	324	BY SIMILARITY.					
FT	DISULFID	327	347	BY SIMILARITY.	QY	154	-VPGSP 159		
FT	DISULFID	350	359	BY SIMILARITY.	Db	1042	NLLGTDP 1048		
FT	DISULFID	352	377	BY SIMILARITY.					
FT	DISULFID	380	389	BY SIMILARITY.					
FT	DISULFID	392	410	BY SIMILARITY.					
FT	DISULFID	413	426	BY SIMILARITY.					
FT	DISULFID	415	441	BY SIMILARITY.					
FT	DISULFID	443	452	BY SIMILARITY.					
FT	DISULFID	455	470	BY SIMILARITY.					
FT	DISULFID	473	487	BY SIMILARITY.					
FT	DISULFID	475	494	BY SIMILARITY.					
FT	DISULFID	496	505	BY SIMILARITY.					
FT	DISULFID	508	522	BY SIMILARITY.					
FT	DISULFID	784	796	BY SIMILARITY.					
FT	DISULFID	786	803	BY SIMILARITY.					
FT	DISULFID	805	814	BY SIMILARITY.					
FT	DISULFID	817	829	BY SIMILARITY.					
FT	DISULFID	832	844	BY SIMILARITY.					
FT	DISULFID	834	851	BY SIMILARITY.					
FT	DISULFID	853	862	BY SIMILARITY.					
FT	DISULFID	865	875	BY SIMILARITY.					
FT	DISULFID	878	887	BY SIMILARITY.					
FT	DISULFID	880	894	BY SIMILARITY.					
FT	DISULFID	897	906	BY SIMILARITY.					
FT	DISULFID	909	925	BY SIMILARITY.					
FT	DISULFID	928	944	BY SIMILARITY.					
FT	DISULFID	930	955	BY SIMILARITY.					
FT	DISULFID	957	966	BY SIMILARITY.					
FT	DISULFID	969	984	BY SIMILARITY.					
FT	DISULFID	987	1001	BY SIMILARITY.					
FT	DISULFID	989	1008	BY SIMILARITY.					
FT	DISULFID	1011	1020	BY SIMILARITY.					
FT	DISULFID	1023	1036	BY SIMILARITY.					
FT	DISULFID	1096	1108	BY SIMILARITY.					
FT	DISULFID	1098	1115	BY SIMILARITY.					
FT	DISULFID	1117	1126	BY SIMILARITY.					
FT	DISULFID	1129	1141	BY SIMILARITY.					
FT	DISULFID	1144	1156	BY SIMILARITY.					
FT	DISULFID	1146	1163	BY SIMILARITY.					
FT	DISULFID	1165	1174	BY SIMILARITY.					
FT	DISULFID	1177	1188	BY SIMILARITY.					
FT	DISULFID	1191	1191	INTERCHAIN (PROBABLE).					
FT	DISULFID	1194	1194	INTERCHAIN (PROBABLE).					

DR PFAM: PF00020; TNFR\_C6; 4;  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1;  
 DR KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 >269 CD40L RECEPTOR.  
 FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 194 215 POTENTIAL.  
 FT DOMAIN 216 >269 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 187 4 X TNFR-CYS.  
 FT REPEAT 25 60 TNFR-CYS 1.  
 FT REPEAT 61 103 TNFR-CYS 2.  
 FT REPEAT 104 144 TNFR-CYS 3.  
 FT REPEAT 145 187 TNFR-CYS 4.  
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT NON\_TER 269  
 SQ SEQUENCE 269 AA; 29983 MW; 746903F30F95F387 CRC64;

Query Match 12.6%; Score 122.5; DB 1; Length 269;  
 Best Local Similarity 28.7%; Pred. No. 0.00048;  
 Matches 37; Conservative 9; Mismatches 70; Indels 13; Gaps 5;

QY 34 CGPGRLLLTGTDARCRVHTTCRDYPGEECCSEWD-----CMCVQPEFHCGDPCCT 87  
 DB 62 CGRGEFLTNWREKY---HEHRYCNPLNLRIQSEGLTNTDTTCVCGEQ-HCTSHTC 117  
 QY 88 TCRHHP-CPGQGVOSGKSFQICDCASGTFSGGHEG--HCKPTWDTCTQFGLVFP 144  
 DB 118 SCTPHSLCLPFGVKQIATGLLDTVCBPCPLGFFSNVSSAFKCRWTSCKRKLGVQHV 177  
 QY 145 GNKTHNAVC 153  
 DB 178 GTNKTDVVC 186

RESULT 10  
 TNFR2\_HUMAN  
 ID TNFR2\_HUMAN STANDARD; PRT; 461 AA.  
 AC P20333;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR  
 BINDING PROTEIN 2) (TPB1) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).  
 GN TNFRSF1B OR TNFR2 OR TNFR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90260639; PubMed=2160731;  
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,  
 RA Dower S.K., Cosman D., Goodwin R.G.;  
 RT "A receptor for tumor necrosis factor defines an unusual family of  
 RT cellular and viral proteins";  
 RL Science 248:1019-1023(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91045991; PubMed=2172983;  
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,  
 RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;  
 RT "A second tumor necrosis factor receptor gene product can shed a  
 RT naturally occurring tumor necrosis factor inhibitor";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96299745; PubMed=8661109;  
 RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,  
 RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,  
 RA Brodeur G.M.;

"Physical mapping and genomic structure of the human TNFR2 gene."; Genomics 35:94-100(1996).  
 [4]  
 RN SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=90349572; PubMed=2166946;  
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D., Ringold G.M.;  
 RT "Complementary DNA cloning of a receptor for tumor necrosis factor  
 RT and demonstration of a shed form of the receptor."; Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).  
 [5]  
 RN SEQUENCE OF 27-31.  
 RX MEDLINE=90110215; PubMed=2153136;  
 RA Engelmann H., Novick D., Wallach D.;  
 RT "Two tumor necrosis factor-binding proteins purified from human  
 RT urine. Evidence for immunological cross-reactivity with cell surface  
 RT tumor necrosis factor receptors."; J. Biol. Chem. 265:1531-1536(1990).  
 [6]  
 RN SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.  
 RX MEDLINE=91056048; PubMed=2173696;  
 RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W., Brockhaus M.;  
 RT "Purification and partial amino acid sequence analysis of two  
 RT distinct tumor necrosis factor receptors from HL60 cells."; J. Biol. Chem. 265:20131-20138(1990).  
 [7]  
 RN CHARACTERIZATION.  
 RX MEDLINE=93016040; PubMed=1328224;  
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M., Lipari M.T., Goeddel D.V.;  
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.  
 RT Characterization of ligand binding, internalization, and receptor phosphorylation."; J. Biol. Chem. 267:21172-21178(1992).  
 [8]  
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.  
 RX MEDLINE=99221490; PubMed=10206649;  
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;  
 RT "Structural basis for self-association and receptor recognition of human TRAF2"; Nature 398:533-538(1999).  
 CC -|- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.  
 CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -|- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW LEVEL ON THREONINE RESIDUES.  
 CC -|- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND WYETH-AVERST); USED TO TREAT MODERATE TO SEVERE RHEUMATOID ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING PORTION OF TNFR2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.  
 CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -|- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".  
 CC -|- DATABASE: NAME=Enbrel; NOTE=Clinical information On Enbrel; WWW="http://www.enbrelinfo.com/".  
 CC -----  
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 CC -----  
 CC EMBL; M32315; AAA59929.1; -;  
 DR EMBL; M35857; AAA63262.1; -;  
 DR EMBL; U52165; AAC50622.1; -;  
 DR EMBL; U52156; AAC50622.1; JOINED.  
 DR EMBL; U52157; AAC50622.1; JOINED.  
 DR EMBL; U52158; AAC50622.1; JOINED.  
 DR EMBL; U52159; AAC50622.1; JOINED.





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FT DISULFID 786 798 BY SIMILARITY.
FT DISULFID 788 805 BY SIMILARITY.
FT DISULFID 807 816 BY SIMILARITY.
FT DISULFID 819 831 BY SIMILARITY.
FT DISULFID 834 846 BY SIMILARITY.
FT DISULFID 836 853 BY SIMILARITY.
FT DISULFID 855 864 BY SIMILARITY.
FT DISULFID 867 877 BY SIMILARITY.
FT DISULFID 880 889 BY SIMILARITY.
FT DISULFID 882 896 BY SIMILARITY.
FT DISULFID 899 908 BY SIMILARITY.
FT DISULFID 911 927 BY SIMILARITY.
FT DISULFID 930 946 BY SIMILARITY.
FT DISULFID 932 957 BY SIMILARITY.
FT DISULFID 959 968 BY SIMILARITY.
FT DISULFID 971 986 BY SIMILARITY.
FT DISULFID 989 1003 BY SIMILARITY.
FT DISULFID 991 1010 BY SIMILARITY.
FT DISULFID 1013 1022 BY SIMILARITY.
FT DISULFID 1025 1038 BY SIMILARITY.
FT DISULFID 1098 1110 BY SIMILARITY.
FT DISULFID 1100 1117 BY SIMILARITY.
FT DISULFID 1119 1128 BY SIMILARITY.
FT DISULFID 1131 1143 BY SIMILARITY.
FT DISULFID 1146 1158 BY SIMILARITY.
FT DISULFID 1148 1165 BY SIMILARITY.
FT DISULFID 1167 1176 BY SIMILARITY.
FT DISULFID 1179 1190 BY SIMILARITY.
FT DISULFID 1193 1193 INTERCHAIN (PROBABLE).
FT DISULFID 1196 1196 INTERCHAIN (PROBABLE).
FT DISULFID 1800 1800 INTERCHAIN (PROBABLE).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 371 371 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1088 1088 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1252 1252 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1311 1311 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1351 1351 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1502 1502 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1801 AA: 196473 MW: 97AEF32F8F31FA75 CRC64:

Query Match 13.9%; Score 134.5; DB 1; Length 1801;
Best Local Similarity 26.9%; Pred. No. 0.00018;
Matches 63; Conservative 6; Mismatches 60; Indels 105; Gaps 15;

QY 8 GAFRALC-GLALLCALSIG-----QRTGG-PCGCP-----GRLLGTGTDARQCRV 52
Db 840 GALSALCEGTSGQCLRTGAFGLRCDHCQRCQGWGFPCRCVCNGR-----ADECA 891

QY 53 HTRTC--CRDYPGEECCSEWDCMCVPEFHCGDPCCT---TCRHHPCPPGQVSGQKFS 107
Db 892 HTGACLCGRDYGTEGHCER-----CI-AGFH-GDPRLPYGGQCRPCPCPEGPG--SQRHFA 943

QY 108 -----FGFCIDCAGTFF----- 120
Db 944 TSHRDGYSQQIVCHCRAGYTGFLRCEACAPGHDPSPKPGRCOLCRCSGNIDPTDFPAC 1003

QY 121 -----SGGHEGHCKPWTDTQFGFLTVFPGNKTHNAV-VPGSPP 159
Db 1004 DPHGTQCLRLHHTGPHGCHKP-----GFGQAARQSCHRCTCNLLGTDP 1050

RESULT 8
LMB2_MOUSE STANDARD; PRT; 1799 AA.
AC Q61252; Q62182;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE LAMININ BETA-2 CHAIN PRECURSOR.
GN LAMB2 OR S-LAM OR LAMS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=129/J;
RX MEDLINE=96278760; PubMed=8662701;
RA Durkin M.E., Gautam M., Loechel S., Sanes J.R., Merlie J.P.,
RT "Structural organization of the human and mouse laminin beta2 chain
RT genes, and alternative splicing at the 5' end of the human
RT transcript.";
RL J. Biol. Chem. 271:13407-13416(1996).
RN [2]
RN SEQUENCE OF 348-428 FROM N.A.
RP TISSUE=Lung;
RX MEDLINE=94319092; PubMed=8043959;
RA Aberdam D., Galliano M.F., Mattei M.-G., Ortonne J.P., Meneguzzi G.;
RT "S-laminin gene (Lams) maps to F1 band of mouse chromosome 9.";
RL Mamm. Genome 5:393-394(1994).
RN [3]
RN FUNCTION.
RP STRAIN=129/J;
RX MEDLINE=95191650; PubMed=7885444;
RA Noakes P.G., Gautam M., Mudd J., Sanes J.R., Merlie J.P.;
RT "Aberrant differentiation of neuromuscular junctions in mice lacking
RT s-laminin/laminin beta 2.";
RL Nature 374:258-262(1995).
CC -1- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
CC IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
CC CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
CC -1- FUNCTION: LAMININ-3 (S-LAMININ) REGULATES THE FORMATION OF MOTOR
CC NERVE TERMINALS.
CC -1- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4
CC (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
CC MEMBRANES (MAJOR COMPONENT).
CC -1- TISSUE SPECIFICITY: NEUROMUSCULAR SYNAPSE AND KIDNEY GLOMERULUS.
CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -1- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -1- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
CC -----
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CC -----
CC EMBL; U43541; AAC53535.1; -.
CC EMBL; U42624; AAC53535.1; JOINED.
CC EMBL; X75928; CAA53532.1; -.
CC HSSP; P02468; IKLO.
CC MGD; MGI:99916; Lamb2.
CC InterPro; IPR001886; -.
CC InterPro; IPR002049; -.
CC Pfam; PF00053; laminin_EGF; 13.
CC Pfam; PF00055; laminin_Nterm; 1.
CC PRINTS; PR00011; EGF_LAMININ.
CC PROSITE; PS00022; EGF_1; 10.
CC PROSITE; PS01186; EGF_2; 2.
CC PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
CC Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.

```

```

RN [3]
RA REVISION TO 107.
RA Schwarz H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95347766; PubMed=7622190;
RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,
RT Kwon B.S.;
RL "Characterization of human homologue of 4-lbb and its ligand.";
IMMUNOL. Lett. 45:67-73(1995)
CC -!- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-LBB. POSSIBLY
CC ACTIVE DURING T CELL ACTIVATION.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T
CC CELLS.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw137.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U03397; AAA53133.1; -
DR EMBL; L12964; AAA62478.2; -
DR HSSP; P19438; 1EXT.
DR MIM; 602250; -
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
FT SIGNAL 1 17
FT CHAIN 18 255
FT DOMAIN 18 186
FT TRANSMEM 187 213
FT DOMAIN 214 255
FT REPEAT 47 159
FT REPEAT 87 118
FT REPEAT 119 159
FT CARBOHYD 138 138
FT CARBOHYD 149 149
SQ SEQUENCE 255 AA; 27899 MW; F3A563FE5EF00460 CRC64;

Query Match 16.6%; Score 160.5; DB 1; Length 255;
Best Local Similarity 30.9%; Pred. No. 2.3e-07;
Matches 47; Conservative 12; Mismatches 52; Indels 41; Gaps 9;

QY 34 CGPGRLLLTGTDARCCRVHTTCCRDYGP-----EECCS-----EWDKMCVQPEFHCGRP 84
DB 48 CPNPFSSAGG--QRTCDI-----CRQKGVTRFKESSTNAECDC---TPGFHCLGA 97
QY 85 CQTCRRHHPCPGQVQSGKFSFGFCQIDCASGTFSGGHEGCKPWTDTCTQFGFLTVFP 144
DB 98 GCSMC-EQDCKQSQELTKKG-----CKDCCFGTFNDQKRGICRWTNCSLDGKSVLNV 149
QY 145 GNKTHNAVCPVG-----SPPA-----EP 162
DB 150 GTERDVVCGPSPADLSPGASSVTPPAPAREP 181

RESULT 4
ID 4LBB_MOUSE STANDARD; PRT; 256 AA.
AC P20334;
```

Query Match	15.68;	Score 151;	DB 1;	Length 271;
Best Local Similarity	28.5%;	Pred. No. 1.6e-06;		
Matches	47;	Conservative	12;	Mismatches 62; Indels 44; Gaps 8;
QY	26	QRPTGGPGCGPGRLLG	--TGTARCCRVHTT-----RCCRD-YGPEBCCSEWD-----	71
DB	6	QQPT-----AFLLGLSLGVTVKLNCVKDTYPSGHKCCRCQPGHGMVSRCDTRDTV	58	
QY	72	CMCVOPEFHCG-----DPC--CTTCRRH-----PCPPGQGVQSGKFSF	108	
DB	59	CHPCPEGFYNEAVNDYCKQCTQCNRHSRGSSELKONCTPTEDTVCCQCRGTPQRODSSHL	118	
QY	109	GFQCIDCASGTFSGHGHGCKPWTDCQFGFLTVPFGNKTHNAV	153	
DB	119	GVDCVCPGPGHFGSPGNOACKPWTNCTLSGKQIRHPASNSLDTVC	163	
RESULT 6				
CD40_MOUSE				
ID	CD40_MOUSE	STANDARD;	PRT;	289 AA.
AC	P27512;			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).			
GN	TNFRSF5 OR CD40.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
LN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=92105763; PubMed=1370315;			
RA	Torres R.M., Clark E.A.;			
RT	"Differential increase of an alternatively polyadenylated mRNA			
RT	species of murine CD40 upon B lymphocyte activation.";			
RL	J. Immunol. 148:620-626(1992).			
LN	[2]			
RP	REVISTONS			
RC	SPRAIN-BALB/C;			
RC	Torres R.M.;			
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.			
LN	[3]			
RP	SEQUENCE FROM N.A.			
RP	SPRAIN-BALB/C; TISSUE=Liver;			
RC	MEDLINE=93094586; PubMed=1281194;			
RX	Grimaldi J.C., Torres R., Korak C.A., Chang R., Clark E.A.,			
RA	Howard M., Cockayne D.A.;			
RT	"Genomic structure and chromosomal mapping of the murine CD40 gene.";			
RT	J. Immunol. 149:3921-3926(1992).			
CC	-!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.			
CC	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
EMBL;	M83312; AAB08705.1; -			
DR	EMBL; M94126; AAA37404.1; -			
DR	EMBL; M94129; AAA37404.1; JOINED.			
DR	EMBL; M94128; AAA37404.1; JOINED.			
DR	EMBL; M94127; AAA37404.1; JOINED.			
DR	PIR; A6476; A46476.			
DR	HSP; P25942; ICDF.			
DR	MGI; M83336; Tnfrsf5.			
DR	InterPro; IPR001368; -			

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:15:20 ; Search time 43.78 Seconds  
(without alignments)  
126.756 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_1\_162  
Perfect score: 969  
Sequence: 1 MAQHGANGAPRALCGLALIC.....FPGNKTHNAVCPGSPAP 162

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	162	16.7	272	1	OX40_MOUSE	P47741 mus musculus
2	162	16.7	277	1	OX40_HUMAN	P43489 homo sapien
3	160.5	16.6	255	1	41BB_HUMAN	Q07011 homo sapien
4	153	15.8	256	1	41BB_MOUSE	P20334 mus musculus
5	151	15.6	271	1	OX40_RAT	P15725 rattus norv
6	135.5	14.0	289	1	OX40_MOUSE	P27512 mus musculus
7	134.5	13.9	1801	1	LMB2_RAT	P15800 rattus norv
8	127.5	13.2	1799	1	LMB2_MOUSE	Q61292 mus musculus
9	122.5	12.6	269	1	CD40_BOVIN	Q28203 bos taurus
10	121	12.5	461	1	TNR2_HUMAN	P25119 mus musculus
11	119	12.3	474	1	TNR2_MOUSE	P25942 homo sapien
12	118.5	12.2	277	1	CD40_HUMAN	P36941 homo sapien
13	117	12.1	435	1	TNRC_HUMAN	P24062 rattus norv
14	115.5	11.9	1370	1	IGIR_RAT	P55268 homo sapien
15	111.5	11.5	1798	1	LMB2_HUMAN	Q61555 mus musculus
16	110.5	11.4	2907	1	FN2_MOUSE	Q01705 mus musculus
17	109.5	11.3	2531	1	NTC1_MOUSE	Q61001 mus musculus
18	109	11.2	3635	1	LMA5_MOUSE	Q60751 mus musculus
19	108.5	11.2	1373	1	IGIR_MOUSE	P35556 homo sapien
20	106.5	11.0	2911	1	FN2_HUMAN	P35442 homo sapien
21	105	10.8	1172	1	TSP2_HUMAN	Q07375 gallus gall
22	104.5	10.8	684	1	FBL1_CHICK	Q05895 mus musculus
23	102.5	10.6	956	1	TSP3_MOUSE	P08069 homo sapien
24	101.5	10.5	1367	1	IGIR_HUMAN	Q61982 mus musculus
25	101.5	10.5	2318	1	NTC3_MOUSE	P98157 gallus gall
26	101	10.4	4543	1	LRP1_CHICK	Q07008 rattus norv
27	100.5	10.4	2531	1	NTC1_RAT	P10969 tritricum ae
28	100	10.3	186	1	AGI3_WHEAT	Q64716 rattus norv
29	100	10.3	581	1	IRR_RAT	P40798 drosophila
30	100	10.3	1106	1	STC_DROME	P26371 homo sapien
31	99.5	10.3	169	1	KRUA_HUMAN	P11219 oryza sativ
32	99.5	10.3	227	1	AGI_ORYSA	Q61789 mus musculus
33	99.5	10.3	2569	1	LMA3_MOUSE	

ALIGNMENTS

RESULT 1	OX40_MOUSE	STANDARD;	PRT;	272 AA.
ID	OX40_MOUSE			
AC	P47741;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).			
GN	TNFRSF4 OR TXGP1 OR OX40.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/C;			
RX	MEDLINE=94044750; PubMed=8238223;			
RA	Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J.,			
RA	Claassen E., Noelle R.J., Fell H.;			
RT	"Cloning of mouse OX40: a T cell activation marker that may mediate			
RT	T-B cell interactions."			
RL	J. Immunol. 151:5261-5271(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95255413; PubMed=7737295;			
RA	Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,			
RA	Barclay A.N.;			
RT	"Gene structure and chromosomal localization of the mouse homologue			
RT	of rat OX40 protein."			
RL	Eur. J. Immunol. 25:926-930(1995).			
CC	-1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
CC	-----			
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CC	-----			
CC	EMBL; Z21674; CAA79772.1; -			
DR	EMBL; X85214; CAA59476.1; -			
DR	HSSP; P25942; ICDF.			
DR	MGI; MGI:104512; Tnfrsf4.			
DR	InterPro; IPR001368; -			
DR	Pfam; PF00020; TNFR_c6; 3.			
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.			
DR	PROSITE; PS00050; TNFR_NGFR_2; 2.			
KW	Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;			
KW	Signal.			
FT	SIGNAL. 1 19 POTENTIAL.			
FT	CHAIN 20 272 OX40L RECEPTOR.			
FT	DOMAIN 20 211 EXTRACELLULAR (POTENTIAL).			
FT	TRANSMEM 212 236 POTENTIAL.			

P02876 triticum ae  
Q07934 homo sapien  
P35444 rattus norv  
P10040 drosophila  
P18519 gallus gall  
Q16787 homo sapien  
P98133 bos taurus  
P10968 tritricum ae  
P21512 homo sapien  
P22105 homo sapien  
P50284 mus musculus  
Q01279 mus musculus

```

FT DOMAIN 237 272 CYTOPLASMIC (POTENTIAL).
FT REPEAT 26 165 4 X TNFR-CYS.
FT REPEAT 26 61 TNFR-CYS 1.
FT REPEAT 62 103 TNFR-CYS 2.
FT REPEAT 104 124 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 125 165 TNFR-CYS 4.
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 15 15 A > G (IN REF. 2).
SQ SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;

Query Match 16.7%; Score 162; DB 1; Length 272;
Best Local Similarity 28.3%; Pred. No. 1.8e-07;
Matches 45; Conservative 11; Mismatches 51; Indels 52; Gaps 7;

QY 39 LLLGTGTDAR--CCRVIT-----TRCCRD-YPG-----ECCSEWDCMCVQPEFHGDCPC-- 85
DB 14 LAUTLGLVTARLNLCKVITYPSGHKKCCRCQPGHGMVSRCDHTRDLTC-----HPCET 65
QY 86 -----CTTCRHHP-----CPCGQGVQSGKFSFGFCID 114
DB 66 GFYNEAVNYDTCKCTOCNHRSGSELKQNCPTPTQDTCRCRPGTQPRQDSGYKLGVDVCP 125
QY 115 CASGTFSGHGHGCKPWTCTQFGFLTVFPGNKTHNAV 153
DB 126 CPCGHFSPGNQACKPWTNCTLTKGQTRHPASDLDVAVC 164

RESULT 2
OX40_HUMAN STANDARD; PRT; 277 AA.
ID OX40_HUMAN
AC P43489; Q13663;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY
DE ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).
GN TNFRSF4 OR TXGPIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94170844; PubMed=7510240;
RA Latza U., Duerkop H., Schnitzger S., Ringeling J., Eitelbach F.,
RA Hummel M., Fonatsch C., Stein H.;
RT "The human OX40 homologue: cDNA structure, expression and chromosomal
RT assignment of the ACT35 antigen."
RL Eur. J. Immunol. 24:677-683(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95219871; PubMed=7704935;
RA Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A.,
RA Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.;
RT "Identification of OX40 ligand and preliminary characterization of
RT its activities on OX40 receptor."
RL Circ. Shock 44:30-34(1994).
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD134 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd134.htm".
CC -----
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EMBL; X75962; CAA53576.1; -

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DR EMBL; S76792; AAB33944.1; ALT_INIT.
DR HSP; P25942; ICDF.
DR MIM; 600315; -
DR InterPro; IPR001368; -
DR Pfam; PF00020; TNFR_C6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW Signal.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 277 OX40L RECEPTOR.
FT DOMAIN 29 214 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 215 235 POTENTIAL.
FT DOMAIN 236 277 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 30 169 4 X TNFR-CYS.
FT REPEAT 30 65 TNFR-CYS 1.
FT REPEAT 66 107 TNFR-CYS 2.
FT REPEAT 108 126 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 127 167 TNFR-CYS 4.
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 277 AA; 29340 MW; 49F15525941550BF CRC64;

Query Match 16.7%; Score 162; DB 1; Length 277;
Best Local Similarity 29.7%; Pred. No. 1.8e-07;
Matches 51; Conservative 11; Mismatches 92; Indels 18; Gaps 5;

QY 5 GAMGAFRALCGLALICALSLG-----QRTGGGCGGPRLLLTGTGTDCRCRVHT 54
DB 4 GARRLGRGPCAALLLLGLGLSTVTLGHCVGDTYPSNDRCCHECR--PGNGMYSRCRSQN 61
QY 55 TRCCRDYPG--ECCSEWDCM-CVQPEFHGCD---PCCTTCRHHPCCPGQGVQSGKFSF 108
DB 62 TVCRPCGPGFYNDVVSXKPCPCPCWCNLSRSGERKQLCTATQDTCRCRAGTQPLDSYKP 121
QY 109 GFQCIDCASGTFSGHGHGCKPWTCTQFGFLTVFPGNKTHNAVCPVSPPA 160
DB 122 GVDCAPCPPGHFSPCDNQACKPWTNCTLAKGHTLQPASNSSDAICEDRDPPA 173

RESULT 3
41BB_HUMAN STANDARD; PRT; 255 AA.
ID 41BB_HUMAN
AC Q07011;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE 4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB HOMOLOG)
DE (T-CELL ANTIGEN ILA) (CD137 ANTIGEN).
GN TNFRSF9 OR ILA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=94374434; PubMed=8088337;
RA Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J.,
RA Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;
RT "Molecular and biological characterization of human 4-1BB and its
RT ligand."
RL Eur. J. Immunol. 24:2219-2227(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=94085794; PubMed=8262389;
RA Schwarz H., Tuckwell J., Lotz M.;
RT "A receptor induced by lymphocyte activation (ILA): a new member of
RT the human nerve-growth-factor/tumor-necrosis-factor receptor
RT family."
RL Gene 134:295-298(1993).

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Db      107 EIRACTQQRNVKACAGRYCAL-----KTHSGS--CROCMRLUSKCGPGGVASSR 155
QY      80 KFSFGFCIDCASGTFSG--GHEGHCKPWTDCDTQGFGLTVFPNGKNTHNVCVPGSP 133
        :   ||| |||| |. |   :   :   : ||| | ||
Db     156 APNGNLVKACAPCTFSDTTSSTDVCRHRICS----ILAIPGNASTDAVCAPESP 207

RESULT 12
A60771
N:Cell activation protein CD40 precursor - human
N:Alternate names: B-cell surface antigen bp50
C:Species: Homo sapiens (man)
C>Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: S04460; A60771
R:Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
A:Reference number: S04460; MUID:89356608
A:Accession: S04460
A:Molecule type: mRNA
A:Residues: 1-277 <STA>
A:Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851
R:Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-
A:Reference number: A60771; MUID:89093941
A:Accession: A60771
A:Molecule type: protein
A:Residues: 21-50 <BKA>
A:Experimental source: Burkitt lymphoma cell line Raji
C:Genetics:
A:Gene: GDB:CD40
A:Cross-references: GDB:215268; OMIM:109535
A:Map position: 20q12-20q13.2
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane prot
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAP>
F:21-193/Domain: extracellular #status predicted <EXT>
F:194-215/Domain: transmembrane status predicted <TM>
F:216-277/Domain: intracellular status predicted <CYT>
F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          14.1%; Score 118.5; DB 2; Length 277;
Best Local Similarity 27.7%; Pred. No. 0.01;
Matches 36; Conservative 10; Mismatches 73; Indels 11; Gaps 5;

QY      9 CGPGRLLGTGDARCCRVHTRTCRDYPG---EECCSEMDCMCVQPE-FHCGRPCCTT 63
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     62 CGESEFLDWNRETHC---HQHKYCDPNLGRVQQKTSETDITCTCEGWHCSTSEACS 118

QY      64 C-RHIPCPGGVGVSQSKFFEGFOCIDASGTFSSGGHEG--HCKPWTDCTQFGFLTVPFG 120
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    119 CVLHRCSPGFGVKQIATGVSVDITCEPCPVGFSSNSAFEEKCHPWTSCETKDLVVQOAG 178

QY      121 NKTHNAVVCVP 130
        : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     179 TNKTDVVVCGP 188

RESULT 13
I54182
tumor necrosis factor receptor 2-related protein - human
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C:Accession: I54182
R:Baens, M.; Chalfanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed seq
A:Reference number: I54182; MUID:93252381
A:Accession: I54182
A>Status: preliminary; translated from GB/EMBL/DDBBJ

```

A;Molecule type: mRNA  
A;Residues: 1-435 <RES>  
A;Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762  
C;Genetics:  
A;Gene: GDB:LTBR  
A;Cross-references: GDB:1230195; OMIM:600979  
A;Map position: 12p13.3-12p13.1  
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 13.9%; Score 117; DB 2; Length 435;  
Best Local Similarity 25.6%; Pred. No. 0.018;  
Matches 42; Conservative 12; Mismatches 66; Indels 44; Gaps 10;

Qy	9	CGGRLLLGTGDARCRVHTTRC-----CRDPGEE---C	41
Db	62	CPP-----GTVSAKCSRIRDTVCATCAENSYNEHMYLTICQLRCRCDPVMGLEIAPC	116
Qy.	42	CS--EWDNCMVQPEFHCGDPC--CTTCR--HHCPPGGVQSGQKFSEF--QCIDCAGTF	95
		:   :   :   :   :   :   :   :   :   :   :   :	
Db	117	TSRRKTQCR--QPGMFAAWALECTHCELLSDCPPGTEAELEKDEVKGNNHCVPCKAGHF	175
Qy	96	--SGHGHGCHKPWTDCTQGFGLTVFPGNKTHNAVCPGSPPAEP	137
		:   :   :   :   :   :   :   :   :   :   :   :	
Db	176	QNTSSSPARQPHTRCENQGLVEAAPGTAQSDTTC---KNPLEP	216

RESULT 14  
S53869 laminin beta-2 chain precursor (version 2) - human  
N;Alternate names: s-laminin  
C;Species: Homo sapiens (man)  
C;Date: 27-Oct-1995 #sequence\_revision 23-Feb-1996 #text\_change 24-Sep-1998  
C;Accession: S53869  
R;Iivanainen, A.; Vuolteenaho, R.; Sainio, K.; Eddy, R.; Shows, T.B.; Sariola, H.; Tryggvason, M.; Liggan, C.A. Matrix Biol. 14, 489-497, 1994  
A;Title: The human laminin beta-2 chain (S-laminin): structure, expression in fetal tissues and localization in adult tissues  
A;Reference number: S53869  
A;Accession: S53869  
A;Molecule type: mRNA  
A;Residues: 1-1798 <II>

C; Gene: GDB:150325  
A; Gene: GDB: LAMB2  
A; Cross-references: GDB:132363; OMIM:150325  
A; Map position: 3p21.3-3p21.2  
C; Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C; Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer  
F; 1-32/Domain: signal sequence #status predicted <SIG>  
F; 33-1798/Product: laminin beta-2 chain #status predicted <MAT>  
F; 283-344/Domain: laminin-type EGF-like homology <LE01>  
F; 347-407/Domain: laminin-type EGF-like homology <LE02>  
F; 410-467/Domain: laminin-type EGF-like homology <LE03>  
F; 470-519/Domain: laminin-type EGF-like homology <LE04>  
F; 522-552/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F; 783-828/Domain: laminin-type EGF-like homology <LE06>  
F; 831-874/Domain: laminin-type EGF-like homology <LE07>  
F; 877-924/Domain: laminin-type EGF-like homology <LE08>  
F; 927-983/Domain: laminin-type EGF-like homology <LE09>  
F; 986-1035/Domain: laminin-type EGF-like homology <LE10>  
F; 1038-1092/Domain: laminin-type EGF-like homology <LE11>  
F; 1095-1140/Domain: laminin-type EGF-like homology <LE12>  
F; 1143-1187/Domain: laminin-type EGF-like homology <LE13>

Query Match 13.7%; Score 115; DB 2; Length 1798;  
Best Local Similarity 23.9%; Pred. No. 0.067;  
Matches 49; Conservative 8; Mismatches 50; Indels 98; Gaps 12;

**QY**    5   GGPGCGPGRLLLTGTGDARC-----CRVHTTRC--CRDYPGECCSEWDCMCVQPFF 54  
| | | | | | | | | | | | | | | | |  
**Db**    870 GFPSCR-----CVCNGHADECNTHTGACLGCRDHTGGEHCR-----CI-AGF 912  
| | | | | | | | | | | | | | | | |  
**QY**    55 HCGDPDCT--TCRHHPCPPGGVGQ-----SQGFKS-----FGQCICDCASS 93

Db	913	H	GDRLPYGGQKPCPCPEGPGSRHFAT	SHQDEYSQ	IVCHCRAGYTG	LRCEACAPG	971
Qy	94	TF	-----	-----	SGHGEGHKPMT	DCTQF	112
Db	972	HFGDSPRGRC	CECSGNIDPMD	PDADCPHTGQ	CLRHHTGEPHCA	CKP	1024
Qy	113	GFLTVFPGN	KNTHNAV	-VPGSPPAE			136
Db	1025	GFHGQAARQ	SCHRCTCN	LLGTNPQ			1049

RESULT 15

hypothetical protein C06A1.6 - *Caenorhabditis elegans*  
 C/Species: *Caenorhabditis elegans*  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C/Accession: T18975

R;McMurray, A.

submitted to the EMBL Data Library, June 1995

A: Reference number: 219054

A;reference number: Z19034  
A;accession: T19075

A;Accession: T18975

A;Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA

A; Residues: 1-152 &lt;WIL&gt;

A; Cross-references: EMB:

A: Experimental source: clone C06A1

A; Experimental source  
C: Genetics.

C;Genetics:  
A:Cond. Cond. Cond. C

A;Gene: CESP:CO

A;Map position:

A; Introns: 22/3

Query Match 13 38: score 112: DB 2: Length 152:

Query Match 13.38; Score 112; DB 2; Length 152;  
Post Local Similarity 24.08; Prod No 0.022.

Best Local Similarity 34.9%; Pred. No. 0.022;

**Matches 30; Conservative 0; Mismatches 32; Indels 24; Gaps**

Y 8 GCGPGRLLGGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFFHCGDPPCCTTCRHH 67

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b 61 GCGGG---GGGGGCCCCR---PRCC-----CCCRPKCCCTCCRTCCCTCCCTCCB--10

D 01 GGGG---GGGGCCCCCR---PRCC---

[illegible]

68 PCPPGQGVQSQGKFSFGFQCIDCAG 93

b 105 PCCCGGC-----GCCCGCGGG 12

Search completed: September 4, 2001, 16:12:11  
Job time: 1108 sec





C;Keywords: growth factor receptor; transmembrane protein  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-271/Product: OX40 antigen #status predicted <MAT>  
F;211-235/Domain: transmembrane #status predicted <TM>

Query Match 18.0%; Score 151; DB 2; Length 271;  
Best Local Similarity 28.5%; Pred. No. 2.6e-05;  
Matches 47; Conservative 12; Mismatches 62; Indels 44; Gaps 8;  
QY 1 QRPVGGPCGGRLLG--TGTDAACCRVHTT-----RCCRD-YGEECCSEWD----- 46  
Db 6 QPPT-----AFLLGLSLGVTVKLVKNDYTPSGHKCCRCQGHGVMVSRCDHTRDTV 58  
QY 47 CMVQPEFHCG----DPC--CTTCRHH-----PCPPQGVQSQGKFSF 83  
Db 59 CHPCEGFYNEAVNYDTCKQCTQCNHRSSELKQNCITPTDVTVCQCRGTPQRODSSHL 118  
QY 84 GFQCIDASGTFSGHGCHCKPWTDTQFGTLTVFPGNKTHNAV 128  
Db 119 GVDCVPCPGHFSPGNSQACKPWTNCTLSGKQIRHPASNSLDTVC 163

RESULT 6  
JC5559  
lectin-B - Virginian pokeweed  
C;Species: Phytolacca americana (Virginian pokeweed)  
C;Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 17-Mar-2000  
C;Accession: JC5559  
R;Yamaguchi, K.; Yurino, N.; Kino, M.; Ishiguro, M.; Funatsu, G.  
Biotech. Biotechnol. Biochem. 61, 690-698, 1997  
A;Title: The amino acid sequence of mitogenic lectin-B from the roots of pokeweed (Phytolacca americana)  
A;Reference number: JC5559; MUID:97290889  
A;Accession: JC5559  
A;Molecule type: protein  
A;Residues: 1-295 <YAM>  
A;Experimental source: root  
C;Comment: This protein is a lectin specific for N-acetylglucosamine-containing saccharide  
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p  
C;Keywords: glycoprotein  
F;96,139/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.5%; Score 138.5; DB 2; Length 295;  
Best Local Similarity 31.7%; Pred. No. 0.00027;  
Matches 33; Conservative 17; Mismatches 31; Indels 23; Gaps 7;  
QY 9 CGPGRLLGTGTDAACCRVHTTRCCRDYPG-----EECCSEWDCMCVQPEFHCGDPCCCTT 63  
Db 154 CGITEGYGEGCQSQC---NHQRCGKDFAGRTCLNDLCCSEWG-WCGSSEAHCGGCGQSN 209  
QY 64 CRHHPCPPGQGVQSGKFSFGQ-C---IDCASGTFSGHGHC 103  
Db 210 CNYNRC-----GR-NFGFRTPNELCCSSGCGWGSNDARC 243

RESULT 7  
A46476  
B cell-associated surface molecule CD40, long splice form - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Nov-2000  
C;Accession: A46476; A46515  
R;Torres, R.M.; Clark, E.A.  
J. Immunol. 148, 620-626, 1992  
A;Title: Differential increase of an alternatively polyadenylated mRNA species of murine CD40  
A;Reference number: A46476; MUID:92105763  
A;Accession: A46476  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-305 <TOR>  
A;Cross-references: GB:M83312; NID:g1553058  
A;Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)  
A;Note: this translation is not annotated in GenBank entry MUSCDA0A, release 113.0

R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockay  
J. Immunol. 149, 3921-3926, 1992  
A;Title: Genomic structure and chromosomal mapping of the murine CD40 gene.  
A;Reference number: A46515; MUID:93094586  
A;Accession: A46515  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-287, 'LV' <GRI>  
A;Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126  
A;Experimental source: BALB/c, liver  
A;Note: sequence extracted from NCBI backbone (NCBIP:120357)  
C;Comment: For an alternative splice form, see PIR:A46515.  
C;Superfamily: CD27 antigen; NGF receptor repeat homology  
C;Keywords: alternative splicing; transmembrane protein  
F;105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 15.2%; Score 127.5; DB 2; Length 305;  
Best Local Similarity 28.9%; Pred. No. 0.0021;  
Matches 37; Conservative 8; Mismatches 72; Indels 11; Gaps 5;  
QY 9 CGPGRLLGTGTDAACCRVHTTRCCRDYPG-----EECCSEWDCMCVQPE-FHCGDPCCCTT 63  
Db 62 CDSGEFSAQWNRIRCI---QHRRHCEPNQGLRVKKEGTAESDVTCTCKEQGHCTSKDCEA 118  
QY 64 C-RHHPCPPGQGVQSGKFSFGQCIDCASGTFSGGHE--GHCKPWTDTCTQFGFLTVFPG 120  
Db 119 CAQHTPCIPGFGVMEMATETDTVCHPCVPVGFSSNOSSLFERKCPWTSCBKNLEVLQKG 178  
QY 121 NKTHNAV 128  
Db 179 TSQTNVIC 186

RESULT 8  
MMRTS  
laminin beta-2 chain precursor - rat  
N;Alternate names: laminin chain B3; S-laminin  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 10-Dec-1999  
C;Accession: S03539  
R;Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.  
Nature 338, 229-234, 1989  
A;Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neocortex  
A;Reference number: S03539; MUID:89159410  
A;Accession: S03539  
A;Molecule type: mRNA  
A;Residues: 1-1801 <HUN>  
A;Cross-references: EMBL:X16563; NID:g57250; PIDN:CAA34561.1; PID:g57251  
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C;Function:  
A;Description: interact with cells and with other basement membrane proteins to promote cell adhesion  
A;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular matrix  
F;1-35/Domain: signal sequence #status predicted <SIG>  
F;36-1801/Product: laminin beta-2 chain #status predicted <MAT>  
F;36-285/Domain: VI <DOM6>  
F;286-555/Domain: V <DOM5>  
F;286-347/Domain: laminin-type EGF-like homology <LE01>  
F;350-410/Domain: laminin-type EGF-like homology <LE02>  
F;413-470/Domain: laminin-type EGF-like homology <LE03>  
F;473-522/Domain: laminin-type EGF-like homology <LE04>  
F;525-555/Domain: laminin-type EGF-like homology <LE05>  
F;556-784/Domain: IV <DOM4>  
F;786-831/Domain: laminin-type EGF-like homology <LE06>  
F;788-1196/Domain: III <DOM3>  
F;834-877/Domain: laminin-type EGF-like homology <LE07>  
F;880-927/Domain: laminin-type EGF-like homology <LE08>  
F;930-986/Domain: laminin-type EGF-like homology <LE09>  
F;989-1038/Domain: laminin-type EGF-like homology <LE10>  
F;1041-1095/Domain: laminin-type EGF-like homology <LE11>  
F;1098-1143/Domain: laminin-type EGF-like homology <LE12>

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:12:11 ; Search time 80.15 Seconds  
(without alignments)  
130.205 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_26\_162

Perfect score: 841

Sequence: 1 QPRTGPGCGRLLGTGT.....FPGKTHNAVCPGSPPAEP 137

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_68.\*

1: p1r1.\*

2: p1r2.\*

3: p1r3.\*

4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	19.3	272	2 148700	gene ox40 protein
2	160.5	19.1	255	2 138436	lymphocyte activat
3	158.5	18.8	277	2 137552	OX40 homolog - hum
4	153	18.2	256	2 832393	T-cell antigen 4-1
5	151	18.0	271	2 512783	OX40 antigen precu
6	138.5	16.5	295	2 JC5559	lectin-B - Virgini
7	127.5	15.2	305	2 A46476	B cell-associated
8	125	14.9	1801	1 MWRTS	laminin beta-2 cha
9	120.5	14.3	459	2 148854	gene murine tumour
10	119	14.1	461	1 A35356	tumor necrosis fac
11	119	14.1	474	2 B38634	tumor necrosis fac
12	118.5	14.1	277	2 A60771	B-cell activation
13	117	13.9	435	2 154182	tumor necrosis fac
14	115	13.7	1798	2 S53859	laminin beta-2 cha
15	112	13.3	152	2 T18975	hypothetical prote
16	111	13.2	1371	2 A33837	insulin-like growt
17	110	13.1	329	2 A48805	insulin-like growt
18	109	13.0	1574	2 T13954	MEGF6 protein - ra
19	109	13.0	3635	2 T10053	laminin alpha 5 ch
20	108	12.8	2907	2 A57278	fibrillin-2 precu
21	107	12.7	164	2 T24272	hypothetical prote
22	106	12.6	1797	2 A55677	laminin beta-2 cha
23	104	12.4	2918	2 A54105	fibrillin-2 precu
24	102.5	12.2	188	2 T15651	hypothetical prote
25	102.5	12.2	956	1 A46016	thrombospondin 3 -
26	101	12.0	1367	1 IGHURI	insulin-like growt
27	100	11.9	540	2 B47417	insulin receptor-r
28	100	11.9	1106	2 T13938	gene shuttle craft
29	99	11.8	1820	2 A55494	latent transformin

30	98	11.7	1111	2 T26972	hypothetical prote
31	97.5	11.6	1713	2 A55347	adhesive ligand ep
32	97	11.5	1106	2 T44598	hypothetical prote
33	97	11.5	1251	2 A57293	latent transformin
34	96.5	11.5	3623	2 T08618	intrinsic factor-B
35	96	11.4	416	1 JN0006	nerve growth facto
36	96	11.4	1364	2 T00250	MEGF2 protein - hu
37	95.5	11.4	1172	1 TSHUP2	thrombospondin 2 p
38	95.5	11.4	1786	1 MMHUB1	laminin beta-1 cha
39	95	11.3	1268	2 B36502	insulin receptor-r
40	95	11.3	2825	2 T14271	doc4 protein, stre
41	94.5	11.2	956	2 A57121	thrombospondin 3 p
42	94.5	11.2	1408	2 S16148	gene serrate prote
43	94	11.2	1203	2 A49175	Motch B protein -
44	94	11.2	1737	2 T00209	MEGF8 protein - hu
45	94	11.2	2871	2 A55567	fibrillin I - bovi

## ALIGNMENTS

RESULT 1

I48700  
gene ox40 protein - mouse  
N:Alternate names: OX40 antigen  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 11-Jan-2000  
C:Accession: I48700; I48334; S34377  
R:Calderhead, D.W.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J  
J. Immunol. 151, 5261-5271, 1993  
A:Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell  
A:Reference number: I48700; MUID:94044750  
A:Accession: I48700  
A>Status: translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-272 <RES>  
A:Cross-references: EMBL:221674; NID:g312827; PIDN:CAA79772.1; PID:g312828  
R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.  
Eur. J. Immunol. 25, 926-930, 1995  
A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX  
A:Reference number: I48334; MUID:95255413  
A:Accession: I48334  
A>Status: translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-14, 'G', 16-272 <RE2>  
A:Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819  
C:Genetics:  
A:Gene: ox40  
A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1  
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match	19.3%;	Score 162;	DB 2;	Length 272;
Best Local Similarity	28.3%;	Pred. No. 3.5e-06;		
Matches	45;	Conservative 11;	Mismatches 51;	Indels 52; Gaps 7;
QY	14	LLLTGTGDAR--CCRVHT-----TRCCRD-YPG-----ECCSEWDCMCVQPEFHCGDPC--	60	

\* RESULT 2

I38426  
lymphocyte activation-induced receptor ILA precursor - human  
C:Species: Homo sapiens (man)

C>Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 01-Dec-2000  
C:Accession: I38426; JT0752  
R:Allderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; R  
Eur. J. Immunol. 24, 2219-2227, 1994  
A>Title: Molecular and biological characterization of human 4-1BB and its ligand.  
A:Reference number: I38426; MUID:94374434  
A:Accession: I38426  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-255 <RES>  
A:Cross-references: EMBL:U03397; NID:g571320; PIDN:AAA53133.1; PID:g571321  
R:Schwarz, H.; Tuckwell, J.; Lotz, M.  
Gene 134, 295-298, 1993  
A>Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne  
A:Reference number: JT0752; MUID:94085794  
A:Accession: JT0752  
A:Molecule type: mRNA  
A:Residues: 1-106, R', 108-255 <SCH>  
C:Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necro  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT>  
F:187-213/Domain: transmembrane #status predicted <TM>  
F:138,149/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:234,235/Binding site: phosphate (Thr) (covalent) (by casein kinase II)  
F:242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 19.1%; Score 160.5; DB 2; Length 255;  
Best Local Similarity 30.9%; Pred. No. 4.4e-06;  
Matches 47; Conservative 12; Mismatches 52; Indels 41; Gaps 9;

QY 9 CGPGRLLGTTDARCCRVHTTRCCRDYPC-----EBCCS-----EWDGCMCVQPEFHGDP 59  
Db 48 CPNPSFSSAGG--QRTCDI-----CROCKGVFTRKCSSTSAECCD---TPGFHCLGA 97

QY 60 CTVTCHRHPPGQGVQSGQKFSFGFCIDCASGTFSGHGHGCKPWTDCDTQFGFLTVFP 119  
Db 98 GCSMC-EQDCKQGEELTKG-----CKDCGFTFNDQKRGICRPWTNCSLDGKSLVN 149

QY 120 GNKTHNAVCPG-----SPPA---EP 137  
Db 150 GTRERDVVCGSPADLSPGASVTPPAPAREP 181

RESULT 3  
I37552  
OX40 homolog - human  
C:Species: Homo sapiens (man)  
C>Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000  
C:Accession: I37552  
R:Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fona  
Eur. J. Immunol. 24, 677-683, 1994  
A>Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment  
A:Reference number: I37552; MUID:94170844  
A:Accession: I37552  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-277 <RES>  
A:Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958  
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 18.8%; Score 158.5; DB 2; Length 277;  
Best Local Similarity 31.6%; Pred. No. 6.7e-06;  
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QY 9 CGPGRLLGTTDARCCRVHTTRCCRDYPC--ECCSEWDCM-CVQPEFHGCD---PCCT 62  
Db 46 CRP-----GNGMVSRCSRSONTCVRCGPGGFYNDVVSSKPKCTWCNLSRSGSERKOLCT 100

C>Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 01-Dec-2000  
C:Accession: I38426; JT0752  
R:Allderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; R  
Eur. J. Immunol. 24, 2219-2227, 1994  
A>Title: Molecular and biological characterization of human 4-1BB and its ligand.  
A:Reference number: I38426; MUID:94374434  
A:Accession: I38426  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-255 <RES>  
A:Cross-references: EMBL:U03397; NID:g571320; PIDN:AAA53133.1; PID:g571321  
R:Schwarz, H.; Tuckwell, J.; Lotz, M.  
Gene 134, 295-298, 1993  
A>Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne  
A:Reference number: JT0752; MUID:94085794  
A:Accession: JT0752  
A:Molecule type: mRNA  
A:Residues: 1-106, R', 108-255 <SCH>  
C:Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necro  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT>  
F:187-213/Domain: transmembrane #status predicted <TM>  
F:138,149/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:234,235/Binding site: phosphate (Thr) (covalent) (by casein kinase II)  
F:242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

QY 63 TCRHHPCPPGQGVQSGQKFSFGFCIDCASGTFSGHGHGCKPWTDCDTQFGFLTVFP 122  
Db 101 ATQDTVCRACRATQPLDSYKPGVDCAPCPGPHFSPGDNQACKPWTNCTLAGKHTLQPASN 160

QY 123 THNAVCPGSPPA 135  
Db 161 SSDAICEDRDPPA 173

RESULT 4  
B32393  
T-cell antigen 4-1BB precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 21-Jul-2000  
C:Accession: B32393; I48879  
R:Kwon, B.S.; Weissman, S.M.  
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989  
A>Title: cDNA sequence of two inducible T-cell genes.  
A:Reference number: A32393; MUID:89184547  
A:Accession: B32393  
A:Molecule type: mRNA  
A:Residues: 1-256 <KWO>  
A:Cross-references: GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122  
R:Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.F.  
J. Immunol. 152, 2256-2262, 1994  
A>Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1B  
A:Reference number: I48879; MUID:94179805  
A:Accession: I48879  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-256 <RES>  
A:Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178  
C:Genetics:  
A:Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: transmembrane protein  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-256/Product: 4-1BB protein #status predicted <MAT>

Query Match 18.2%; Score 153; DB 2; Length 256;  
Best Local Similarity 31.5%; Pred. No. 1.7e-05;  
Matches 40; Conservative 17; Mismatches 52; Indels 18; Gaps 7;

QY 9 CGPGRLLGTTDARCCRVHTTRCCRDYPCGEECCSEW---DCMCVQPEFHGDCPCCTTC 64  
Db 47 CPPTFSSIGGQPNICRV---CAGYFRFKKCSSTHNAECCIE-GFHCGLGQCCTRC 101

QY 65 RHHPCCPPGQGVQSGQKFSFGFCIDCASGTFSGHGHGCKPWTDCDTQFGFLTVFP 123  
Db 102 -EKDCRPQELTKQG-----CKTCSLGTFDQNGTGVCRPWTNCSLDGSRVLKGTTE 153

QY 124 HNAYCVP 130  
Db 154 KDVVCGP 160

RESULT 5  
S12783  
OX40 antigen precursor - rat  
N:Alternate names: nerve growth factor receptor homolog  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 05-Nov-1999  
C:Accession: S12783; S08036  
R:Mallett, S.; Fossum, S.; Barclay, A.N.  
EMBO J. 9, 1063-1068, 1990  
A>Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphoc  
A:Reference number: S12783; MUID:90214614  
A:Accession: S12783  
A:Molecule type: mRNA  
A:Residues: 1-271 <MAL>  
A:Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831  
C:Superfamily: CD27 antigen; NGF receptor repeat homology

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FT DOMAIN 1832 1887 LAMININ EGF-LIKE 18.
FT DOMAIN 1888 1941 LAMININ EGF-LIKE 19.
FT DOMAIN 1942 1988 LAMININ EGF-LIKE 20.
FT DOMAIN 1989 2035 LAMININ EGF-LIKE 21.
FT DOMAIN 2036 2085 LAMININ EGF-LIKE 22.
FT DOMAIN 2086 2678 LAMININ EGF-LIKE 4.
FT DOMAIN 2679 3635 5 X LAMININ G-LIKE REPEATS (DOMAIN G).
FT DOMAIN 3636 3679 LAMININ G-LIKE 1.
FT DOMAIN 3680 3850 LAMININ G-LIKE 2.
FT DOMAIN 3851 4021 LAMININ G-LIKE 3.
FT DOMAIN 4022 4292 LAMININ G-LIKE 4.
FT DOMAIN 4293 4563 LAMININ G-LIKE 5.
FT DOMAIN 4564 4834 COILED COIL (POTENTIAL).
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Best Local Similarity 27.8%; Pred. No. 0.032;
Matches 44; Conservative 9; Mismatches 51; Indels 54; Gaps 10;
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Db 1994 AAKGSECHPQSGOCHCQPG-----TTGPQCLCAPGYWGLPEKGCRRRCQPRGHCD 2044
QY 105 PWTDTCTQFGFLVFPG-----NKTNAVCPVGPSP 133
Db 2045 PHT-----GHCTCPPLSGERCDCSCQHQ--VPVPCKP 2076
Search completed: September 4, 2001, 16:15:22
Job time: 1134 sec
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CC DR EMBL; L04270; AAA36757.1; -.
CC DR HSSP; P25942; 1CDF.
CC DR MIN; 600979; -.
CC DR InterPro; IPR001368; -.
CC DR Pfam; PF00020; TNFR_C6; 4.
CC DR PROSITE; PS00652; TNFR_NGFR_1; 2.
CC DR PROSITE; PS00500; TNFR_NGFR_2; 3.
CC KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
CC FT SIGNAL 1 30
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CC FT DISULFID 139 148
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CC FT DISULFID 170 185
CC FT CARBOHYD 40 40
CC FT CARBOHYD 177 177
CC SQ SEQUENCE 435 AA; 46709 MW; 624626E6022F656F CRC64;

Query Match 13.9%; Score 117; DB 1; Length 435;
Best Local Similarity 25.6%; Pred. No. 0.0013;
Matches 42; Conservative 12; Mismatches 66; Indels 44; Gaps 10;

Qy 9 CGPGLLLGTGTDARCRVHTRC-----CRDYPGEE-----C 41
Db 62 CPP-----GTVSAKCSIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVNGLEEIAPC 116
Qy 42 CS--EWDGCMQVQPEPHCGDPC--CTTCR-HHPCPPGQVGOSGKFSFG-FQCIDCASGTF 95
Db 117 TSKRKTQRC-OPGMFCAANALECTHCELLSDCPPTGAELKDEVGKGNHNCVPCRAGHF 175
Qy 96 --SGGHEGCRPWTCTDQFGFLTVPPGNKTHNAVCPGSPPAEP 137
Db 176 QNTSSPSARCQPHTRCENQGLVEAPAGTAQSDTTC--KNPLEP 216

RESULT 14
IGIR_RAT
ID IGIR_RAT STANDARD; PRV; 1370 AA.
AC P24062;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR (EC 2.7.1.112).
GN IGfR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

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RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=95277910; PubMed=7758167;
RA Du J., Delafontaine P.;
RT "Inhibition of vascular smooth muscle cell growth through antisense
transcription of a rat insulin-like growth factor I receptor cDNA.";
RL Circ. Res. 76:963-972(1995).
RN [2]
RP SEQUENCE OF 1-364 FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=90017496; PubMed=2477843;
RA Werner H., Woloschak M., Adamo M., Shen-Orr Z., Roberts C.T. Jr.,
RA Leroith D.;
RT "Developmental regulation of the rat insulin-like growth factor I
receptor gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:7451-7455(1989).
RN [3]
RP SEQUENCE OF 913-1017 FROM N.A.
RX MEDLINE=92412145; PubMed=1530648;
RA Kurachi H., Jobo K., Ohta M., Kawasaki T., Itoh N.;
RT "A new member of the insulin receptor family, insulin
receptor-related receptor, is expressed preferentially in the
kidney.";
RL Biochem. Biophys. Res. Commun. 187:934-939(1992).
CC CC -!- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)
WITH A HIGH AFFINITY AND IGF II WITH A LOWER AFFINITY. IT HAS A
CC CC TYROSINE-PROTEIN KINASE ACTIVITY.
CC CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
CC CC -!- SUBUNIT: Tetramer of 2 alpha and 2 beta chains linked by disulfide
bonds. The alpha chains contribute to the formation of the ligand-
binding domain, while the beta chain carries the kinase domain.
CC CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC CC -!- SIMILARITY: Belongs to the insulin receptor family of tyrosine-
protein kinases.
CC CC -!- SIMILARITY: Contains 2 fibronectin type III-like domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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CC EMBL; L29232; AAA11392.1; -.
CC DR EMBL; M27293; AAA41384.1; -.
CC DR PIR; A33837; A33837.
CC DR HSSP; P06213; 1IRK.
CC DR InterPro; IPR000494; -.
CC DR InterPro; IPR000719; -.
CC DR InterPro; IPR001245; -.
CC DR InterPro; IPR001777; -.
CC DR InterPro; IPR002011; -.
CC DR InterPro; IPR002174; -.
CC DR Pfam; PF00757; Furin-like; 1.
CC DR Pfam; PF01030; Recep_L_domain; 2.
CC DR Pfam; PF00041; pkinase; 2.
CC DR Pfam; PF00069; pkinase; 1.
CC DR PRINTS; PR00109; TYRKINASE.
CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
CC DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
CC DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
CC DR Transferrase; Tyrosine-protein kinase; Receptor; Transmembrane;
KW Glycoprotein; ATP-binding; Phosphorylation; Repeat; Signal.
CC SIGNAL 1 30
CC FT CHAIN 31 741
CC FT CHAIN 742 1370
CC FT DOMAIN 742 936
CC FT TRANSMEM 937 960

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FT DOMAIN 961 1370 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 608 829 FIBRONECTIN TYPE-III.
FT DOMAIN 830 929 FIBRONECTIN TYPE-III.
FT DOMAIN 1000 1275 PROTEIN KINASE.
FT NP_BIND 1006 1014 ATP (BY SIMILARITY).
FT BINDING 1034 1034 ATP (BY SIMILARITY).
FT ACT_SITE 1136 1136 BY SIMILARITY.
FT MOD_RES 1166 1166 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 51 51 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 245 245 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 314 314 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 418 418 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 439 439 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 535 535 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 641 641 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 748 748 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 757 757 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 765 765 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 901 901 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 914 914 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 985 986 AD -> PY (IN REF. 3).
SQ SEQUENCE 1370 AA; 155395 MW; A5946897A41CB145 CRC64;

Query Match 13.2%; Score 111; DB 1; Length 1370;
Best Local Similarity 27.2%; Pred. No. 0.01;
Matches 46; Conservative 17; Mismatches 44; Indels 62; Gaps 16;

QY 9 CG----PGLR-----LLGTGTDARCCRVHTTRC---CRDYPGECSCSEWDCMCVQPE 53
|| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 178 CGDLCPGCTLEKPMCKETTTINNEYRCWT--TNRCKMCPSCVGRACTE--NNECCHPE 234

QY 54 FHCGDPC-----CTTCRRH-----PCPPGQGVQSGKFSEF--GFQCID---CAS- 92
|| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 235 --CLGSCHTPDNTTCVACRHHYKYGVCVPACPP-----GTYRFGRCVDRDFCANI 285

QY 93 ----GTFSGG---HEGCKPWTCTQFGFLTVPFGNKNTHNACVPGSP 134
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 286 PNAESSDSGFIHGDGEC--MQECPGSGFIR-----NSTQSMYCIPEGP 327

RESULT 15
LMA5_MOUSE STANDARD; PRT; 3635 AA.
AC Q61001;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE LAMININ ALPHA-5 CHAIN (FRAGMENT).
GN LMA5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Lung;
RX MEDLINE=96081906; PubMed=7499364;
RA Miner J.H., Lewis R.M., Sanes J.R.;
RT "Molecular cloning of a novel laminin chain, alpha 5, and widespread
expression in adult mouse tissues";
RL J. Biol. Chem. 270:28523-28526(1995).
RN [2]
RP REVISIONS.
RA Miner J.H., Lewis R.M., Sanes J.R.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR. LAMININ
IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATING OF
CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING

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CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
CC -!- FUNCTION: ALPHA-5 CHAIN MAY BE THE MAJOR LAMININ ALPHA CHAIN OF
CC ADULT EPITHELIAL AND/OR ENDOTHELIAL BASAL LAMINAE.
CC -!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
CC MEMBRANES (MAJOR COMPONENT).
CC -!- TISSUE SPECIFICITY: IN ADULT, HIGH LEVELS IN HEART, LUNG, AND
CC KIDNEY; LOWER IN BRAIN, MUSCLE AND TESTIS; VERY LOW IN LIVER, GUT
CC AND SKIN. EXPRESSED IN MANY TISSUES IN EMBRYONIC DAY 11.
CC -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -!- SIMILARITY: CONTAINS 21-5 LAMININ EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
CC -!- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
CC -!- SIMILARITY: ALPHA-5 CHAIN IS MORE RELATED TO DROSOPHILA ALPHA
CC CHAIN THAN TO MAMMALIAN ALPHA CHAINS 1-4.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U37501; AAC53430.1; -.
CC HSSP; P02468; ITLE.
CC DR MGD; MGI:105382; Lama5.
CC DR InterPro; IPR000034; -.
CC DR InterPro; IPR000561; -.
CC DR InterPro; IPR001791; -.
CC DR InterPro; IPR001886; -.
CC DR InterPro; IPR002049; -.
CC DR Pfam; PF00052; laminin_B; 1.
CC DR Pfam; PF00053; laminin_EG; 19.
CC DR Pfam; PF00054; laminin_G; 2.
CC DR Pfam; PF00055; laminin_Nterm; 1.
CC DR PROSITE; PS00022; EGF_1; 19.
CC DR PROSITE; PS01186; EGF_2; 3.
CC DR PROSITE; PS01248; LAMININ_TYPE_EGF; 19.
CC DR Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
CC KW Laminin EGF-like domain; Cell adhesion; Repeat.
CC FT NON_TER 1 1
CC FT DOMAIN <1 221 LAMININ N-TERMINAL (DOMAIN VI).
CC FT DOMAIN 222 772 10.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
CC V).
CC FT DOMAIN 280 280 LAMININ EGF-LIKE 1.
CC FT DOMAIN 281 350 LAMININ EGF-LIKE 2.
CC FT DOMAIN 351 396 LAMININ EGF-LIKE 3.
CC FT DOMAIN 417 463 LAMININ EGF-LIKE 4.
CC FT DOMAIN 464 509 LAMININ EGF-LIKE 5.
CC FT DOMAIN 510 554 LAMININ EGF-LIKE 6.
CC FT DOMAIN 555 599 LAMININ EGF-LIKE 7.
CC FT DOMAIN 600 645 LAMININ EGF-LIKE 8.
CC FT DOMAIN 646 698 LAMININ EGF-LIKE 9.
CC FT DOMAIN 699 750 LAMININ EGF-LIKE 10.
CC FT DOMAIN 751 772 LAMININ EGF-LIKE 11 (INCOMPLETE).
CC FT DOMAIN 773 1359 LAMININ DOMAIN IV 1 (DOMAIN IV B).
CC FT DOMAIN 1360 1559 4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
CC III B).
CC FT DOMAIN 1360 1405 LAMININ EGF-LIKE 12.
CC FT DOMAIN 1406 1449 LAMININ EGF-LIKE 13.
CC FT DOMAIN 1450 1498 LAMININ EGF-LIKE 14.
CC FT DOMAIN 1499 1549 LAMININ EGF-LIKE 15.
CC FT DOMAIN 1550 1559 LAMININ EGF-LIKE 16 (N-TERMINAL).
CC FT DOMAIN 1560 1748 LAMININ DOMAIN IV 2 (DOMAIN IV A).
CC FT DOMAIN 1749 2085 6.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
CC III A).
CC FT

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FT DISULFID 853 862 BY SIMILARITY.
FT DISULFID 865 875 BY SIMILARITY.
FT DISULFID 878 887 BY SIMILARITY.
FT DISULFID 880 894 BY SIMILARITY.
FT DISULFID 897 906 BY SIMILARITY.
FT DISULFID 909 925 BY SIMILARITY.
FT DISULFID 928 944 BY SIMILARITY.
FT DISULFID 930 955 BY SIMILARITY.
FT DISULFID 957 966 BY SIMILARITY.
FT DISULFID 969 984 BY SIMILARITY.
FT DISULFID 987 1001 BY SIMILARITY.
FT DISULFID 989 1008 BY SIMILARITY.
FT DISULFID 1011 1020 BY SIMILARITY.
FT DISULFID 1023 1036 BY SIMILARITY.
FT DISULFID 1036 1108 BY SIMILARITY.
FT DISULFID 1098 1115 BY SIMILARITY.
FT DISULFID 1117 1126 BY SIMILARITY.
FT DISULFID 1129 1141 BY SIMILARITY.
FT DISULFID 1144 1156 BY SIMILARITY.
FT DISULFID 1165 1174 BY SIMILARITY.
FT DISULFID 1177 1188 BY SIMILARITY.
FT DISULFID 1191 1191 INTERCHAIN (PROBABLE).
FT DISULFID 1194 1194 INTERCHAIN (PROBABLE).
FT DISULFID 1798 1798 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1086 1086 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1250 1250 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1309 1309 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1349 1349 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1500 1500 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1799 AA; 196352 MW; 1F28967A67AEDE33 CRC64;

Query Match 14.3%; Score 120; DB 1; Length 1799;
Best Local Similarity 25.9%; Pred. No. 0.0021;
Matches 52; Conservative 6; Mismatches 49; Indels 94; Gaps 12;

Qy 5 GPGGCGP---GRLLTGTDARCCRVTTTC--CRDYPGECCESEWDCMCVQPFHCGD 58
Db 871 GPNCRPCVNGR-----ADECDTHTGACLGCRDRTYGGHCHER-----CI-AGFH-GD 916

Qy 59 PCCT---TCRHPCPPGQGVQSQGRFS-----FGFQCIDCASGTF 95
Db 917 PRLPYGGQCRPCPEGPG--SQRFATFSCHRDGYSQIVCHCRAGYGLRCEACAPGPF 974

Qy 96 -----SGGHEGCKPWTDCQTQGF 114
Db 975 GDSKPGRCQCECSGNIDPMDPCDPHTGQCLRLHNTGPHGVCYK-----GF 1027

Qy 115 LTVPGNKTHNAV-CVPGSPP 134
Db 1028 HQAARQSCHRCTCNLLGTD 1048

RESULT 11
TNR2_MOUSE
ID TNR2_MOUSE STANDARD; PRT; 474 AA.
AC P25119; P97893;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (p75).
GN TNFRSF1B OR TNFR2 OR TNFR-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9118785; PubMed=1849278;
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,

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RA Wong G.H., Chen E.Y., Goeddel D.V.;
RT "Cloning and expression of cDNAs for two distinct murine tumor
RT necrosis factor receptors demonstrate one receptor is species
RT specific.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91246168; PubMed=1645445;
RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA Copeland N.G., Jenkins N.A., Smith C.A.;
RT "Molecular cloning and expression of the type 1 and type 2 murine
RT receptors for tumor necrosis factor.";
RL Mol. Cell. Biol. 11:3020-3026(1991).
RN [3]
RP SEQUENCE OF 1-26 FROM N.A.
RC STRAIN=NOD;
RA Jacob C.O., Liu J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-22 FROM N.A.
RC TISSUE=Liver;
RA Kissoneghis M., Fellowes R., Feldmann M., Chernajovsky Y.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M50469; AAA39752.1; -
DR EMBL; M59378; AAA40463.1; -
DR EMBL; U39488; AAA85021.1; -
DR EMBL; X87128; CAA60618.1; -
DR PIR; B38634; B38634.
DR HSP; P19438; INCF.
DR MGD; MGI:1314883; Tnfrsf1b.
DR InterPro; IPR001368; -
DR Pfam; PF00020; TNFR_c6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 22
FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 259 288 POTENTIAL.
FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 39 203 4 X TNFR-CYS.
FT REPEAT 39 77 TNFR-CYS 1.
FT REPEAT 78 119 TNFR-CYS 2.
FT REPEAT 120 164 TNFR-CYS 3.
FT REPEAT 165 203 TNFR-CYS 4.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 55 68 BY SIMILARITY.
FT DISULFID 58 76 BY SIMILARITY.
FT DISULFID 79 94 BY SIMILARITY.
FT DISULFID 97 111 BY SIMILARITY.
FT DISULFID 101 119 BY SIMILARITY.
FT DISULFID 121 127 BY SIMILARITY.
FT DISULFID 136 145 BY SIMILARITY.
FT DISULFID 139 163 BY SIMILARITY.
FT DISULFID 166 181 BY SIMILARITY.
FT CARBOHYD 69 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Query Match 14.1%; Score 119; DB 1; Length 474;

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Best Local Similarity 31.08; Pred. No. 0.00093;
Matches 36; Conservative 8; Mismatches 54; Indels 18; Gaps 5;

QY 21 DARCRRVHTTRCCRDYGECECCSEWDCMCVQPEHFGDPCCTTC-RHHPCPPGGGVQSOG 79
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 107 EIRACTQQRNVKACAGRYCAL-----KTHSSS--CRQCMRLSKCGFGGVASSR 155
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 80 KFSFGFCIDCAGSTFGS--GHEGHCKPWTDTQFGFLTVPFGKNTNAVCVPGSP 133
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 156 APNGNVLCKACAPGCTFSDTTSVDVCRPHRTCS----ILAIPGNASTDAVCAPESP 207
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
CD40_HUMAN CD40_HUMAN STANDARD; PRT; 277 AA.
ID ID
AC P25942;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)
DE (TUMOR NECROSIS FACTOR RECEPTOR 5).
DE TNFRSF5 OR CD40.
DE GN
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RX MEDLINE=89356608; PubMed=2475341;
RA Stamenkovic I., Clark E.A., Seed B.;
RT "A B-lymphocyte activation molecule related to the nerve growth
RT factor receptor and induced by cytokines in carcinomas.",
RL EMBO J. 8:1403-1410(1989).
RN [2]
RX 3D-STRUCTURE MODELING OF 24-144.
RA Bajorath J., Aruffo A.;
RT "Construction and analysis of a detailed three-dimensional model of
RT the ligand binding domain of the human B cell receptor CD40.";
RL Proteins 27:59-70(1997).
RN [3]
RX 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
RA MEDLINE=98266353; PubMed=9605317;
RX Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
RX Zheng Z., Naismith J.H., Thomas D.;
RT "The role of polar interactions in the molecular recognition of CD40L
RT with its receptor CD40.";
RL Protein Sci. 7:1124-1135(1998).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME=PROW; NOTE=cd guide CD40 entry;
CC WWW: http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm.
CC -----
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CC -----
DR EMBL; X60592; CAA43045.1; -.
DR PIR; S044601; S04460.
DR PDB; 1CDF; 01-APR-97.
DR MIM; 109535; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
DR Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
DR 3D-structure.
KW

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DR Pfam: PF00020; TNFR\_C6: 4.  
 DR PROSITE: PS00652; TNFR\_NGRF\_1; 1.  
 DR PROSITE: PS0050; TNFR\_NGRF\_2; 4.  
 KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 289 CD40L RECEPTOR.  
 FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 194 215 POTENTIAL.  
 FT DOMAIN 216 289 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 187 4 X TNFR-CYS.  
 FT REPEAT 25 60 TNFR-CYS 1.  
 FT REPEAT 61 103 TNFR-CYS 2.  
 FT REPEAT 104 144 TNFR-CYS 3.  
 FT REPEAT 145 187 TNFR-CYS 4.  
 FT CARBOHYD 153 153 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 289 AA; 3211 MW; C791CB6D2FEA574E CRC64;

Query Match 15.2%; Score 127.5; DB 1; Length 289;  
 Best Local Similarity 28.9%; Pred. No. 0.00011;  
 Matches 37; Conservative 8; Mismatches 72; Indels 11; Gaps 5;

Qy 9 CGPGRLLGTGDARCRVHTTRCCRDYGP-----EECCSEWDCMCVQPE-RHCGDPCCYTT 63  
 Db 62 CDSGEFSQWNRIRC---HQRHCEPQGLRVKRGTAESDTCTCKEGQCHTCKDCEA 118  
 Qy 64 C-RHHPCCPGGVQSGQSFSGFQICDASGTFSGGHE--GHCKPWTDCQFGFLTVFPG 120  
 Db 119 CAQHTPCIPGFGVEMATETDTTCHPCVPVGFSSQSSIFKCYPTWSCDKNLEVLQKG 178  
 Qy 121 NKTHNAV 128  
 Db 179 TSQTNVIC 186

RESULT 7  
 LMB2\_RAT ID LMB2\_RAT STANDARD; PRT; 1801 AA.  
 AC P15800;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-JUL-1999 (Rel. 39, Last annotation update)  
 DE LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3).  
 GN LAMB2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=89159410; PubMed=2922051;  
 RA Hunter D.D., Shah V., Merlie J.P., Sanes J.R.;  
 RT "A laminin-like adhesive protein concentrated in the synaptic cleft  
 of the neuromuscular junction.";  
 RL Nature 338:229-234(1989).  
 CC -1- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ  
 IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF  
 CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING  
 WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.  
 CC -1- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE  
 DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND  
 TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE  
 COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.  
 CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4  
 (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).  
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR  
 COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC  
 CLEFT OF THE NEUROMUSCULAR JUNCTION.  
 CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT  
 WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.  
 CC -1- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.

CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).  
 CC -1- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL: X16563; CAA34561.1; -.  
 DR PIR: S03539; MWRYS.  
 DR HSSP: P02468; IKLO.  
 DR InterPro: IPR000561; -.  
 DR InterPro: IPR001896; -.  
 DR InterPro: IPR002049; -.  
 DR Pfam: PF00053; laminin\_EGF; 13.  
 DR Pfam: PF00055; laminin\_Nterm; 1.  
 DR PRINTS: PR00011; EGFLAMININ.  
 DR PROSITE: PS00022; EGF\_1; 10.  
 DR PROSITE: PS01186; EGF\_2; 2.  
 DR PROSITE: PS01248; LAMININ\_TYPE\_EGF; 12.  
 KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
 KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
 FT SIGNAL 1 35  
 FT CHAIN 36 1801  
 FT DOMAIN 36 283  
 FT DOMAIN 286 555  
 FT DOMAIN 286 349  
 FT DOMAIN 350 412  
 FT DOMAIN 413 472  
 FT DOMAIN 473 524  
 FT DOMAIN 525 555  
 FT DOMAIN 556 785  
 FT DOMAIN 786 1192  
 FT DOMAIN 786 833  
 FT DOMAIN 834 879  
 FT DOMAIN 880 929  
 FT DOMAIN 930 988  
 FT DOMAIN 989 1040  
 FT DOMAIN 1041 1097  
 FT DOMAIN 1098 1145  
 FT DOMAIN 1146 1192  
 FT DOMAIN 1193 1412  
 FT DOMAIN 1413 1445  
 FT DOMAIN 1446 1801  
 FT DOMAIN 1259 1306  
 FT DOMAIN 1475 1529  
 FT DOMAIN 1576 1793  
 FT DISULFID 286 295  
 FT DISULFID 288 313  
 FT DISULFID 315 324  
 FT DISULFID 327 347  
 FT DISULFID 350 359  
 FT DISULFID 352 377  
 FT DISULFID 380 389  
 FT DISULFID 392 410  
 FT DISULFID 413 426  
 FT DISULFID 415 441  
 FT DISULFID 443 452  
 FT DISULFID 455 470  
 FT DISULFID 473 487  
 FT DISULFID 495 494  
 FT DISULFID 496 505  
 FT DISULFID 508 522  
 FT DISULFID 786 798  
 FT DISULFID 788 805  
 FT DISULFID 807 816  
 FT DISULFID 819 831

-----  
 -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).  
 -1- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.  
 -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 EMBL: X16563; CAA34561.1; -.  
 PIR: S03539; MWRYS.  
 HSSP: P02468; IKLO.  
 InterPro: IPR000561; -.  
 InterPro: IPR001896; -.  
 InterPro: IPR002049; -.  
 Pfam: PF00053; laminin\_EGF; 13.  
 Pfam: PF00055; laminin\_Nterm; 1.  
 PRINTS: PR00011; EGFLAMININ.  
 PROSITE: PS00022; EGF\_1; 10.  
 PROSITE: PS01186; EGF\_2; 2.  
 PROSITE: PS01248; LAMININ\_TYPE\_EGF; 12.  
 Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
 Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
 SIGNAL 1 35  
 CHAIN 36 1801  
 DOMAIN 36 283  
 DOMAIN 286 555  
 DOMAIN 286 349  
 DOMAIN 350 412  
 DOMAIN 413 472  
 DOMAIN 473 524  
 DOMAIN 525 555  
 DOMAIN 556 785  
 DOMAIN 786 1192  
 DOMAIN 786 833  
 DOMAIN 834 879  
 DOMAIN 880 929  
 DOMAIN 930 988  
 DOMAIN 989 1040  
 DOMAIN 1041 1097  
 DOMAIN 1098 1145  
 DOMAIN 1146 1192  
 DOMAIN 1193 1412  
 DOMAIN 1413 1445  
 DOMAIN 1446 1801  
 DOMAIN 1259 1306  
 DOMAIN 1475 1529  
 DOMAIN 1576 1793  
 DISULFID 286 295  
 DISULFID 288 313  
 DISULFID 315 324  
 DISULFID 327 347  
 DISULFID 350 359  
 DISULFID 352 377  
 DISULFID 380 389  
 DISULFID 392 410  
 DISULFID 413 426  
 DISULFID 415 441  
 DISULFID 443 452  
 DISULFID 455 470  
 DISULFID 473 487  
 DISULFID 495 494  
 DISULFID 496 505  
 DISULFID 508 522  
 DISULFID 786 798  
 DISULFID 788 805  
 DISULFID 807 816  
 DISULFID 819 831

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FT DISULFID 834 846 BY SIMILARITY.
FT DISULFID 853 BY SIMILARITY.
FT DISULFID 855 864 BY SIMILARITY.
FT DISULFID 867 877 BY SIMILARITY.
FT DISULFID 880 889 BY SIMILARITY.
FT DISULFID 882 896 BY SIMILARITY.
FT DISULFID 899 908 BY SIMILARITY.
FT DISULFID 911 927 BY SIMILARITY.
FT DISULFID 930 946 BY SIMILARITY.
FT DISULFID 932 957 BY SIMILARITY.
FT DISULFID 959 968 BY SIMILARITY.
FT DISULFID 971 986 BY SIMILARITY.
FT DISULFID 989 1003 BY SIMILARITY.
FT DISULFID 991 1010 BY SIMILARITY.
FT DISULFID 1013 1022 BY SIMILARITY.
FT DISULFID 1025 1038 BY SIMILARITY.
FT DISULFID 1098 1110 BY SIMILARITY.
FT DISULFID 1100 1117 BY SIMILARITY.
FT DISULFID 1119 1128 BY SIMILARITY.
FT DISULFID 1131 1143 BY SIMILARITY.
FT DISULFID 1146 1158 BY SIMILARITY.
FT DISULFID 1148 1165 BY SIMILARITY.
FT DISULFID 1167 1176 BY SIMILARITY.
FT DISULFID 1179 1190 BY SIMILARITY.
FT DISULFID 1193 1193 INTERCHAIN (PROBABLE).
FT DISULFID 1196 1196 INTERCHAIN (PROBABLE).
FT DISULFID 1800 1800 INTERCHAIN (PROBABLE).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1088 1088 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1252 1252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1311 1311 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1351 1351 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1502 1502 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1801 AA; 196473 MW; 97AEF32F8F31FA75 CRC64;

Query Match 14.9%; Score 125; DB 1; Length 1801;
Best Local Similarity 26.4%; Pred. No. 0.00075;
Matches 53; Conservative 5; Mismatches 49; Indels 94; Gaps 12;

QY 5 GPGCGCP-----GRLLGTGTDCRCRVHTRC---CRDYPGECCSEWDCMCVQPEFHCGD 58
Db 873 GFPCNRCPCVNGR-----ADECDATGACLGCRDYGTEGHCER-----CI-AGEFH-GD 918

QY 59 PCCT---TCRHHP-CPGQGVQSGKES-----FGFQCIDCASGTF 95
Db 919 PRLPYGGQCRPCPCPGPG--SORHFATSCHRDGYSOQIVCHCRAGYTGURCACPAGHF 976

QY 96 -----SGGHEGHCCKPWTDCQTQGF 114
Db 977 GDSKPGRCQLCECSGNIDPTDPGACDHPITGQCLRLHHTEGPHGCHKP-----GF 1029

QY 115 LTVFPNGKTHNAV-VPGSPP 134
Db 1030 HGQAARQSCRCCTCNLLGTDP 1050

RESULT 8
CD40_BOVIN
ID CD40_BOVIN STANDARD; PRT; 269 AA.
AC Q28203;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).
GN TNFRSF5 OR CD40.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bos.
OX NCBI_TaxID=9913;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=97281252; PubMed=9135560;
RA Hirano A., Brown W.C., Estes D.M.;
RT "Cloning" expression and biological function of the bovine CD40
RT homologue: role in B-lymphocyte growth and differentiation in
RT cattle.";
RL Immunology 90:294-300(1997).
CC -I- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC -----
DR EMBL; U57745; AAC48710.1; -.
DR HSSP; P25942; ICDF.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_c6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00505; TNFR_NGFR_2; 1.
KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 >269 CD40L RECEPTOR.
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194 215 POTENTIAL.
FT DOMAIN 216 >269 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 187 4 X TNFR-CYS.
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 269 269
SQ SEQUENCE 269 AA; 25983 MW; 746903F30F95F387 CRC64;

Query Match 14.6%; Score 122.5; DB 1; Length 269;
Best Local Similarity 28.7%; Pred. No. 0.0003;
Matches 37; Conservative 9; Mismatches 70; Indels 13; Gaps 5;

QY 9 CGGRLLLGTGTDCRCRVHTRC---CRDYPGECCSEWD-----CMCVQPEFHCGDPCCT 62
Db 62 CGKGEFLSTWNRKYC---HEHRYCNPNLGRISQEGTLNTDTICVCVEGQ-HCTSHTC 117

QY 63 TCRHHP-CPGQGVQSGKESFGFQCIDCASGTFSGGHEG--HCKPWTDCQTQGF 119
Db 118 SCTPHSLCLPGFGVKQIATGLLDTVCEPLGFFSNVSSAFEKCHRWTSCKRGLVQHV 177

QY 120 GNKTHNAV 128
Db 178 GTNKTDVVC 186

RESULT 9
TNFR2_HUMAN
ID TNFR2_HUMAN STANDARD; PRT; 461 AA.
AC P20333;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR
DE BINDING PROTEIN 2) (TNF1) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).
GN TNFRSF1B OR TNFR2 OR TNFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

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RA Latza U., Duerkop H., Schnittger S., Ringeling J., Eitelbach F.,  
 RA Hummel M., Fonatsch C., Stein H.;  
 RT "The human OX40 homolog: cDNA structure, expression and chromosomal  
 RT assignment of the ACT35 antigen.";  
 RL Eur. J. Immunol. 24:677-683(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=952119871; PubMed=7704935;  
 RA Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A.,  
 RA Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.;  
 RT "Identification of OX40 ligand and preliminary characterization of  
 RT its activities on OX40 receptor";  
 RL Circ. Shock 44:30-34(1994).  
 CC -|- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.  
 CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -|- DATABASE: NAME=PROW; NOTE=CD guide CD134 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd134.htm".  
 CC -----  
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 CC -----  
 DR EMBL; X75962; CAA53576.1; -;  
 DR EMBL; S76792; AAB33944.1; ALT\_INIT.  
 DR HSP; P25942; ICDF.  
 DR MIN; 600315; -;  
 DR InterPro; IPR001368; -;  
 DR Pfam; PF00020; TNFR\_C6; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
 KW Signal.  
 FT SIGNAL 1 28  
 FT CHAIN 29 277  
 FT DOMAIN 29 214  
 FT TRANSMEM 215 235  
 FT DOMAIN 236 277  
 FT DOMAIN 30 169  
 FT REPEAT 30 65  
 FT REPEAT 66 107  
 FT REPEAT 108 126  
 FT REPEAT 127 167  
 FT CARBOHYD 146 146  
 FT CARBOHYD 160 160  
 FT CARBOHYD 160 160  
 SQ SEQUENCE 277 AA; 29340 MW; 49F15525941550BF CRC64;

Query Match 18.8%; Score 158.5; DB 1; Length 277;  
 Best Local Similarity 31.6%; Pred. No. 2.1e-07;  
 Matches 42; Conservative 10; Mismatches 70; Indels 11; Gaps 4;  
 QY 9 CGPGRLLGTGDACRCRVRHTRCCRDYFG--EECCSEWDCH-CYQPEFHCGD---PCCT 62  
 Db 46 CRP-----GNGMYVSCRSQNTVCRPCGFGFYNDVVVSSKPCPCTWCNLRSGSERKQLCT 100  
 QY 63 TCRHHPCPPGQVQSGKPSFGFCIDCASGTFSGHGHCCKPWTCTQFGFLTVPFGNK 122  
 Db 101 ATQDIVCRACRAGTQPLDSYKPGVDCACPGPHSGPDNQACAPWNTCTLAGKHTLPASN 160  
 QY 123 THNAVCPGSPPA 135  
 Db 161 SSDAICEDRDPPA 173  
 RESULT 4  
 ID 41BB\_MOUSE STANDARD; PRY; 256 AA.  
 AC P20334;

DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE 4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB).  
 GN TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89184547; PubMed=2784565;  
 RA Kwon B.S., Weissman S.M.;  
 RT "cDNA sequences of two inducible T-cell genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C;  
 RX MEDLINE=94179805; PubMed=8133039;  
 RA Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;  
 RT "Genomic organization and chromosomal localization of the T-cell  
 RT antigen 4-1BB";  
 RL J. Immunol. 152:2256-2262(1994).  
 RN [3]  
 RP CHARACTERIZATION, AND SEQUENCE OF 25-29.  
 RX MEDLINE=93139510; PubMed=7678621;  
 RA Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T.,  
 RA Kwon B.S.;  
 RT "Inducible T cell antigen 4-1BB. Analysis of expression and  
 RT function.";  
 RL J. Immunol. 150:771-781(1993).  
 CC -|- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY  
 CC ACTIVE DURING T CELL ACTIVATION.  
 CC -|- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.  
 CC -|- ASSOCIATES WITH P56-LCK.  
 CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -|- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.  
 CC -|- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.  
 CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -----  
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 CC -----  
 DR EMBL; J04492; AAA40167.1; -;  
 DR EMBL; U02567; AAA93113.1; -;  
 DR PIR; B32393; B32393.  
 DR HSP; P25942; ICDF.  
 DR MGD; MGI:1101059; Tnfrsf9.  
 DR InterPro; IPR001368; -;  
 DR Pfam; PF00020; TNFR\_C6; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; FALSE\_NEG.  
 KW Receptor; Glycoprotein; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 24  
 FT CHAIN 25 256  
 FT DOMAIN 25 187  
 FT TRANSMEM 188 208  
 FT DOMAIN 209 256  
 FT DOMAIN 17 159  
 FT REPEAT 17 45  
 FT REPEAT 46 85  
 FT REPEAT 86 117  
 FT REPEAT 118 159  
 FT CARBOHYD 128 128  
 FT CARBOHYD 138 138  
 FT CARBOHYD 138 138  
 SQ SEQUENCE 256 AA; 27598 MW; 93A10D03C60813C4 CRC64;

Query Match 18.2%; Score 153; DB 1; Length 256;  
 Best Local Similarity 31.5%; Pred. No. 6e-07;  
 Matches 40; Conservative 17; Mismatches 52; Indels 18; Gaps 7;

QY 9 CGGRL-LLGTGTDARCCRVHTRCCRDYPGEECCSEW---DCMVOPFHCQDPCCTTC 64  
 DB 47 CPSTSSIGQGNICRV-----CAGYFRFKFCSTHNAECIB-GFHCIGPQCTRC 101  
 QY 65 RHHPCCPPGQVQSGRFSFGQCIDCASGTFSGGH-BGHCKPWTDCQTFGLTFVFPNK 123  
 DB 102 -BKDRPGQLTKQG-----CKTCSLGTFDQNGVGCRPWTNCSLGRSLVLTGTTE 153  
 QY 124 HNAVCP 130  
 DB 154 KDVCVCP 160

RESULT 5  
 OX40\_RAT STANDARD; PRT; 271 AA.  
 AC P15725;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).  
 GN TNFRSF4 OR TXGPIL OR OX40.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=T-cell;  
 RX MEDLINE=90214614; PubMed=2157591;  
 RA Mallett S., Fossum S., Barclay A.N.;  
 RT "Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes -- a molecule related to nerve growth factor receptor.";  
 RL EMBO J. 9:1063-1068(1990).  
 CC 1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.  
 CC 1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC 1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.  
 CC 1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC  
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 CC  
 CC EMBL; X17037; CAA34897.1; -;  
 DR PIR; S08036; S08036.  
 DR PIR; S12783; S12783.  
 DR HSP; P25942; ICDF.  
 DR InterPro; IPR001368; -;  
 DR Pfam; PF00020; TNFR\_C6; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR.1; 3.  
 DR PROSITE; PS00500; TNFR\_NGFR.2; 2.  
 DR Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
 KW Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 271 OX40L RECEPTOR.  
 FT DOMAIN 20 210 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 211 235 POTENTIAL.  
 FT DOMAIN 236 271 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 164 4 X TNFR-CYS.  
 FT REPEAT 25 60 TNFR-CYS 1.  
 FT REPEAT 61 102 TNFR-CYS 2.  
 FT REPEAT 103 123 TNFR-CYS 3 (INCOMPLETE).  
 FT REPEAT 124 164 TNFR-CYS 4.  
 FT CARBOHYD 143 143 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;

Query Match 18.0%; Score 151; DB 1; Length 271;  
 Best Local Similarity 28.5%; Pred. No. 9.4e-07;  
 Matches 47; Conservative 12; Mismatches 62; Indels 44; Gaps 8;

QY 1 QRPYGGCGGGRLLLG--TCTDARCCRVHIT-----RCCRD-YPGECCSEWD----- 46  
 DB 6 QQPT-----AFLLLGLSLGTVTKLNCVKDTPYSGHKRCRCQPGHGMVSRCDTRDTV 58  
 QY 47 CMVQCPFHCG---DPC--CTTCRHH-----PCPPGQGVQSGKFSF 83  
 DB 59 CHPCEPGFNEAVNYDCKQTCQNHRSSELKQNCQCTPTEDTVCCRCPTQPRDSSHL 118  
 QY 84 GFQCIDCASGTFSGGHEGCHKPWTDCQTFGLTFVFPGNKTHNAV 128  
 DB 119 GVDVCPGPGHFGSPGQACKPWNTCLSGKQIRHPASNSLDTVC 163

RESULT 6  
 CD40\_MOUSE STANDARD; PRT; 289 AA.  
 AC P27512;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).  
 GN TNFRSF5 OR CD40.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92105763; PubMed=1370315;  
 RA Torres R.M., Clark E.A.;  
 RT "Differential increase of an alternatively polyadenylated mRNA species of murine CD40 upon B lymphocyte activation.";  
 RL J. Immunol. 148:620-626(1992).  
 CC 1-  
 CC 2-  
 CC REVISIONS.  
 CC STRAIN-BALB/C;  
 RA Torres R.M.;  
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
 CC [3]  
 CC SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C; TISSUE=Liver;  
 RX MEDLINE=93094586; PubMed=1281194;  
 RA Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A., Howard M., Cockayne D.A.;  
 RT "Genomic structure and chromosomal mapping of the murine CD40 gene.";  
 RL J. Immunol. 149:3921-3926(1992).  
 CC 1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
 CC 1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC 1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC  
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 CC  
 CC EMBL; M83312; AAB08705.1; -;  
 DR EMBL; M94126; AAA37404.1; -;  
 DR EMBL; M94129; AAA37404.1; JOINED.  
 DR EMBL; M94128; AAA37404.1; JOINED.  
 DR EMBL; M94127; AAA37404.1; JOINED.  
 DR PIR; A46476; A46476.  
 DR HSP; P25942; ICDF.  
 DR MGD; MGI:88336; Tnfrsf5.  
 DR InterPro; IPR001368; -;



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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:15:21 ; Search time 43.78 Seconds  
(without alignments)  
107.195 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_26\_162

Perfect score: 841

Sequence: 1 QRPTGGPGCGPGRLLLTGT.....FFGNKTHNAVCPGPPAP 137

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	162	19.3	272	1	OX40_MOUSE
2	160.5	19.1	255	1	41BB_HUMAN
3	158.5	18.8	277	1	OX40_HUMAN
4	153	18.2	256	1	41BB_MOUSE
5	151	18.0	271	1	OX40_RAT
6	127.5	15.2	289	1	CD40_MOUSE
7	125	14.9	1801	1	LMB2_RAT
8	122.5	14.6	269	1	CD40_BOVIN
9	121	14.4	461	1	TNR2_HUMAN
10	120	14.3	1799	1	LMB2_MOUSE
11	119	14.1	474	1	TNR2_MOUSE
12	118.5	14.1	277	1	CD40_HUMAN
13	117	13.9	435	1	TNR2_HUMAN
14	111	13.2	1370	1	IG1R_RAT
15	109	13.0	3635	1	LMA5_MOUSE
16	108	12.8	2907	1	FBN2_MOUSE
17	107	12.7	1798	1	LMB2_HUMAN
18	104	12.4	1373	1	IG1R_MOUSE
19	104	12.4	2911	1	FBN2_HUMAN
20	102.5	12.2	956	1	TSP3_MOUSE
21	101	12.0	1367	1	IG1R_HUMAN
22	100	11.9	581	1	IRR_RAT
23	100	11.9	1106	1	STC_DROME
24	99.5	11.8	2569	1	LMA3_MOUSE
25	97.5	11.6	1713	1	LMA3_HUMAN
26	96	11.4	416	1	NGFR_CHICK
27	95.5	11.4	415	1	TNR2_MOUSE
28	95.5	11.4	1172	1	TSP2_HUMAN
29	95.5	11.4	1786	1	LMB1_HUMAN
30	95	11.3	1297	1	IRR_HUMAN
31	94.5	11.2	956	1	TSP3_HUMAN
32	94.5	11.2	1408	1	SERR_DROME
33	94	11.2	2871	1	FBN1_BOVIN

34 94 11.2 2871 1 FBN1\_HUMAN p35555 homo sapien  
35 93.5 11.1 212 1 AG1\_HORVU p15312 hordeum vul  
36 93.5 11.1 1786 1 LMB1\_MOUSE p02469 mus musculu  
37 93.5 11.1 1964 1 NTC4\_MOUSE p31695 mus musculu  
38 93 11.1 213 1 AG12\_WHEAT p02876 triticum ae  
39 93 11.1 555 1 DP87\_DICDI Q04503 dictyoscell  
40 93 11.1 2318 1 NTC3\_MOUSE Q61982 mus musculu  
41 92.5 11.0 169 1 KRU4\_HUMAN p26371 homo sapien  
42 92.5 11.0 2139 1 CRB\_DROME p10040 drosophila  
43 92 10.9 2531 1 NTC1\_MOUSE Q01705 mus musculu  
44 92 10.9 4289 1 TENX\_HUMAN p22105 homo sapien  
45 91.5 10.9 186 1 AG13\_WHEAT p10969 triticum ae

#### ALIGNMENTS

RESULT 1  
ID OX40\_MOUSE STANDARD; PRT; 272 AA.  
AC P47741;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).  
GN TNFRSF4 OR TXGP1 OR OX40.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OC NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C.  
RX MEDLINE=94044750; PubMed=8228223;  
RA Calderhead D.M., Buhlmann J.E., van den Bortwegh A.J.,  
RT Claassen E., Noelle R.J., Fell H.;  
RT Cloning of mouse OX40: a T cell activation marker that may mediate  
RT T-B cell interactions.;  
RL J. Immunol. 151:5261-5271(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95255413; PubMed=7737295;  
RA Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,  
RA Barclay A.N.;  
RT "Gene structure and chromosomal localization of the mouse homologue  
RT of rat OX40 protein.";  
RL Eur. J. Immunol. 25:926-930(1995).  
CC -|- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.  
CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
CC  
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CC  
CC EMBL; 221674; CAA79772.1; -;  
CC EMBL; X85214; CAA59476.1; -;  
CC HSSP; P25942; 1CDF.  
CC MGD; MGI:104512; Tnfrsf4.  
CC InterPro; IPR001368; -;  
CC Pfam; PF00020; TNFR\_C6; 3.  
CC PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
CC PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
CC Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
CC Signal.  
CC  
CC CHAIN 1 19 POTENTIAL.  
CC DOMAIN 20 272 OX40L RECEPTOR.  
CC TRANSMEM 21 211 EXTRACELLULAR (POTENTIAL).  
CC TRANSMEM 212 236 POTENTIAL.

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FT DOMAIN 237 272 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 165 4 X TNFR-CYS.
FT REPEAT 26 61 TNFR-CYS 1.
FT REPEAT 62 103 TNFR-CYS 2.
FT REPEAT 104 124 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 125 165 TNFR-CYS 4.
FT CARBOHYD 144 144 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CONFLICT 15 15 A -> G (IN REF. 2).
SQ SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;

Query Match 19.3%; Score 162; DB 1; Length 272;
Best Local Similarity 28.3%; Pred. No. 1e-07;
Matches 45; Conservative 11; Mismatches 51; Indels 52; Gaps 7;

QY 14 LLLGTGTGTDAR--CCRVT-----TRCCRD-YPG-----EECCSEWDCMCVQPEFHCGDPC-- 60
Db 14 LALTGLVTARRLNCVHTVPSGHKKCRCPQGHGMVSRCDHTDRLC-----HPCET 65

QY 61 -----CTTCRHPP-----CPQGQVQSQKFSFGFCID 89
Db 66 GFYNEAVNYDTCKQCQCNHRSSSELKQNCPTPTQDVTVCRCRPGTQPRQDSGYKLGVDVCP 125

QY 90 CASGTFSGGHEGCKPWTCTQFGFLTVPGNKTHNAV 128
Db 126 CPPGHFSPGNQACKPWTNCTLSGKQTRHPASDSDAVC 164

RESULT 2
41BB_HUMAN STANDARD; PRT; 255 AA.
AC Q07011;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE 4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB HOMOLOG)
DE (T-CELL ANTIGEN ILA) (CD137 ANTIGEN).
GN TNFRSF9 OR ILA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=94374434; PubMed=8088337;
RA Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J.,
RA Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;
RT "Molecular and biological characterization of human 4-1BB and its
RT ligand.";
RL Eur. J. Immunol. 24:2219-2227(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=94085794; PubMed=8262389;
RA Schwarz H., Tuckwell J., Lotz M.;
RT "A receptor induced by lymphocyte activation (ILA): a new member of
RT the human nerve-growth-factor/tumor-necrosis-factor receptor
RT family.";
RL Gene 134:295-298(1993).
RN [3]
RP REVISION TO 107.
RA Schwarz H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95347766; PubMed=7622190;
RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,
RA Kwon B.S.;
RT "Characterization of human homologue of 4-1BB and its ligand.";
RL Immunol. Lett. 45:67-73(1995).
CC -!- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY
```

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CC ACTIVE DURING T CELL ACTIVATION.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T
CC CELLS.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw137.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U01397; AAA5133.1; -
CC EMBL: L12964; AAA62478.2; -
CC HSP: P19438; TEXT.
CC MIM: 602250; -
CC InterPro: IPR001368; -
CC Pfam: PF00020; TNFR_C6; 2.
CC PROSITE: PS00652; TNFR_NGFR_1; 1.
CC PROSITE: PS00500; TNFR_NGFR_2; 1.
CC KW Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
CC SIGNAL 1 17 POTENTIAL.
CC FT CHAIN 18 255 4-1BB LIGAND RECEPTOR.
CC FT DOMAIN 18 186 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 187 213 POTENTIAL.
CC FT DOMAIN 214 255 CYTOPLASMIC (POTENTIAL).
CC FT REPEAT 47 159 3 X TNFR-CYS.
CC FT REPEAT 87 86 TNFR-CYS 1.
CC FT REPEAT 119 159 TNFR-CYS 2.
CC FT REPEAT 138 138 TNFR-CYS 3.
CC FT CARBOHYD 149 149 N-LINKED (GLCNAC... ) (POTENTIAL).
CC FT CARBOHYD 149 149 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 255 AA; 27899 MW; F3A563FE5EF00460 CRC64;

Query Match 19.1%; Score 160.5; DB 1; Length 255;
Best Local Similarity 30.9%; Pred. No. 1.3e-07;
Matches 47; Conservative 12; Mismatches 52; Indels 41; Gaps 9;

QY 9 CGPGRLLLTGTARCCRVHTTCCRDYPG-----EECCS-----EWDCMCVQPEFHCGDPP 59
Db 48 CPPNSFSAGG--QRTCDI-----CROCKGVFRTRKESSTSNACDC--TPGFHCLGA 97

QY 60 CCTTCRHPPGPPGVQSQKFSFGFCIDCASGTFSGGHEGCKPWTCTQFGFLTVFP 119
Db 98 GCSMC-EQDCKQGOELTKG-----CKDCFCFTNDQKRGICRPWTNCSLDGKSVLVN 149

QY 120 GNKTHNAVCPG-----SPPA---EP 137
Db 150 GTRERDVVCGPSPADLSFGASSVTPPAPAREP 181

RESULT 3
OX40_HUMAN STANDARD; PRT; 277 AA.
AC P43489; Q13663;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY
DE ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).
GN TNFRSF4 OR TXGP1L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94170844; PubMed=7510240;
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F:1142-1186/Domain: laminIn-type EGF-like homology <LE13>

```

Query Match          14.9%; Score 106; DB 2; Length 1797;
Best Local Similarity 29.5%; Pred. No. 0.2;
Matches 39; Conservative 5; Mismatches 38; Indels 50; Gaps 10;

QY  5  GGPGCGRLLLTGTGDARC-----CRVHTTRC--CRDYPGECCSWMDCMCVQPEF 54
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   870  GFPSCRP-----CVCNGHADECNTHTGACLCGRDLTGGEHCR---CI-AGF  912
                                     ||| ||| ||| ||| ||| ||| ||| |||
QY  55  HCGDPPC---TTCRRHPCPPGQGVQ-----SQGKFS-----FGQCIDCAGS  93
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   913  H-GDPLPYGAQCRPCPCPGPGSGRHFATSCHQDEYSQQIVCHCRAGYTGLRCEACAPG 971
                                     ||| ||| ||| ||| ||| ||| ||| |||
QY  94  TFSG-GHEGHCK 104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   972  QFGDPSRPGACQ 983
                                     ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
A57278
fibrillin-2 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 11-Jan-2000
C:Accession: A57278
R:Zhang, H.; Hu, W.; Ramirez, F.
J. Cell Biol. 129, 1165-1176, 1995
A:Title: Developmental expression of fibrillin genes suggests heterogeneity of extrac
A:Reference number: A57278; MUID:95263670
A:Accession: A57278
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2907 <ZHA>
A:Cross-references: GB:L39790; NID:g762830; PIDN:AAA74908.1; PID:g762831
C:Superfamily: unassigned EGF-related proteins; EGF homology
F:1239-1274/Domain: EGF homology <EGF1>
F:2488-2523/Domain: EGF homology <EGF>

Query Match          14.8%; Score 105.5; DB 2; Length 2907;
Best Local Similarity 26.8%; Pred. No. 0.3;
Matches 33; Conservative 11; Mismatches 40; Indels 39; Gaps 8;

QY  9  CGPCRLLLTGTGDARCC-----RVHTTRCCRDYPGECCSWMDCMCVQPEFHCG 57
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   677  CPPG---LAVGVGRCVCDTHMRSTCTGKVGCVRPFFGAVTKSE---CCCANPDYGGC 731
                                     ||| ||| ||| ||| ||| ||| ||| |||
QY  58  DPCQTCRRHPCPPGQGVQSGQKFSFGF-----QC-ID---CAGS---TFSGGHE 100
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   732  EPC-----QPCPAKNSAEFHGLCSSGIGITVDGRDINECALPDICANGICENLRGTYR 785
                                     ||| ||| ||| ||| ||| ||| ||| |||
QY  101  GHC 103
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   786  CNC 788
                                     ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
TL13954
MEGF6 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C:Accession: TL13954
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like moti
A:Reference number: Z14126; MUID:98360089
A:Accession: TL13954
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1574 <NAK>
A:Cross-references: EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g3449294
A:Experimental source: strain Sprague-Dawley; brain
```

C:Genetics:  
A:Gene: MEGF6

Query Match 14.8%; Score 105; DB 2; Length 1574;  
Best Local Similarity 28.8%; Pred. No. 0.22;  
Matches 34; Conservative 8; Mismatches 36; Indels 40; Gaps 8;  
QY 6 GPGCGPGRLLGTGTIDARCRVHTTRC-----CR-DYPGECCSEWD----- 46  
Db 651 GPGC-----SEDCLEQSHTRSCNPKDGSCKAGFQGERCAECESGFFGPGCRH 701  
QY 47 -CMCVQPEFHCGDPCCCTTCRHHPCPPGQVQSQGKFSFGFCIDCASGTFSGGHEGHC 103  
Db 702 RCTC-QPGVAC-DPVSGERCTQ-CPEGYQGEDCGQ-----ECPVGTFGVNCSCGSC 748

Search completed: September 4, 2001, 16:12:12  
Job time: 1109 sec

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Query Match      19.1%; Score 135.5; DB 2; Length 255;
Best Local Similarity 32.5%; Pred. No. 0.00022;
Matches 37; Conservative 9; Mismatches 41; Indels 27; Gaps 7;

QY 9 CGPGRLLLGTTDARCCRVHTTRCCRDYPG-----EECCS-----EWDCCMCVQPERFHCDDP 59
Db 48 CPPNSFSSAGG--QRTCDI-----CROCKGVFTRKKECSSTNAECDC---TPGFHCLGA 97

QY 60 CCTTCRHHPCCPPGGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTDCQTFG 113
Db 98 GCSMC-EQDCKQGOELTKKG-----CKDCFCFTFNDQKRGICRPWTNCSLDG 143

RESULT 6
I37552
OX40 homolog - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C:Accession: I37552
R:Latza, U.; Durrkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat
Eur. J. Immunol. 24, 677-683, 1994
A:Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment o
A:Reference number: I37552; MUID:94170844
A:Accession: I37552
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-277 <RES>
A:Cross-references: EMBL:X75962; NID:9472957; PIDN:CAA53576.1; PID:9472958
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match      17.4%; Score 123.5; DB 2; Length 277;
Best Local Similarity 31.5%; Pred. No. 0.0022;
Matches 35; Conservative 5; Mismatches 60; Indels 11; Gaps 4;

QY 9 CGPGRLLLGTTDARCCRVHTTRCCRDYPG--EECCSEWDCM-CVQPFHCGD---PQCT 62
Db 46 CRP-----GNGMVSRCSRSQNTVCRPCGPGFYNDVWSSKPCPKCTWNCNLRSGERKQLCT 100

QY 63 TCRHHPCCPPGGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTDCQTFG 113
Db 101 ATQDTVCRCRAGTQPLDSYKFGVDCAPCPGPFSGDNGQACKPWTNCTLAG 151

RESULT 7
MMRTS
laminin beta-2 chain precursor - rat
N:Alternate names: laminin chain B3; S-laminin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 10-Dec-1999
C:Accession: S03539
R:Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.
Nature 338, 229-234, 1989
A:Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neuro
A:Reference number: S03539; MUID:89159410
A:Accession: S03539
A:Molecule type: mRNA
A:Residues: 1-1801 <HUN>
A:Cross-references: EMBL:X16563; NID:957250; PIDN:CAA34561.1; PID:957251
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C:Function:
A:Description: Interact with cells and with other basement membrane proteins to promote
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F:1-35/Domain: signal sequence #status predicted <SIG>
F:36-1801/Product: laminin beta-2 chain #status predicted <MAT>
F:36-285/Domain: VI <DOM4>
F:286-555/Domain: V <DOM5>
F:286-347/Domain: laminin-type EGF-like homology <LE01>
F:350-410/Domain: laminin-type EGF-like homology <LE02>
F:413-470/Domain: laminin-type EGF-like homology <LE03>
F:473-522/Domain: laminin-type EGF-like homology <LE04>
F:525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>

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F:556-784/Domain: IV <DOM4>
F:786-831/Domain: laminin-type EGF-like homology <LE06>
F:788-1196/Domain: III <DOM3>
F:834-877/Domain: laminin-type EGF-like homology <LE07>
F:880-927/Domain: laminin-type EGF-like homology <LE08>
F:930-986/Domain: laminin-type EGF-like homology <LE09>
F:989-1038/Domain: laminin-type EGF-like homology <LE10>
F:1041-1095/Domain: laminin-type EGF-like homology <LE11>
F:1098-1143/Domain: laminin-type EGF-like homology <LE12>
F:1146-1190/Domain: laminin-type EGF-like homology <LE13>
F:1197-1412/Domain: II <DOM2>
F:1197-1412/Region: heptad repeats
F:1413-1445/Domain: alpha <ALP>
F:1446-1801/Region: heptad repeats
F:1446-1801/Domain: I <DOM1>
F:45-50/Disulfide bonds: #status predicted
F:251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #statu
F:1193,1196,1800/Disulfide bonds: Interchain #status predicted

Query Match      17.2%; Score 122; DB 1; Length 1801;
Best Local Similarity 27.5%; Pred. No. 0.01;
Matches 47; Conservative 3; Mismatches 35; Indels 86; Gaps 10;

QY 5 GGPGGCGP-----GRLLLGTTDARCCRVHTTRC--CRDYPGEECCSEWDCMCVQPFHCGD 58
Db 873 GFPNCRPCVCNGR-----ADECDHAHTGACLCGRDYGGEHCER----CI-AGFH-GD 918

QY 59 PQCT---TCRHHPCCPPGGVQSGKFS-----FGQCIDCASGTF 95
Db 919 PRLPYGGQCRPCPEPGG--SQRHEATSCHRDGYQQIVCHCRAGYTGURCEACAPGHF 976

QY 96 -----SGGHEGCHKP 105
Db 977 GDSRPGGRGRCQCESGNIDPTDPGACDPHTGQCRLCLHHTGPHGCHKP 1027

RESULT 8
A46476
B cell-associated surface molecule CD40, long splice form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C:Accession: A46476; A46515
R:Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A:Title: Differential increase of an alternatively polyadenylated mRNA species of mur
A:Reference number: A46476; MUID:92105763
A:Accession: A46476
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-305 <TOR>
A:Cross-references: GB:M83312; NID:91553058
A:Note: sequence extracted from NCBI backbone (NCBI:75206, NCBI:75207)
A:Note: this translation is not annotated in Genbank entry MUSCD40A, release 113.0
R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockay
J. Immunol. 149, 3921-3926, 1992
A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A:Reference number: A46515; MUID:93094586
A:Accession: A46515
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-287 'LV' <GRI>
A:Cross-references: GB:M83312; NID:91553058; PIDN:AAB08705.1; PID:91553059; GB:M941126
A:Experimental source: BALB/c, liver
A:Comment: For an alternative splice form, see PIR:A46515
C:Comment: For an alternative splice form, see PIR:A46476.
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: alternative splicing; transmembrane protein
F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match      16.4%; Score 116.5; DB 2; Length 305;

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**RESULT**    10  
S53869  
laminin beta-2 chain precursor (version 2) - human  
N;Alternate names: s-laminin  
C;Species: Homo sapiens (man)  
C;Date: 27-Oct-1995 #sequence\_revision 23-Feb-1996 #text\_change 24-Sep-1998  
R;Accession: S53869  
R;Iivanainen, A.; Vuolteenaho, R.; Sainio, K.; Eddy, R.; Shows, T.B.; Sariola, H.; Tryggn Matrix Biol. 14, 489-497, 1994  
A;Title: The human laminin beta-2 chain (S-laminin): structure, expression in fetal tissue  
A;Reference number: S53869  
A;Accession: S53869  
A;Molecule type: mRNA  
A;Residues: 1-1798 <II>  
C;Genetics:  
A;Gene: GDB:LAMB2  
A;Cross-references: CDB:132363; OMIM:150325  
A;Map position: 3p21.3-3p21.2  
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C;Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer  
F;1-32/Domain: signal sequence #status predicted <SIG>  
F;33-1798/Product: laminin beta-2 chain #status predicted <MAT>  
F;283-344/Domain: laminin-type EGF-like homology <LE01>  
F;347-407/Domain: laminin-type EGF-like homology <LE02>  
F;410-467/Domain: laminin-type EGF-like homology <LE03>  
F;470-519/Domain: laminin-type EGF-like homology <LE04>  
F;522-552/Domain: laminin-type EGF-like homology #status atypical <LE05>

64 C-RHHPCPPGOGVOSOGKFSFGFOCIDCASGTFSGGHEG--HCKPWTDC 109

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	143	20.1	272	2	I48700	gene ox40 protein
2	141	19.8	271	2	S12783	OX40 antigen precursor
3	140	19.7	256	2	B32393	T-cell antigen 4-1
4	138.5	19.5	295	2	JC5559	lectin-B - Virgin
5	135.5	19.1	255	2	I38426	lymphocyte activat
6	123.5	17.4	277	2	I37552	OX40 homolog - hum
7	122	17.2	1801	1	MMRTS	laminin beta-2 cha
8	116.5	16.4	305	2	A46476	B cell-associated
9	112	15.8	152	2	T18975	hypothetical prote
10	112	15.8	1798	2	S53869	laminin beta-2 cha
11	108.5	15.3	277	2	A60771	B-cell activation
12	107	15.0	164	2	T24272	hypothetical prote
13	106	14.9	1797	2	A55677	laminin beta-2 cha
14	105.5	14.8	2907	2	A57278	fibrillin-2 precu
15	105	14.8	1374	2	T13954	MEGF6 protein - ra
16	103.5	14.6	2918	2	A54105	fibrillin-2 precu
17	102.5	14.4	188	2	T15651	hypothetical prote
18	98	13.8	3635	2	T10053	laminin alpha 5 ch
19	97.5	13.7	1713	2	A55347	adhesive ligand ep
20	96.5	13.6	540	2	B47417	insulin receptor-r
21	96.5	13.6	1820	2	A53494	latent transformin
22	95.5	13.4	1786	1	MMHUB1	laminin beta-1 cha
23	94.5	13.3	435	2	I54182	tumor necrosis fac
24	94.5	13.3	1268	2	B36502	insulin receptor-r
25	94	13.2	1203	2	A48175	Mo1ch B protein -
26	93.5	13.2	212	2	T05936	agglutinin isolect
27	93.5	13.2	644	2	A36325	epidermal growth f
28	93.5	13.2	1786	1	MMMSB1	laminin beta-1 cha
29	92.5	13.0	329	2	A48805	insulin-like growt

C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 05-Nov-1999  
C:Accession: S12783; S08036  
R:Mallett, S.; Fossum, S.; Barclay, A.N.  
EMBO J. 9, 1063-1068, 1990  
A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte  
A:Reference number: S12783; MUID:90214614  
A:Accession: S12783

A:Molecule type: mRNA  
A:Residues: 1-271 <NAL>  
A:Cross-references: EMBL:XL7037; NID:g57830; PIDN:CRA34897.1; PID:g57831  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: growth factor receptor; transmembrane protein  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-271/Product: OX40 antigen #status predicted <MAT>  
F:211-235/Domain: transmembrane #status predicted <TM>

Query Match 19.8%; Score 141; DB 2; Length 271;  
Best Local Similarity 29.3%; Pred. No. 8.3e-05;  
Matches 44; Conservative 9; Mismatches 53; Indels 44; Gaps 8;

QY 1 ORPTGGPGGPGRLLG--TGTDAACRVHTT-----RCRD-YPGECCSEWD----- 46  
DB 6 QOPT-----AFLILSLGVTVKLVKVDTPVSGHKCCRCQPGRGVMVSRCDHTRDTV 58

QY 47 CMCVQPEFHCG-----DPC--CITCRHH-----PCPPGGQVQSGKFSF 83  
DB 59 CHPCPGFNEAVNYDTCKQTCNHRSGSELKQNCPTEDTVCCRCRGTQPRQDSSHLK 118

QY 84 GFQICDASGTSGGHGHCKPWTDTCTQFG 113  
DB 119 GVDVCPGPHFSPGNSQACKPWNTCLSG 148

RESULT 3  
B32393  
T-cell antigen 4-1BB precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 21-Jul-2000  
C:Accession: B32393; I48879  
R:Kwon, B.S.; Weisman, S.M.  
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989  
A:Title: cDNA sequence of two inducible T-cell genes.  
A:Reference number: A32393; MUID:89184547  
A:Accession: B32393  
A:Molecule type: mRNA  
A:Residues: 1-256 <KW>  
A:Cross-references: GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122  
R:Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.  
J. Immunol. 152, 2256-2262, 1994  
A:Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1BB.  
A:Reference number: I48879; MUID:94179805  
A:Accession: I48879  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-256 <RES>  
A:Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178  
C:Genetics:

A:Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: transmembrane protein  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-256/Product: 4-1BB protein #status predicted <MAT>

Query Match 19.7%; Score 140; DB 2; Length 256;  
Best Local Similarity 32.7%; Pred. No. 9.6e-05;  
Matches 36; Conservative 15; Mismatches 41; Indels 18; Gaps 7;

QY 9 CGPGRLLGTGTDAACRVHTTCCRDYPGECCSEW---DCMCVQPEFHCGDPCCTTC 64  
DB 47 CPPSTSSIGQPNICRV---CAGYFRFKFCSSTHNAECEIE-GFHCILGPQCTRC 101

QY 65 RHHPCPGPGVQSGKFSFGQICDASGTSFGGH-BGHCKPWTDTCTQFG 113  
DB 102 -EKDCRPGQELTKQG-----CKTCSLGTFDQNGTGVCPRWNTCSLDG 143

RESULT 4  
JC5559  
lectin-B - Virginian pokeweed  
C:Species: Phytolacca americana (Virginian pokeweed)  
C:Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 17-Mar-2000  
C:Accession: JC5559  
R:Yamaguchi, K.; Yurino, N.; Kino, M.; Ishiguro, M.; Funatsu, G.  
Biosci. Biotechnol. Biochem. 61, 690-698, 1997  
A:Title: The amino acid sequence of mitogenic lectin-B from the roots of pokeweed (Ph)  
A:Reference number: JC5559; MUID:97290889  
A:Accession: JC5559

A:Molecule type: protein  
A:Residues: 1-295 <YAM>  
A:Experimental source: root  
C:Comment: This protein is a lectin specific for N-acetylglucosamine-containing saccha  
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;  
C:Keywords: glycoprotein  
F:96,139/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.5%; Score 138.5; DB 2; Length 295;  
Best Local Similarity 31.7%; Pred. No. 0.00014;  
Matches 33; Conservative 17; Mismatches 31; Indels 23; Gaps 7;

QY 9 CGPGRLLLTGTDAACRVHTTCCRDYPG-----ECCSEWDCMCVQPEFHCGDPCCTT 63  
DB 154 CGITEGYCGEGCSQC---NHQRCGKDFAGRTCLNDLCCSEWG-WCGSSEAHCGGCGQSN 209

QY 64 CRHHPCPGPGVQSGKFSFGQ-C-----IDCAGTFFSGGHEHC 103  
DB 210 CNYNRC-----GR-NFGFRTCPNELCCSGGCGGSDAHC 243

RESULT 5  
I38426  
lymphocyte activation-induced receptor ILA precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 01-Dec-2000  
C:Accession: I38426; JT0752  
R:Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.  
Eur. J. Immunol. 24, 2219-2227, 1994  
A:Title: Molecular and biological characterization of human 4-1BB and its ligand.  
A:Reference number: I38426; MUID:94374434  
A:Accession: I38426  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-255 <RES>  
A:Cross-references: EMBL:U03397; NID:g571320; PIDN:AAA53133.1; PID:g571321  
R:Schwarz, H.; Tuckwell, J.; Lotz, M.  
Gene 134, 295-298, 1993  
A:Title: A receptor induced by lymphocyte activation (ILA): a new member of the human  
A:Reference number: JT0752; MUID:94085794  
A:Accession: JT0752

A:Molecule type: mRNA  
A:Residues: 1-106,'R',108-255 <SCH>  
C:Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-ne  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT>  
F:187-213/Domain: transmembrane #status predicted <TM>  
F:138,149/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:234,235/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status pred  
F:242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted



FT	DOMAIN	3036	3241	FT	DISULFID	2086	2086	INTERCHAIN (PROBABLE).
FT	DOMAIN	3422	3427	FT	DISULFID	2089	2089	INTERCHAIN (PROBABLE).
FT	DOMAIN	3428	3635	FT	CARBOHYD	17	17	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	2122	2174	FT	CARBOHYD	65	65	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	2247	2381	FT	CARBOHYD	165	165	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	2521	2538	FT	CARBOHYD	300	300	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	2556	2622	FT	CARBOHYD	374	374	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SITE	1640	1642	FT	CARBOHYD	402	402	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SITE	1756	1758	FT	CARBOHYD	822	822	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	222	231	FT	CARBOHYD	843	843	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	224	244	FT	CARBOHYD	881	881	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	246	255	FT	CARBOHYD	1252	1252	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	258	278	FT	CARBOHYD	1451	1451	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	281	290	FT	CARBOHYD	1938	1938	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	283	315	FT	CARBOHYD	2115	2115	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	318	327	FT	CARBOHYD	2128	2128	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	330	348	FT	CARBOHYD	2282	2282	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	351	362					
FT	DISULFID	353	369					
FT	DISULFID	371	380					
FT	DISULFID	383	393					
FT	DISULFID	417	429					
FT	DISULFID	419	438					
FT	DISULFID	440	449					
FT	DISULFID	452	461					
FT	DISULFID	464	476					
FT	DISULFID	466	483					
FT	DISULFID	485	494					
FT	DISULFID	497	507					
FT	DISULFID	510	522					
FT	DISULFID	512	528					
FT	DISULFID	530	539					
FT	DISULFID	542	552					
FT	DISULFID	555	567					
FT	DISULFID	557	573					
FT	DISULFID	575	584					
FT	DISULFID	587	597					
FT	DISULFID	600	612					
FT	DISULFID	602	619					
FT	DISULFID	621	630					
FT	DISULFID	633	643					
FT	DISULFID	1360	1372					
FT	DISULFID	1362	1379					
FT	DISULFID	1381	1390					
FT	DISULFID	1393	1403					
FT	DISULFID	1450	1465					
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FT	DISULFID	1501	1518					
FT	DISULFID	1520	1529					
FT	DISULFID	1532	1547					
FT	DISULFID	1782	1791					
FT	DISULFID	1784	1798					
FT	DISULFID	1801	1810					
FT	DISULFID	1813	1829					
FT	DISULFID	1832	1847					
FT	DISULFID	1834	1856					
FT	DISULFID	1858	1867					
FT	DISULFID	1870	1885					
FT	DISULFID	1888	1903					
FT	DISULFID	1890	1910					
FT	DISULFID	1913	1922					
FT	DISULFID	1925	1939					
FT	DISULFID	1989	2000					
FT	DISULFID	1991	2007					
FT	DISULFID	2009	2018					
FT	DISULFID	2021	2033					
FT	DISULFID	2036	2043					
FT	DISULFID	2038	2050					
FT	DISULFID	2052	2061					
FT	DISULFID	2064	2083					

Query Match 13.8%; Score 98; DB 1; Length 3635;  
Best Local Similarity 28.3%; Pred. No. 0.15;  
Matches 36; Conservative 7; Mismatches 44; Indels 40; Gaps 8;

Qy 3 PTGGGCGGP--GRLLLTGTDAKCCRVHTTRCCRDYPG--EECCSEWDCMCVQPEFHCGDP 59  
Db 1946 PGGTETCDPQSGRCLCKAGVTGQRC----DRCLGYGFEGCQCQCRPCAC-----GP 1993

Qy 60 CCTTCRHHP-----CPPGGGVQSQGKSFSGFQCIDCASGTFSSGHE-----GHCK 104  
Db 1994 AAKGSECHPQSGQCHCQPG-----TTGPOCLECAPGYWGLPKRGCRRCQCPRGHCD 2044

Qy 105 PWT-DCT 110  
Db 2045 PHTGHT 2051

Search completed: September 4, 2001, 16:15:23  
Job time: 1135 sec

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FT DISULFID 804 813 BY SIMILARITY.
FT DISULFID 816 828 BY SIMILARITY.
FT DISULFID 831 843 BY SIMILARITY.
FT DISULFID 833 850 BY SIMILARITY.
FT DISULFID 852 861 BY SIMILARITY.
FT DISULFID 864 874 BY SIMILARITY.
FT DISULFID 877 886 BY SIMILARITY.
FT DISULFID 879 893 BY SIMILARITY.
FT DISULFID 896 905 BY SIMILARITY.
FT DISULFID 908 924 BY SIMILARITY.
FT DISULFID 927 943 BY SIMILARITY.
FT DISULFID 929 954 BY SIMILARITY.
FT DISULFID 956 965 BY SIMILARITY.
FT DISULFID 968 983 BY SIMILARITY.
FT DISULFID 986 1000 BY SIMILARITY.
FT DISULFID 988 1007 BY SIMILARITY.
FT DISULFID 1010 1019 BY SIMILARITY.
FT DISULFID 1022 1035 BY SIMILARITY.
FT DISULFID 1095 1107 BY SIMILARITY.
FT DISULFID 1097 1114 BY SIMILARITY.
FT DISULFID 1116 1125 BY SIMILARITY.
FT DISULFID 1128 1140 BY SIMILARITY.
FT DISULFID 1143 1155 BY SIMILARITY.
FT DISULFID 1145 1162 BY SIMILARITY.
FT DISULFID 1164 1173 BY SIMILARITY.
FT DISULFID 1176 1187 BY SIMILARITY.
FT DISULFID 1190 1190 INTERCHAIN (PROBABLE).
FT DISULFID 1193 1193 INTERCHAIN (PROBABLE).
FT DISULFID 1797 1797 INTERCHAIN (PROBABLE).
FT CARBOHYD 248 248 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 368 368 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1085 1085 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1249 1249 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1308 1308 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1348 1348 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1499 1499 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 914 914 R -> G (IN REF. 2).
FT CONFLICT 1179 1179 G -> A (IN REF. 2).
SQ SEQUENCE 1798 AA; 196079 MW; 9555CF5B24850CB7 CRC64;

Query Match 14.68; Score 104; DB 1; Length 1798;
Best Local Similarity 23.8%; Pred. No. 0.026;
Matches 41; Conservative 5; Mismatches 38; Indels 88; Gaps 9;

QY 5 GPGCGPGRLLGGTDARC-----CRVHTTRC--CRDYPGEECCSEWDCMCVQPEF 54
DQ 870 GFPSCR-----CVCNGHADECNTHTGACLCGRDHTGGEHCE-----CI-AGF 912
QY 55 HCGD--PCCTTCRHHPPGGGVQ-----SOGKFS-----FGFQCIDCAGST 94
DQ 913 HRDPRLYGGGCRPCPCPEGPGSGRHFATSCQDEYSQOIVCHRCAGYTGRLCEACAPGH 972
QY 95 F-----SGHEGHCKP 105
DQ 973 FGDPSPRGRCQLCECSGNIDPMDPDACDPTGQCLRLHHTGPHCAHCKP 1024

RESULT 13
FBN2_HUMAN
ID FBN2_HUMAN STANDARD; PRT; 2911 AA.
AC P35556;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE FIBRILLIN 2 PRECURSOR.
GN FBN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE-94165150; PubMed-8120105;
RA Zhang H., Apfeiroth S.D., Hu W., Davis E.C., Sanguineti C.,
RA Bonadio J., Mecham R.P., Ramirez F.;
RT "Structure and expression of fibrillin-2, a novel microfibrillar
RT component preferentially located in elastic matrices.";
RL J. Cell Biol. 124:855-863(1994).
[2]
RN SEQUENCE OF 752-1505 FROM N.A.
RX MEDLINE-91304567; PubMed-1852206;
RA Lee B., Godfrey M., Vitale E., Hori H., Mattei M.-G., Sarfarazi M.,
RA Tsipouras P., Ramirez F., Hollister D.;
RT "Linkage of Marfan syndrome and a phenotypically related disorder to
RT two different fibrillin genes.";
RL Nature 352:330-334(1991).
[3]
RN VARIANT'S CCA TYR-1252 AND SER-1433, AND VARIANT ILE-964.
RX MEDLINE-96083599; PubMed-7493032;
RA Putnam E.A., Zhang H., Ramirez F., Milewicz D.M.;
RT "Fibrillin-2 (FBN2) mutations result in the Marfan-like disorder,
RT congenital contractural arachnodactyly.";
RL Nat. Genet. 11:456-458(1995).
CC -!- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
CC THAT BINDS CALCIUM. FIBRILLIN-2-CONTAINING MICROFIBRILS REGULATE
CC THE EARLY PROCESS OF ELASTIC FIBER ASSEMBLY.
CC -!- DISEASE: DEFECTS IN FBN2 ARE THE CAUSE OF CONGENITAL CONTRACTURAL
CC ARACHNOIDACTYLY (CCA) (ALSO KNOWN AS BEALS SYNDROME). CCA IS
CC PHENOTYPICALLY SIMILAR TO MARFAN SYNDROME, BUT DOES NOT EFFECT THE
CC AORTA AND THE EYES.
CC -!- SIMILARITY: CONTAINS 43 CALCIUM-BINDING AND 4 NON-CALCIUM BINDING
CC EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U03272; AAA18950.1;
DR EMBL; X62009; -; NOT_ANNOTATED_CDS.
DR PIR; S17063; S17063.
DR PIR; S31101; S31101.
DR HSSP; P35555; 1EMO.
DR MIM; 121050; -;
DR InterPro; IPR000152; -;
DR InterPro; IPR000561; -;
DR InterPro; IPR001438; -;
DR InterPro; IPR001881; -;
DR InterPro; IPR002212; -;
DR Pfam; PF000008; EGF_46;
DR Pfam; PF00683; TB; 9;
DR PRINTS; PR00010; EGFBL00D.
DR PROSITE; PS00010; ASX_HYDROXYL; 43.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 37.
DR PROSITE; PS01187; EGF_CA; 43.
DR Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;
DR Repeat; Signal; Multigene family; Disease mutation; Polymorphism.
FT SIGNAL 1 28
FT CHAIN 29 2911 FIBRILLIN 2.
FT DOMAIN 111 142 EGF-LIKE 1, NON-CALCIUM BINDING.
FT DOMAIN 145 176 EGF-LIKE 2, NON-CALCIUM BINDING.
FT DOMAIN 176 207 EGF-LIKE 3, NON-CALCIUM BINDING.
FT DOMAIN 275 316 EGF-LIKE 4, CALCIUM-BINDING.
FT DOMAIN 317 358 EGF-LIKE 5, CALCIUM-BINDING.
FT REPEAT 359 425 TGFBP 1.
FT DOMAIN 493 533 EGF-LIKE 6, NON-CALCIUM BINDING.
FT DOMAIN 534 573 EGF-LIKE 7, CALCIUM-BINDING.
FT DOMAIN 574 615 EGF-LIKE 8, CALCIUM-BINDING.
FT DOMAIN 616 656 EGF-LIKE 9, CALCIUM-BINDING.
FT DOMAIN 657 697 EGF-LIKE 10, CALCIUM-BINDING.

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DR	InterPro; IPR000822; -	FT	DISULFID	153	164	BY SIMILARITY.
DR	InterPro; IPR001436; -	FT	DISULFID	166	175	BY SIMILARITY.
DR	InterPro; IPR001881; -	FT	DISULFID	180	190	BY SIMILARITY.
DR	InterPro; IPR002212; -	FT	DISULFID	184	196	BY SIMILARITY.
DR	Pfam; PF00008; EGF; 46.	FT	DISULFID	198	207	BY SIMILARITY.
DR	Pfam; PF00683; TB; 9.	FT	DISULFID	280	292	BY SIMILARITY.
DR	PRINTS; PR00010; EGFBL00D.	FT	DISULFID	287	301	BY SIMILARITY.
DR	PROSITE; PS00010; ASX-HYDROXYL; 43.	FT	DISULFID	303	316	BY SIMILARITY.
DR	PROSITE; PS00022; EGF_1; 2.	FT	DISULFID	322	334	BY SIMILARITY.
DR	PROSITE; PS01186; EGF_2; 36.	FT	DISULFID	329	343	BY SIMILARITY.
DR	PROSITE; PS01187; EGF_CA; 43.	FT	DISULFID	345	358	BY SIMILARITY.
KW	Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;	FT	DISULFID	491	503	BY SIMILARITY.
KW	Repeat; Signal; Multigene family.	FT	DISULFID	498	512	BY SIMILARITY.
FT	SIGNAL 1 28	FT	DISULFID	514	526	BY SIMILARITY.
FT	CHAIN 29 2907	FT	DISULFID	532	542	BY SIMILARITY.
FT	POTENTIAL.	FT	DISULFID	553	566	BY SIMILARITY.
FT	FIBRILLIN 2.	FT	DISULFID	572	584	BY SIMILARITY.
FT	EGF-LIKE 1, NON-CALCIUM BINDING.	FT	DISULFID	579	593	BY SIMILARITY.
FT	EGF-LIKE 2, NON-CALCIUM BINDING.	FT	DISULFID	608	625	BY SIMILARITY.
FT	EGF-LIKE 3, NON-CALCIUM BINDING.	FT	DISULFID	614	625	BY SIMILARITY.
FT	EGF-LIKE 4, CALCIUM-BINDING.	FT	DISULFID	620	634	BY SIMILARITY.
FT	EGF-LIKE 5, CALCIUM-BINDING.	FT	DISULFID	636	649	BY SIMILARITY.
FT	TGFBBP 1.	FT	DISULFID	655	666	BY SIMILARITY.
FT	EGF-LIKE 6, NON-CALCIUM BINDING.	FT	DISULFID	661	675	BY SIMILARITY.
FT	EGF-LIKE 7, CALCIUM-BINDING.	FT	DISULFID	677	690	BY SIMILARITY.
FT	EGF-LIKE 8, CALCIUM-BINDING.	FT	DISULFID	765	777	BY SIMILARITY.
FT	EGF-LIKE 9, CALCIUM-BINDING.	FT	DISULFID	772	786	BY SIMILARITY.
FT	EGF-LIKE 10, CALCIUM-BINDING.	FT	DISULFID	788	801	BY SIMILARITY.
FT	TGFBBP 2.	FT	DISULFID	807	819	BY SIMILARITY.
FT	EGF-LIKE 11, CALCIUM-BINDING.	FT	DISULFID	814	828	BY SIMILARITY.
FT	EGF-LIKE 12, CALCIUM-BINDING.	FT	DISULFID	830	843	BY SIMILARITY.
FT	EGF-LIKE 13, CALCIUM-BINDING.	FT	DISULFID	849	859	BY SIMILARITY.
FT	EGF-LIKE 14, CALCIUM-BINDING.	FT	DISULFID	854	868	BY SIMILARITY.
FT	TGFBBP 3.	FT	DISULFID	870	883	BY SIMILARITY.
FT	EGF-LIKE 15, CALCIUM-BINDING.	FT	DISULFID	952	964	BY SIMILARITY.
FT	EGF-LIKE 16, CALCIUM-BINDING.	FT	DISULFID	959	973	BY SIMILARITY.
FT	EGF-LIKE 17, CALCIUM-BINDING.	FT	DISULFID	1077	1082	BY SIMILARITY.
FT	EGF-LIKE 18, CALCIUM-BINDING.	FT	DISULFID	1091	1091	BY SIMILARITY.
FT	EGF-LIKE 19, CALCIUM-BINDING.	FT	DISULFID	1112	1124	BY SIMILARITY.
FT	EGF-LIKE 20, CALCIUM-BINDING.	FT	DISULFID	1119	1133	BY SIMILARITY.
FT	EGF-LIKE 21, CALCIUM-BINDING.	FT	DISULFID	1135	1149	BY SIMILARITY.
FT	EGF-LIKE 22, CALCIUM-BINDING.	FT	DISULFID	1155	1167	BY SIMILARITY.
FT	EGF-LIKE 23, CALCIUM-BINDING.	FT	DISULFID	1162	1176	BY SIMILARITY.
FT	EGF-LIKE 24, CALCIUM-BINDING.	FT	DISULFID	1178	1191	BY SIMILARITY.
FT	EGF-LIKE 25, CALCIUM-BINDING.	FT	DISULFID	1197	1209	BY SIMILARITY.
FT	EGF-LIKE 26, CALCIUM-BINDING.	FT	DISULFID	1204	1218	BY SIMILARITY.
FT	TGFBBP 4.	FT	DISULFID	1220	1233	BY SIMILARITY.
FT	EGF-LIKE 27, CALCIUM-BINDING.	FT	DISULFID	1239	1250	BY SIMILARITY.
FT	EGF-LIKE 28, CALCIUM-BINDING.	FT	DISULFID	1246	1259	BY SIMILARITY.
FT	TGFBBP 5.	FT	DISULFID	1261	1274	BY SIMILARITY.
FT	EGF-LIKE 29, CALCIUM-BINDING.	FT	DISULFID	1280	1292	BY SIMILARITY.
FT	EGF-LIKE 30, CALCIUM-BINDING.	FT	DISULFID	1287	1301	BY SIMILARITY.
FT	EGF-LIKE 31, CALCIUM-BINDING.	FT	DISULFID	1303	1316	BY SIMILARITY.
FT	EGF-LIKE 32, CALCIUM-BINDING.	FT	DISULFID	1322	1334	BY SIMILARITY.
FT	EGF-LIKE 33, CALCIUM-BINDING.	FT	DISULFID	1334	1343	BY SIMILARITY.
FT	EGF-LIKE 34, CALCIUM-BINDING.	FT	DISULFID	1345	1358	BY SIMILARITY.
FT	EGF-LIKE 35, CALCIUM-BINDING.	FT	DISULFID	1364	1377	BY SIMILARITY.
FT	TGFBBP 6.	FT	DISULFID	1371	1386	BY SIMILARITY.
FT	EGF-LIKE 36, CALCIUM-BINDING.	FT	DISULFID	1388	1399	BY SIMILARITY.
FT	EGF-LIKE 37, CALCIUM-BINDING.	FT	DISULFID	1405	1418	BY SIMILARITY.
FT	EGF-LIKE 38, CALCIUM-BINDING.	FT	DISULFID	1412	1427	BY SIMILARITY.
FT	EGF-LIKE 39, CALCIUM-BINDING.	FT	DISULFID	1429	1440	BY SIMILARITY.
FT	EGF-LIKE 40, CALCIUM-BINDING.	FT	DISULFID	1446	1458	BY SIMILARITY.
FT	TGFBBP 7.	FT	DISULFID	1453	1467	BY SIMILARITY.
FT	EGF-LIKE 41, CALCIUM-BINDING.	FT	DISULFID	1469	1482	BY SIMILARITY.
FT	EGF-LIKE 42, CALCIUM-BINDING.	FT	DISULFID	1488	1499	BY SIMILARITY.
FT	EGF-LIKE 43, CALCIUM-BINDING.	FT	DISULFID	1494	1508	BY SIMILARITY.
FT	EGF-LIKE 44, CALCIUM-BINDING.	FT	DISULFID	1510	1523	BY SIMILARITY.
FT	EGF-LIKE 45, CALCIUM-BINDING.	FT	DISULFID	1529	1540	BY SIMILARITY.
FT	EGF-LIKE 46, CALCIUM-BINDING.	FT	DISULFID	1535	1549	BY SIMILARITY.
FT	EGF-LIKE 47, CALCIUM-BINDING.	FT	DISULFID			
FT	BY SIMILARITY.	FT	DISULFID			
FT	BY SIMILARITY.	FT	DISULFID			
FT	BY SIMILARITY.	FT	DISULFID			

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FT DISULFID 1551 1564 BY SIMILARITY.
FT DISULFID 1647 1659 BY SIMILARITY.
FT DISULFID 1654 1668 BY SIMILARITY.
FT DISULFID 1670 1683 BY SIMILARITY.
FT DISULFID 1689 1701 BY SIMILARITY.
FT DISULFID 1696 1710 BY SIMILARITY.
FT DISULFID 1712 1725 BY SIMILARITY.
FT DISULFID 1805 1817 BY SIMILARITY.

Query Match 14.8%; Score 105.5; DB 1; Length 2907;
Best Local Similarity 26.8%; Pred. No. 0.027;
Matches 33; Conservative 11; Mismatches 40; Indels 39; Gaps 8;

QY 9 CGPGRLLLTGTDAKCC-----RVHTTRCRDYPGECCSEWDCMCVQPFHCG 57
Db 677 CPPG---LAVGDRGVCDVTHMRSTCYGEIKGKGVCRPFPGAVTKSE--CCCANPDYGF 731

QY 58 DPCCTCRHPCPGGVQVSGQKFSFGF-----QC-ID---CAGS---TFSGGHE 100
Db 732 EPC-----QPCPAKNSAEFHGLCSSGIGITVDGRDINECALDPDICANGICENLRGTYR 785

QY 101 GNC 103
Db 786 CMC 788

RESULT 12
ID LMB2_HUMAN STANDARD; PRT; 1798 AA.
AC P55268; Q16321;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ).
GN LMB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95213013; PubMed=7698745;
RA Wever U.M., Gerecke D.R., Durkin M.E., Kurtz K.S., Mattei M.-G.,
RA Champlaud M.F., Burgess R.E., Albrechtsen R.;
RT "Human beta 2 chain of laminin (formerly S chain): cDNA cloning,
RT chromosomal localization, and expression in carcinomas.";
RL Genomics 24:243-252(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95316263; PubMed=7795887;
RA Iivanainen A., Vuolteenaho R., Sainio K., Eddy R., Shows T.B.,
RA Sariola H., Tryggvason K.;
RT "The human laminin beta 2 chain (S-laminin): structure, expression in
RT fetal tissues and chromosomal assignment of the LMB2 gene.";
RL Matrix Biol. 14:489-497(1995).
CC -!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
CC IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
CC CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
CC -!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4
CC (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
CC COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC
CC CLEFT OF THE NEUROMUSCULAR JUNCTION.
CC -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -!- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
CC -!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).

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CC CC -!- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
CC CC -!- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
CC CC -----
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CC CC -----
CC CC EMBL; Z68155; CA92279.1; -.
CC CC EMBL; Z68156; CA92279.1; JOINED.
CC CC EMBL; X75683; AAB36130.1; -.
CC CC EMBL; S77512; AAB34682.2; -.
CC CC HSP; P02468; 1KLO..
CC CC MIM; 150325; -.
CC CC InterPro; IPR000561; -.
CC CC InterPro; IPR001886; -.
CC CC InterPro; IPR002049; -.
CC CC Pfam; PF00053; laminin_EGF; 13.
CC CC PRINTS; PR00011; EGF_LAMININ.
CC CC PROSITE; PS00022; EGF_1; 10.
CC CC PROSITE; PS01186; EGF_2; 2.
CC CC PROSITE; PS01248; LAMININ_Type_EGF; 12.
CC KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
CC Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
CC FT SIGNAL 1 32 POTENTIAL.
CC FT CHAIN 33 1798 LAMININ BETA-2 CHAIN.
CC FT DOMAIN 33 280 LAMININ N-TERMINAL (DOMAIN VI).
CC FT DOMAIN 281 552 4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
CC V).
CC FT DOMAIN 283 346 LAMININ EGF-LIKE 1.
CC FT DOMAIN 347 409 LAMININ EGF-LIKE 2.
CC FT DOMAIN 410 469 LAMININ EGF-LIKE 3.
CC FT DOMAIN 470 521 LAMININ EGF-LIKE 4.
CC FT DOMAIN 522 552 LAMININ EGF-LIKE 5 (INCOMPLETE).
CC FT DOMAIN 553 781 LAMININ DOMAIN IV.
CC FT DOMAIN 782 1190 8 X LAMININ EGF-LIKE REPEATS (DOMAIN
CC III).
CC FT DOMAIN 783 830 LAMININ EGF-LIKE 6.
CC FT DOMAIN 831 876 LAMININ EGF-LIKE 7.
CC FT DOMAIN 877 926 LAMININ EGF-LIKE 8.
CC FT DOMAIN 927 985 LAMININ EGF-LIKE 9.
CC FT DOMAIN 986 1037 LAMININ EGF-LIKE 10.
CC FT DOMAIN 1038 1094 LAMININ EGF-LIKE 11.
CC FT DOMAIN 1095 1142 LAMININ EGF-LIKE 12.
CC FT DOMAIN 1143 1189 LAMININ EGF-LIKE 13.
CC FT DOMAIN 1190 1409 LAMININ EGF-LIKE 13.
CC FT DOMAIN 1410 1442 DOMAIN II.
CC FT DOMAIN 1443 1798 DOMAIN ALPHA.
CC FT DOMAIN 1253 1319 COILED COIL (POTENTIAL).
CC FT DOMAIN 1472 1526 COILED COIL (POTENTIAL).
CC FT DOMAIN 1577 1790 COILED COIL (POTENTIAL).
CC FT DISULFID 283 292 BY SIMILARITY.
CC FT DISULFID 285 310 BY SIMILARITY.
CC FT DISULFID 312 321 BY SIMILARITY.
CC FT DISULFID 324 344 BY SIMILARITY.
CC FT DISULFID 347 356 BY SIMILARITY.
CC FT DISULFID 349 374 BY SIMILARITY.
CC FT DISULFID 377 386 BY SIMILARITY.
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CC FT DISULFID 505 519 BY SIMILARITY.
CC FT DISULFID 785 795 BY SIMILARITY.
CC FT DISULFID 785 802 BY SIMILARITY.

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GN TNFRSF5 OR CD40.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RN [2]  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92105763; PubMed=1370315;  
 RA Torres R.M., Clark E.A.;  
 RT "Differential increase of an alternatively polyadenylated mRNA  
 species of murine CD40 upon B lymphocyte activation.";  
 RL J. Immunol. 148:620-626(1992).  
 RN [2]  
 RP REVISIONS.  
 RC STRAIN=BALB/C;  
 RA Torres R.M.;  
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=Liver;  
 RX MEDLINE=93094586; PubMed=1281194;  
 RA Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,  
 RA Howard M., Cockayne D.A.;  
 RT "Genomic structure and chromosomal mapping of the murine CD40 gene.";  
 RL J. Immunol. 149:3921-3926(1992).  
 CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
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 CC  
 DR EMBL; M83312; AAB08705.1; -  
 DR EMBL; M94126; AAA37404.1; -  
 DR EMBL; M94129; AAA37404.1; JOINED.  
 DR EMBL; M94128; AAA37404.1; JOINED.  
 DR EMBL; M94127; AAA37404.1; JOINED.  
 DR PIR; A46476; A46476.  
 DR HSP; P25942; ICDF.  
 DR MGI; MGI:88336; Tnfrsf5.  
 DR InterPro: IPR001368; -  
 DR Pfam; PF00020; TNFR\_C6; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00505; TNFR\_NGFR\_2; 4.  
 KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 289  
 FT DOMAIN 20 193  
 FT TRANSMEM 194 215  
 FT DOMAIN 216 289  
 FT DOMAIN 25 187  
 FT REPEAT 25 60  
 FT REPEAT 61 103  
 FT REPEAT 104 144  
 FT REPEAT 145 187  
 FT CARBOHYD 153 153  
 FT CARBOHYD 180 180  
 FT NON\_TER 289  
 SQ SEQUENCE 289 AA; 32111 MW; C791CB6D2FEA574E CRC64;  
 Query Match 16.4%; Score 116.5; DB 1; Length 289;  
 Best Local Similarity 31.2%; Pred. No. 0.00048;  
 Matches 34; Conservative 6; Mismatches 58; Indels 11; Gaps 5;  
 QY 9 CGPGRLLLTGTDCRCRVHTRCCRDYPG-----EECCSEWDCMCVQPE-FHCGRPCCTT 63  
 Db 62 CDSGEFSQAWNRETRC---HQHRCPEPNOGLRVKRGTAESDTVCTCKREGHCTSKDCEA 118  
 QY 64 C-RHPCPPGGVQSGKFSFGFCIDCASGTFSGGHE--GHCKPWTDC 109

Db 119 CAQHTPCIFGFGVMEATETDTVCHPCPVGFESNQSSLFKEKCPWTSC 167  
 RESULT 9  
 CD40\_BOVIN  
 ID CD40\_BOVIN STANDARD; PRT; 269 AA.  
 AC Q28203;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).  
 GN TNFRSF5 OR CD40.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97281252; PubMed=91355560;  
 RA Hirano A., Brown W.C., Estes D.M.;  
 RT "Cloning, expression and biological function of the bovine CD40  
 homologue: role in B-lymphocyte growth and differentiation in  
 cattle.";  
 RL Immunology 90:294-300(1997).  
 CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC  
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 CC  
 DR EMBL; U57745; AAC48710.1; -  
 DR HSP; P25942; ICDF.  
 DR InterPro: IPR001368; -  
 DR Pfam; PF00020; TNFR\_C6; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00505; TNFR\_NGFR\_2; 1.  
 KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 >269  
 FT DOMAIN 20 193  
 FT TRANSMEM 194 215  
 FT DOMAIN 216 >269  
 FT DOMAIN 25 187  
 FT REPEAT 25 60  
 FT REPEAT 61 103  
 FT REPEAT 104 144  
 FT REPEAT 145 187  
 FT CARBOHYD 153 153  
 FT CARBOHYD 180 180  
 FT NON\_TER 269  
 SQ SEQUENCE 269 AA; 29983 MW; 746903F30F95F387 CRC64;  
 Query Match 15.5%; Score 110.5; DB 1; Length 269;  
 Best Local Similarity 29.8%; Pred. No. 0.0016;  
 Matches 34; Conservative 7; Mismatches 60; Indels 13; Gaps 5;  
 QY 9 CGPGRLLLTGTDCRCRVHTRCCRDYPGEECCSEWDC-----CMCVQPEFHCGRPCCT 62  
 Db 62 CGKGEFLSTWREKVC---HEHRYCNPNLGLRIQSEGLTNTDTCVCVEQ-HCTSHTE 117  
 QY 63 TCRHHP-CPPGGVQSGKFSFGFCIDCASGTFSGGHEG--HCKPWTDCQTG 113  
 Db 118 SCTPHSLCLPGFGVKQIATGLLDTVCEPCPLGFGFSSVSSAFKCHRWTCERKG 171

RESULT 10  
CD40\_HUMAN STANDARD; PRT; 277 AA.  
ID CD40\_HUMAN  
AC P25942;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)  
DE (TUMOR NECROSIS FACTOR RECEPTOR 5).  
GN TNFRSF5 OR CD40.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89356608; PubMed=2475341;  
RA Stamenkovic I., Clark E.A., Seed B.;  
RT "A B-lymphocyte activation molecule related to the nerve growth  
RT factor receptor and induced by cytokines in carcinomas.";  
RL EMBO J. 8:1403-1410(1989).  
RN [2]  
RP 3D-STRUCTURE MODELING OF 24-144.  
RX MEDLINE=97189482; PubMed=9037712;  
RA Bajorath J., Aruffo A.;  
RT "Construction and analysis of a detailed three-dimensional model of  
RT the ligand binding domain of the human B cell receptor CD40L";  
RL Proteins 27:59-70(1997).  
RN [3]  
RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.  
RX MEDLINE=98266353; PubMed=9605317;  
RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,  
RA Zheng Z., Naismith J.H., Thomas D.;  
RT "The role of polar interactions in the molecular recognition of CD40L  
RT with its receptor CD40L";  
RL Protein Sci. 7:1124-1135(1998).  
CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -!- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.  
CC -!- SIMILARITY: CONTAINS A LA-NGER/TNFR-TYPE CYSTEINE-RICH REGION.  
CC -!- DATABASE: NAME-PROW; NOTE-CD guide CD40 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".  
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CC  
CC EMBL; X60592; CAA43045.1; -  
CC PIR; S04460; S04460.  
CC PDB; 1CDF; 01-APR-97.  
CC MIM; 109535; -  
CC InterPro; IPR001368; -  
CC Pfam; PF00020; TNFR\_c6; 4.  
CC PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
CC PROSITE; PS00050; TNFR\_NGFR\_2; 4.  
KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;  
KW 3D-structure.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 277 CD40L RECEPTOR.  
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 194 215 POTENTIAL.  
FT DOMAIN 216 277 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 25 187 4 X TNFR-CYS.  
FT REPEAT 25 60 TNFR-CYS 1.  
FT REPEAT 61 103 TNFR-CYS 2.  
FT REPEAT 104 144 TNFR-CYS 3.  
FT REPEAT 145 187 TNFR-CYS 4.  
FT DISULFID 26 37

FT DISULFID 38 51  
FT DISULFID 41 59  
FT DISULFID 62 77  
FT DISULFID 83 103  
FT DISULFID 105 119  
FT DISULFID 111 116  
FT DISULFID 125 143  
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 277 AA; 30619 MW; BC8776EC2C4A5680 CRC64;  
  
Query Match 15.3%; Score 108.5; DB 1; Length 277;  
Best Local Similarity 29.4%; Pred. No. 0.0025;  
Matches 32; Conservative 8; Mismatches 58; Indels 11; Gaps 5;  
  
QY 9 CGPCRLLLTGTGTDARCCRVHTTRCCRDYPG---EECCSEWDCMCVQPE-FHCGDPCCTT 63  
DB 62 CGSEFLDTWNRTHC---HQHKYCDPNLGRVQOKGTSETDTICTCEGWHCTSEACES 118  
QY 64 C-RHHPGPPGGVQSGQKFSFGFCIDCAGTFSGGHEG--HCKPWTDC 109  
DB 119 CVLHRSCTPGGVKQIATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSC 167  
  
RESULT 11  
FBN2\_MOUSE STANDARD; PRT; 2907 AA.  
ID FBN2\_MOUSE  
AC O61555; O63957;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE FIBRILLIN 2 PRECURSOR.  
GN FBN2 OR FBN-2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95263670; PubMed=7744963;  
RA Zhang H., Hu W., Ramirez F.;  
RT "Developmental expression of fibrillin genes suggests heterogeneity  
RT of extracellular microfibrils";  
RL J. Cell Biol. 129:1165-1176(1995).  
RN [2]  
RP SEQUENCE OF 210-317 FROM N.A.  
RX MEDLINE=94140368; PubMed=8307578;  
RA Li X., Pereira L., Zhang H., Sanguinetti C., Ramirez F., Bonadio J.,  
RA Francke U.;  
RT "Fibrillin genes map to regions of conserved mouse/human synteny on  
RT mouse chromosomes 2 and 18";  
RL Genomics 18:667-672(1993).  
CC -!- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS  
CC THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE  
CC LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.  
CC -!- SIMILARITY: CONTAINS 43 CALCIUM-BINDING AND 4 NON-CALCIUM BINDING  
CC EGF-LIKE DOMAINS.  
CC -!- SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.  
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CC  
CC EMBL; L39790; AAA74908.1; -  
CC EMBL; S69359; AAC60685.1; -  
CC MGD; MGI:95490; Fbn2.  
CC InterPro; IPR000152; -  
CC InterPro; IPR000561; -

FT	DOMAIN	36	283	LAMININ N-TERMINAL (DOMAIN VI).
FT	DOMAIN	286	555	4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN V).
FT	DOMAIN	286	349	LAMININ EGF-LIKE 1.
FT	DOMAIN	350	412	LAMININ EGF-LIKE 2.
FT	DOMAIN	413	472	LAMININ EGF-LIKE 3.
FT	DOMAIN	473	524	LAMININ EGF-LIKE 4.
FT	DOMAIN	525	555	LAMININ EGF-LIKE 5 (INCOMPLETE).
FT	DOMAIN	556	785	LAMININ DOMAIN IV.
FT	DOMAIN	786	1192	8 X LAMININ EGF-LIKE REPEATS (DOMAIN III).
FT	DOMAIN	786	833	LAMININ EGF-LIKE 6.
FT	DOMAIN	834	879	LAMININ EGF-LIKE 7.
FT	DOMAIN	880	929	LAMININ EGF-LIKE 8.
FT	DOMAIN	930	988	LAMININ EGF-LIKE 9.
FT	DOMAIN	989	1040	LAMININ EGF-LIKE 10.
FT	DOMAIN	1041	1097	LAMININ EGF-LIKE 11.
FT	DOMAIN	1098	1145	LAMININ EGF-LIKE 12.
FT	DOMAIN	1146	1192	LAMININ EGF-LIKE 13.
FT	DOMAIN	1193	1412	DOMAIN II.
FT	DOMAIN	1413	1445	DOMAIN ALPHA.
FT	DOMAIN	1446	1801	DOMAIN I.
FT	DOMAIN	1259	1306	COILED COIL (POTENTIAL).
FT	DOMAIN	1475	1529	COILED COIL (POTENTIAL).
FT	DOMAIN	1576	1793	BY SIMILARITY.
FT	DISULFID	286	295	BY SIMILARITY.
FT	DISULFID	288	313	BY SIMILARITY.
FT	DISULFID	315	324	BY SIMILARITY.
FT	DISULFID	327	347	BY SIMILARITY.
FT	DISULFID	350	359	BY SIMILARITY.
FT	DISULFID	352	377	BY SIMILARITY.
FT	DISULFID	380	389	BY SIMILARITY.
FT	DISULFID	392	410	BY SIMILARITY.
FT	DISULFID	413	426	BY SIMILARITY.
FT	DISULFID	415	441	BY SIMILARITY.
FT	DISULFID	443	452	BY SIMILARITY.
FT	DISULFID	455	470	BY SIMILARITY.
FT	DISULFID	473	487	BY SIMILARITY.
FT	DISULFID	475	494	BY SIMILARITY.
FT	DISULFID	496	505	BY SIMILARITY.
FT	DISULFID	508	522	BY SIMILARITY.
FT	DISULFID	786	798	BY SIMILARITY.
FT	DISULFID	788	805	BY SIMILARITY.
FT	DISULFID	807	816	BY SIMILARITY.
FT	DISULFID	819	831	BY SIMILARITY.
FT	DISULFID	834	846	BY SIMILARITY.
FT	DISULFID	836	853	BY SIMILARITY.
FT	DISULFID	855	864	BY SIMILARITY.
FT	DISULFID	867	877	BY SIMILARITY.
FT	DISULFID	880	889	BY SIMILARITY.
FT	DISULFID	882	896	BY SIMILARITY.
FT	DISULFID	899	908	BY SIMILARITY.
FT	DISULFID	911	927	BY SIMILARITY.
FT	DISULFID	930	946	BY SIMILARITY.
FT	DISULFID	932	957	BY SIMILARITY.
FT	DISULFID	959	968	BY SIMILARITY.
FT	DISULFID	971	986	BY SIMILARITY.
FT	DISULFID	989	1003	BY SIMILARITY.
FT	DISULFID	991	1010	BY SIMILARITY.
FT	DISULFID	1013	1022	BY SIMILARITY.
FT	DISULFID	1025	1038	BY SIMILARITY.
FT	DISULFID	1098	1110	BY SIMILARITY.
FT	DISULFID	1100	1117	BY SIMILARITY.
FT	DISULFID	1119	1128	BY SIMILARITY.
FT	DISULFID	1131	1143	BY SIMILARITY.
FT	DISULFID	1146	1158	BY SIMILARITY.
FT	DISULFID	1148	1165	BY SIMILARITY.
FT	DISULFID	1167	1176	BY SIMILARITY.
FT	DISULFID	1179	1190	BY SIMILARITY.
FT	DISULFID	1193	1193	INTERCHAIN (PROBABLE).
FT	DISULFID	1196	1196	INTERCHAIN (PROBABLE).
FT	DISULFID	1800	1800	INTERCHAIN (PROBABLE).
FT	CARBOHYD	251	251	N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 17.2%; Score 122; DB 1; Length 1801;  
Best Local Similarity 27.5%; Pred. No. 0.0006;  
Matches 47; Conservative 3; Mismatches 35; Indels 86; Gaps 10;

QY	5	GGPGCGP----	GRLLLGTTDARCCRVHTTRC--	CRDYPGEECCSEWDCMCVOPFHC	GD 58
Db	873	GFPCNRCPCVNCGR-----	ADECDHAHTCAGLCGRDYGHECHER	---CI-AGPH-GD	918
QY	59	PCCT-----	TCRHHPCPGQGVQSGKFS-----	FGQCIDCASGTF	95
Db	919	PRLPYGGQCRPCPCPRPG--	SQRHEATSHRDGYSQQIVCHCRAGYTG	LCRCACAPGHF	976
QY	96	-----	-----	SGHCHCKP	105
Db	977	GDPSKPGRCQCECSGNIDPTDP	GACDPHTGQCLRLHHTGPHGCHCKP	1027	

RESULT 7  
LMB2\_MOUSE  
ID LMB2\_MOUSE STANDARD; PRT; 1799 AA.  
AC Q61292; Q62182;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE LAMININ BETA-2 CHAIN PRECURSOR.  
GN LMB2 OR S-LAM OR LAMS.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/J;  
RX MEDLINE=96278760; PubMed=8662701;  
RA Durkin M.E., Gautam M., Loechel S., Sanes J.R., Merlie J.P.,  
RA Albrechtsen R., Wewer U.M.;  
RT "Structural organization of the human and mouse laminin beta2 chain  
genes, and alternative splicing at the 5' end of the human  
transcript.";  
RT J. Biol. Chem. 271:13407-13416(1996).  
RN [2]  
RP SEQUENCE OF 348-428 FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=94319092; PubMed=8043959;  
RA Aberdam D., Galliano M.F., Mattei M.-G., Ortonne J.P., Meneguzzi G.;  
RT "S-laminin gene (Lams) maps to F1 band of mouse chromosome 9.";  
RL Mamm. Genome 5:393-394(1994).  
RN [3]  
RP FUNCTION.  
RC STRAIN=129/J;  
RX MEDLINE=95191650; PubMed=7885444;  
RA Noakes P.G., Gautam M., Mudd J., Sanes J.R., Merlie J.P.;  
RT "Aberrant differentiation of neuromuscular junctions in mice lacking  
s-laminin/laminin beta 2.";  
RL Nature 374:258-262(1995).  
CC -!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ  
IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF  
CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING  
WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.  
CC -!- FUNCTION: LAMININ-3 (S-LAMININ) REGULATES THE FORMATION OF MOTOR  
NERVE TERMINALS.  
CC -!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE  
DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND  
TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE

CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.  
 CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4  
 CC (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).  
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT  
 CC MEMBRANES (MAJOR COMPONENT).  
 CC -1- TISSUE SPECIFICITY: NEUROMUSCULAR SYNAPSE AND KIDNEY GLOMERULUS.  
 CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT  
 CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.  
 CC -1- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.  
 CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).  
 CC -1- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.  
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 CC -----  
 CC EMBL: U43541; AAC53535.1; -  
 CC DR EMBL: U42624; AAC53535.1; JOINED.  
 CC DR EMBL: X75928; CAA53532.1; -  
 CC DR HSSP: P02468; IKLO.  
 CC DR MGD; MGI:99916; Lamb2.  
 CC DR InterPro: IPR000561; -  
 CC DR InterPro: IPR001886; -  
 CC DR InterPro: IPR002049; -  
 CC DR Pfam: PF00053; laminin\_EGF; 13.  
 CC DR Pfam: PF00055; laminin\_Nterm; 1.  
 CC DR PRINTS; PRO0011; EGF\_LAMININ.  
 CC DR PROSITE; PS00022; EGF\_1; 10.  
 CC DR PROSITE; PS01186; EGF\_2; 2.  
 CC DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 12.  
 CC KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
 KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
 FT SIGNAL 1 35 POTENTIAL.  
 FT CHAIN 36 1799 LAMININ BETA-2 CHAIN.  
 FT DOMAIN 36 283 LAMININ N-TERMINAL (DOMAIN VI).  
 FT DOMAIN 284 555 4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN  
 FT V).  
 FT DOMAIN 286 349 LAMININ EGF-LIKE 1.  
 FT DOMAIN 350 412 LAMININ EGF-LIKE 2.  
 FT DOMAIN 413 472 LAMININ EGF-LIKE 3.  
 FT DOMAIN 473 524 LAMININ EGF-LIKE 4.  
 FT DOMAIN 525 555 LAMININ EGF-LIKE 5 (INCOMPLETE).  
 FT DOMAIN 556 782 LAMININ DOMAIN IV.  
 FT DOMAIN 783 1191 8 X LAMININ EGF-LIKE REPEATS (DOMAIN  
 FT III).  
 FT DOMAIN 784 831 LAMININ EGF-LIKE 6.  
 FT DOMAIN 832 877 LAMININ EGF-LIKE 7.  
 FT DOMAIN 878 927 LAMININ EGF-LIKE 8.  
 FT DOMAIN 928 986 LAMININ EGF-LIKE 9.  
 FT DOMAIN 987 1038 LAMININ EGF-LIKE 10.  
 FT DOMAIN 1039 1095 LAMININ EGF-LIKE 11.  
 FT DOMAIN 1096 1143 LAMININ EGF-LIKE 12.  
 FT DOMAIN 1144 1190 LAMININ EGF-LIKE 13.  
 FT DOMAIN 1191 1410 DOMAIN II.  
 FT DOMAIN 1411 1443 DOMAIN ALPHA.  
 FT DOMAIN 1444 1799 DOMAIN I.  
 FT DOMAIN 1257 1304 COILED COIL (POTENTIAL).  
 FT DOMAIN 1473 1527 COILED COIL (POTENTIAL).  
 FT DOMAIN 1577 1791 COILED COIL (POTENTIAL).  
 FT DISULFID 286 295 BY SIMILARITY.  
 FT DISULFID 288 313 BY SIMILARITY.  
 FT DISULFID 315 324 BY SIMILARITY.  
 FT DISULFID 327 347 BY SIMILARITY.  
 FT DISULFID 350 359 BY SIMILARITY.  
 FT DISULFID 352 377 BY SIMILARITY.  
 FT DISULFID 380 389 BY SIMILARITY.  
 FT DISULFID 392 410 BY SIMILARITY.  
 FT DISULFID 413 426 BY SIMILARITY.

FT DISULFID 415 441 BY SIMILARITY.  
 FT DISULFID 443 452 BY SIMILARITY.  
 FT DISULFID 455 470 BY SIMILARITY.  
 FT DISULFID 473 487 BY SIMILARITY.  
 FT DISULFID 475 494 BY SIMILARITY.  
 FT DISULFID 496 505 BY SIMILARITY.  
 FT DISULFID 508 522 BY SIMILARITY.  
 FT DISULFID 784 796 BY SIMILARITY.  
 FT DISULFID 786 803 BY SIMILARITY.  
 FT DISULFID 805 814 BY SIMILARITY.  
 FT DISULFID 817 829 BY SIMILARITY.  
 FT DISULFID 832 844 BY SIMILARITY.  
 FT DISULFID 834 851 BY SIMILARITY.  
 FT DISULFID 853 862 BY SIMILARITY.  
 FT DISULFID 865 875 BY SIMILARITY.  
 FT DISULFID 878 887 BY SIMILARITY.  
 FT DISULFID 880 894 BY SIMILARITY.  
 FT DISULFID 897 906 BY SIMILARITY.  
 FT DISULFID 909 925 BY SIMILARITY.  
 FT DISULFID 928 944 BY SIMILARITY.  
 FT DISULFID 930 955 BY SIMILARITY.  
 FT DISULFID 957 966 BY SIMILARITY.  
 FT DISULFID 969 984 BY SIMILARITY.  
 FT DISULFID 987 1001 BY SIMILARITY.  
 FT DISULFID 989 1008 BY SIMILARITY.  
 FT DISULFID 1011 1020 BY SIMILARITY.  
 FT DISULFID 1023 1036 BY SIMILARITY.  
 FT DISULFID 1096 1108 BY SIMILARITY.  
 FT DISULFID 1098 1115 BY SIMILARITY.  
 FT DISULFID 1117 1126 BY SIMILARITY.  
 FT DISULFID 1129 1141 BY SIMILARITY.  
 FT DISULFID 1144 1156 BY SIMILARITY.  
 FT DISULFID 1146 1163 BY SIMILARITY.  
 FT DISULFID 1165 1174 BY SIMILARITY.  
 FT DISULFID 1177 1188 BY SIMILARITY.  
 FT DISULFID 1191 1191 INTERCHAIN (PROBABLE).  
 FT DISULFID 1194 1194 INTERCHAIN (PROBABLE).  
 FT DISULFID 1798 1798 INTERCHAIN (PROBABLE).  
 FT CARBOHYD 251 251 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 371 371 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1086 1086 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1250 1250 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1309 1309 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1349 1349 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1500 1500 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 1799 AA; 196352 MW; 1F28967A67AEDE33 CRC64;  
 Query Match 16.5%; Score 117; DB 1; Length 1799;  
 Best Local Similarity 26.9%; Pred. No. 0.0017;  
 Matches 46; Conservative 4; Mismatches 35; Indels 86; Gaps 10;  
 Qy 5 GGPGCGP-----GRLLLTGTDTARCCRVHTTRC--CRDYPGECCSEWDCMVCQVPEFHCGD 58  
 Db 871 GFPCNRCPCVNGR-----ADECDTHTGACLCRDYTGGEHGER-----CI-AGFH-GD 916  
 Qy 59 PCCT--TCRHPPCPGQVSGQKFS-----FGQCIDCASGTF 95  
 Db 917 PLPLPGGQCRPCPCPEPG--SQRHFTSCHRDGYSQIVCHCRAGYGLRCACAPGPF 974  
 Qy 96 -----SGGHEGCKP 105  
 Db 975 GPSKPGRCQLCECSGNIDPMDPADCPHTGQCLRLCHNTEGPHGCGYCKP 1025  
 RESULT 8  
 CD40\_MOUSE STANDARD; PRT; 289 AA.  
 ID CD40\_MOUSE  
 AC P27512;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 13-JUL-1999 (Rel. 38, Last annotation update)  
 DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDM40).

-----  
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-----  
DR EMBL; J04492; AAA40167.1; -;  
DR EMBL; U02567; AAA93113.1; -;  
DR PIR; B32393; B32393.  
DR HSP; P25942; ICDF.  
DR MGD; MGI:1101059; Tnfrsf9.  
DR InterPro; IPR001368; -;  
DR Pfam; PF00020; TNFR\_C6; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; FALSE\_NEG.  
KW Receptor; Glycoprotein; Repeat; Signal; Transmembrane.  
FT SIGNAL 1 24  
FT CHAIN 25 256 4-1BB LIGAND RECEPTOR.  
FT DOMAIN 25 187 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 188 208 POTENTIAL.  
FT DOMAIN 209 256 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 17 159 4 X TNFR-CYS.  
FT REPEAT 17 45 TNFR-CYS 1.  
FT REPEAT 46 85 TNFR-CYS 2.  
FT REPEAT 86 117 TNFR-CYS 3.  
FT REPEAT 118 159 TNFR-CYS 4.  
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 256 AA; 27598 MW; 93A10D03C60813C4 CRC64;  
  
Query Match 19.7%; Score 140; DB 1; Length 256;  
Best Local Similarity 32.7%; Pred. No. 3.3e-06;  
Matches 36; Conservative 15; Mismatches 41; Indels 18; Gaps 7;  
  
QY 9 CGPGRLLGTGTARCRVHTTRCCRDYPGECSEW---DCMCVQPFHCGDCCTTC 64  
DB 47 CPPTFFSIGQPCNICRV---CAGFRKKFCSSTHNAECEIE-GFCLGFCQTCRC 101  
QY 65 RHHPCCPPGQVQSOGKFSFGQICDASGTFSGGH-EGHCKPWTDCQFG 113  
DB 102 -EKDCRPQQLTKG-----CKTCSLGTENDQNGTGVCRPWTNCSLDG 143  
  
RESULT 4  
ID 41BB\_HUMAN  
AC Q07011; STANDARD; PRT; 255 AA.  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE 4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB HOMOLOG)  
DE (T-CELL ANTIGEN ILA) (CD137 ANTIGEN).  
GN TNFRSF9 OR ILA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=94374434; PubMed=8088337;  
RA Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J.,  
RA Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.,  
RT "Molecular and biological characterization of human 4-1BB and its  
RT ligand";  
RL Eur. J. Immunol. 24:2219-2227(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;

RX MEDLINE=94085794; PubMed=8262389;  
RT Schwarz H., Tuckwell J., Lotz M.;  
RT "A receptor induced by lymphocyte activation (ILA): a new member of  
RT the human nerve-growth-factor/tumor-necrosis-factor receptor  
RT family";  
RL Gene 134:295-298(1993).  
RN [3]  
RP REVISION TO 107.  
RA Schwarz H.;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=95347766; PubMed=7622190;  
RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,  
RA Kwon B.S.;  
RT "Characterization of human homologue of 4-1BB and its ligand.";  
RL Immunol. Lett. 45:67-73(1995).  
CC -|- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY  
CC ACTIVE DURING T CELL ACTIVATION.  
CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -|- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T  
CC CELLS.  
CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
CC -|- DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw137.htm".  
CC -----  
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-----  
DR EMBL; U03397; AAA53133.1; -;  
DR EMBL; L12964; AAA62478.2; -;  
DR HSP; P19438; 1EXT.  
DR MIM; 602250; -;  
DR InterPro; IPR001368; -;  
DR Pfam; PF00020; TNFR\_C6; 2.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 1.  
KW Receptor; Glycoprotein; Repeat; Signal; Transmembrane.  
FT SIGNAL 1 17 POTENTIAL.  
FT CHAIN 18 255 4-1BB LIGAND RECEPTOR.  
FT DOMAIN 18 186 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 187 213 POTENTIAL.  
FT DOMAIN 214 255 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 47 159 3 X TNFR-CYS.  
FT REPEAT 47 86 TNFR-CYS 1.  
FT REPEAT 87 118 TNFR-CYS 2.  
FT REPEAT 119 159 TNFR-CYS 3.  
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 255 AA; 27899 MW; F3A563FE5EEF00460 CRC64;  
  
Query Match 19.1%; Score 135.5; DB 1; Length 255;  
Best Local Similarity 32.5%; Pred. No. 8.3e-06;  
Matches 37; Conservative 9; Mismatches 41; Indels 27; Gaps 7;  
  
QY 9 CGPGRLLGTGTARCRVHTTRCCRDYPG-----EECCS-----EWDCMVQPFHCGDP 59  
DB 48 CPPNSSFSSAGG--QRTCDI-----CRQCKGVFTRKESSTNAECD---TFGFHCLGA 97  
QY 60 CCTTCRHPCPGQVQSOGKFSFGQICDASGTFSGGHGCKPWTDCQFG 113  
DB 98 GCSMC-EQCKQGGQLTKG-----CKDCFGFTNDQKRGICRPWTNCSLDG 143  
  
RESULT 5  
OX40\_HUMAN

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ID   OX40_HUMAN          STANDARD;              PRT;      277 AA.
AC   P43689; Q13663;
DT   01-NOV-1995 (Rel. 32, Created)
DD   01-NOV-1995 (Rel. 32, Last sequence update)
DE   01-OCT-2000 (Rel. 40, Last annotation update)
DE   OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX=TRANSCRIPTIIONALLY
DE   ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).
DE   TNFRSF4 OR TXGPFIL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94170844; PubMed=7510240;
RA   Latza U., Duerkop H., Schnittger S., Ringeling J., Eitelbach F.,
RA   Hummel M., Fonatsch C., Stein H.;
RT   "The human OX40 homolog: cDNA structure, expression and chromosomal
RT   assignment of the ACT35 antigen.";
RL   Eur. J. Immunol. 24:677-683(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95219871; PubMed=7704935;
RA   Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A.,
RA   Watson M.L., Selkin M.F., Clifford K.N., Grabstein K., Alderson M.R.;
RT   "Identification of OX40 ligand and preliminary characterization of
RT   its activities on OX40 receptor.";
RL   Circ. Shock 44:30-34(1994).
CC   -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC   -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -1- SIMILARITY: CONTAINS A LA-NGF/TNFR-TYPE CYSTEINE-RICH REGION.
CC   -1- DATABASE: NAME=PROW; NOTE=CD guide CD134 entry;
CC   WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd134.htm".
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CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; X75962; CAA53576.1; --
DR   EMBL; S76792; AAB33944.1; ALT_INIT.
DR   HSP; P25942; ICDF.
DR   MM; 600315; -.
DR   InterPro; IPR001368; -.
DR   Pfam; PF00020; TNFR_C6; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW   Signal.
FT   SIGNAL                     1..28                      POTENTIAL.
FT   CHAIN                      29..277                    OX40L RECEPTOR.
FT   DOMAIN                     29..214                    EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM                  215..235                    POTENTIAL.
FT   DOMAIN                     236..277                    CYTOPLASMIC (POTENTIAL).
FT   DOMAIN                     30..169                    4 x TNFR-CYS.
FT   REPEAT                     30..65                     TNFR-CYS 1.
FT   REPEAT                     66..107                    TNFR-CYS 2.
FT   REPEAT                     108..126                   TNFR-CYS 3 (INCOMPLETE).
FT   REPEAT                     127..167                   TNFR-CYS 4.
FT   CARBOHYD                   146..146                   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD                   160..160                   N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE                277 AA; 29340 MW; 49F15525941550BF CRC64;
Query Match                                17.4%; Score 123.5; DB 1; Length 277;
Best Local Similarity 31.5%; Pred.No. 0.00011;
Matches 35; Conservative 5; Mismatches 60; Indels 11; Gaps 4;
QY    9 CGPGRLLGTGDARCCRVHTTCRRDPYG--EECCSEWDGM-CVQPEFHCGD---PCQT 62

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46 CRP-----GNCWVSRCSRSQNTVCRCPCGPYNDVSVSKPKCTCWTNLSGSRKQLCT 100

63 TCRHPHCPGGVGQSOGKFSFGFCIDCASGTFFSGHGHCCKPWTDCTQCG 113  
:  
:  
ATQDTCRCRAGTQPLDSYKPGVDCAPCPPGHFSPGDACKPWNTCTLAG 151

RESULT 6  
LMB2\_RAT LMB2\_RAT STANDARD; PRT; 1801 AA.  
AC P15800;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3).  
GN LAMB2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_Taxid=10116;  
[1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Liver;  
RC MEDLINE=49139410; Pubmed=2922051;  
RA Hunter D.D., Shah V., Merlie J.P., Sanes J.R.;  
RX "A laminin-like adhesive protein concentrated in the synaptic cleft  
of the neuromuscular junction.";  
RT Nature 338:229-234(1989).  
RL  
CC -1- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ  
CC IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF  
CC CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING  
CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.  
CC -1- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE  
CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND  
CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE  
CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.  
CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4  
CC (S-MEROBIN), AND LAMININ-7 (KS-LAMININ).  
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
CC -1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR  
CC COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC  
CC CLEFT OF THE NEUROMUSCULAR JUNCTION.  
CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT  
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.  
CC -1- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.  
CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).  
CC -1- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.  
CC -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.  
CC  
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CC -----  
DR EMBL; X16563; CAA34561.1; -.  
DR PIR; S03539; MMRTS.  
DR HSSP; P02468; IKLO.  
DR InterPro; IPR000561; -.  
DR InterPro; IPR001886; -.  
DR InterPro; IPR002049; -.  
DR Pfam; PF00053; laminin\_EGF\_13.  
DR Pfam; PF00055; laminin\_Nterm; 1.  
DR PRINTS; PR00011; EGLFLAMININ.  
DR PROSITE; PS00022; EGF\_1; 10.  
DR PROSITE; PS01186; EGF-2; 2.  
DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 12.  
DR Glycoproteins; Basement membrane; Extracellular matrix; Coiled coil;  
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
FT SIGNAL 1 35  
FT FT 36 1801 LAMININ BETA-2 CHAIN.

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:15:22 ; Search time 43.78 Seconds  
(without alignments)  
89.199 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_26\_139

Perfect score: 711

Sequence: 1 QPRTGPGCGPGRLLGTCT.....FSGHGEHCCKPWTDCQTQGF 114

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	143	20.1	272	1	OX40_MOUSE
2	141	19.8	271	1	OX40_RAT
3	140	19.7	256	1	41BB_MOUSE
4	135.5	19.1	255	1	41BB_HUMAN
5	123.5	17.4	277	1	OX40_HUMAN
6	122	17.2	1801	1	LMB2_RAT
7	117	16.5	1799	1	LMB2_MOUSE
8	116.5	16.4	289	1	CD40_MOUSE
9	110.5	15.5	269	1	CD40_BOVIN
10	108.5	15.3	277	1	CD40_HUMAN
11	105.5	14.8	2907	1	FBN2_MOUSE
12	104	14.6	1798	1	LMB2_HUMAN
13	103.5	14.6	2911	1	FBN2_HUMAN
14	99.5	14.0	2569	1	LMA3_MOUSE
15	98	13.8	3635	1	LMA3_MOUSE
16	97.5	13.7	1713	1	LMA3_HUMAN
17	96.5	13.6	581	1	IRR_RAT
18	95.5	13.4	1786	1	LMB1_HUMAN
19	94.5	13.3	435	1	TNRC_HUMAN
20	94.5	13.3	1297	1	IRR_HUMAN
21	93.5	13.2	212	1	AGI_HORVU
22	93.5	13.2	1786	1	LMB1_MOUSE
23	92.5	13.0	1370	1	IGLR_RAT
24	91.5	12.9	186	1	AGI3_WHEAT
25	91	12.8	2213	1	SORL_MOUSE
26	90.5	12.7	1210	1	EGFR_MOUSE
27	90.5	12.7	4289	1	TENX_HUMAN
28	90	12.7	169	1	KRUA_HUMAN
29	90	12.7	227	1	AGL_ORYSA
30	89	12.5	116	1	MCS_HUMAN
31	89	12.5	755	1	COMP_RAT
32	89	12.5	846	1	ITBX_DROME
33	88.5	12.4	212	1	AGIL_WHEAT

RESULT 1

ID	OX40_MOUSE	STANDARD;	PRT;	272 AA.
AC	P47741;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DE	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).			
GN	TNFRSF4 OR TXGP1 OR OX40.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RP	SEQUENCE FROM N.A.			
RN	[1]			
RC	STRAIN=BA1B/C;			
RX	MEDLINE=94044750; PubMed=8228223;			
RA	Calderhead D.M., Buhlmann J.E., van den Bortwegh A.J.,			
RA	Claassen E., Noelle R.J., Fell H.;			
RT	"Cloning of mouse OX40: a T cell activation marker that may mediate			
RT	T-B cell interactions."			
RL	J. Immunol. 151:5261-5271(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95255413; PubMed=7737295;			
RA	Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,			
RA	Barclay A.N.;			
RT	"Gene structure and chromosomal localization of the mouse homologue			
RT	of rat OX40 protein."			
RL	Eur. J. Immunol. 25:926-930(1995).			
CC	-!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.			
CC	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
CC	-----			
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CC	-----			
DR	EMBL; 221674; CAA79772.1; -			
DR	EMBL; X85214; CAA59476.1; -			
DR	HSSP; P25942; 1CDF			
DR	MGI; 104512; Tnfrsf4.			
DR	InterPro; IPR001368; -			
DR	Pfam; PF00020; TNFR_C6; 3.			
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.			
DR	PROSITE; PS00505; TNFR_NGFR_2; 2.			
KW	Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;			
KW	Signal.			
FT	SIGNAL	1	19	POTENTIAL.
FT	CHAIN	20	272	OX40L RECEPTOR.
FT	DOMAIN	20	211	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	212	236	POTENTIAL.

ALIGNMENTS

FT	CHAIN	20	271	OX40L RECEPTOR.
FT	DOMAIN	20	210	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	211	235	POTENTIAL.
FT	DOMAIN	236	271	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	25	164	4 X TNFR-CYS.
FT	REPEAT	25	60	TNFR-CYS 1.
FT	REPEAT	61	102	TNFR-CYS 2.
FT	REPEAT	103	123	TNFR-CYS 3 (INCOMPLETE).
FT	REPEAT	124	164	TNFR-CYS 4.
FT	CARBOHYD	143	143	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	271 AA;	29895 MW;	C06465136B16E821 CRC64;

Query Match 19.8%; Score 141; DB 1; Length 271;  
 Best Local Similarity 29.3%; Pred. No. 2.8e-06;  
 Matches 44; Conservative 9; Mismatches 53; Indels 44; Gaps

Qy	1	QRPYGGCGGPRLLIG--TGTDAACCRVHTT-----RCCRD-YPGECCSEWD-----	46
Db	6	QOPT-----AFLLLSLGVTVKLCNVKDTYPSGHKCCRECPGHMVSRCDHTRDTV	58
Qy	47	CMCVOPEFHCG-----DPC--CTTCRRH-----PCPPGGVGVSQGKFSE	83
Db	59	CHCPEGFYEAENVYDCKOCTQCNHRSGSELKQNCPTEDTVCCQRPRTGTPRODSSHL	118
Qy	84	GFOCIDCASGTFSGGHEGHCKPMTDCTQFG	113
Db	119	GVDCVCPPGHFSPGSNQACKPWTNCTLSG	148

RESULT 3  
 41BB MOUSE STANDARD; PRT; 256 AA.

ID	41BB MOUSE	STANDARD;	PRT;	256 AA.
AC	P20334;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB).			
GN	TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
ON	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=89184547; PubMed=2784565;			
RA	Kwon B.S., Weissman S.M.;			
RT	"CDNA sequences of two inducible T-cell genes.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).			
RN	[2]			
RC	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/C.			
RA	MEDLINE=941179805; PubMed=8133039;			
RA	Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;			
RT	"Genomic organization and chromosomal localization of the T-cell			
RL	antigen 4-1BB.";			
RL	J. Immunol. 152:2256-2262(1994).			
RN	[3]			
RP	CHARACTERIZATION, AND SEQUENCE OF 25-29.			
RA	MEDLINE=933139510; PubMed=7678621;			
RA	Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kim K.K., Pickard R.T.			
RT	"Inducible T cell antigen 4-1BB. Analysis of expression and			
RL	function.";			
RL	J. Immunol. 150:771-781(1993).			
CC	-1- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY			
CC	ACTIVE DURING T CELL ACTIVATION.			
CC	-1- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.			
CC	ASSOCIATES WITH P56-LCK.			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS			
CC	-1- INDUCTION: OPTIMAL BY PHA AND IONOMYCIN.			
CC	-1- SIMILARITY: CONTAINS A LA-NGER/TNFR-TYPE CYSTEINE-RICH REGION.			



Search completed: September 4, 2001, 16:12:16  
Job time: 1113 sec

F:986-1035/Domain: laminin-type EGF-like homology <LE10>  
F:1038-1092/Domain: laminin-type EGF-like homology <LE11>  
F:1095-1140/Domain: laminin-type EGF-like homology <LE12>  
F:1143-1187/Domain: laminin-type EGF-like homology <LE13>

Query Match 12.2%; Score 119.5; DB 2; Length 1798;  
Best Local Similarity 23.9%; Pred. No. 0.051;  
Matches 57; Conservative 10; Mismatches 62; Indels 109; Gaps 14;  
  
QY 8 GAFRALC-----GLALICALSLGR-----PTGGPGCGPGRLLLTGTGDARC----- 49  
DB 837 GALSSICEKTSQCLRTCAFLRCDCRCRGQGWFFSCR-----CVCNGHAD 884  
  
QY 50 -CRVHTTRC--CRDYPGECCSEWDCMCVQPEFHCDPCCT---TCRHHPCCPPGQGVQ-- 101  
DB 885 ECNTHTGACLCGRDHTGHECHER---CI-AGFH-GDRLPYGGQCRPCPCPEGPGSQRH 938  
  
QY 102 -----SQKFSE-----FGQCIDCASGTF----- 120  
DB 939 FATSCHQDEYSQOIVCHCRAGYTGRLCEACAPGHFGDPSRPGRCQLCECSGNIDPMDPD 998  
  
QY 121 -----SGGHEGHCKPWTCTQFGFLTVFPGNKTHNAV-CVPSPAE 161  
DB 999 ACDPTHGQCLRLHTEGPHCAHCKP-----GFHGQAAROSCHRCTCNLLGTNPQQ 1049

RESULT 12  
A35356  
tumor necrosis factor receptor 2 precursor [validated] - human  
N:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2  
C:Species: Homo sapiens (man)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 08-Dec-2000  
C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094  
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K.  
Science 248, 1019-1023, 1990  
A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular and  
A:Reference number: A35356; MUID:90260639  
A:Accession: A35356  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-461 <SM1>  
A:Cross-references: GB:M32315; NID:g189185; PIDN:AA59929.1; PID:g189186  
R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires,  
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990  
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occur  
A:Reference number: A36475; MUID:91045991  
A:Accession: A36475  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-195, 'R', 197-461 <KOH>  
A:Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758  
R:Demiche, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.  
Cytokine 2, 231-237, 1990  
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular,  
A:Reference number: A48416; MUID:91370690  
A:Accession: A48416  
A:Status: preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 23-461 <DEM>  
A:Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649  
R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990  
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra  
A:Reference number: A36007; MUID:90349572  
A:Accession: A36007  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEU>  
A:Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752  
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.  
J. Biol. Chem. 265, 20131-20138, 1990

A:Title: Purification and partial amino acid sequence analysis of two distinct tumor  
A:Reference number: A23666; MUID:91056048  
A:Accession: A23666  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 23-40; 65-69; 136-141; 300-306 <LOE>  
R:Engelmann, H.; Novick, D.; Wallach, D.  
J. Biol. Chem. 265, 1531-1536, 1990  
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Eviden  
A:Reference number: A35010; MUID:90110215  
A:Accession: B35010  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 27-31 <ENG>  
R:Kuhnert, P.; Kemper, O.; Wallach, D.  
Gene 150, 381-386, 1994  
A:Title: Cloning, sequencing and partial functional characterization of the 5' region  
A:Reference number: I38094; MUID:95121934  
A:Accession: I38094  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-37 <RES>  
A:Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701  
C:Genetics:

A:Gene: GDB:TNFR2  
A:Cross-references: GDB:125914; OMIM:191191  
A:Map position: 1p36.2-1p36.2  
A:Introns: 26/3  
A:Note: the list of introns is incomplete  
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>  
F:40-76/Domain: NGF receptor repeat homology <NG1>  
F:78-119/Domain: NGF receptor repeat homology <NG2>  
F:120-162/Domain: NGF receptor repeat homology <NG3>  
F:164-201/Domain: NGF receptor repeat homology <NG4>  
F:262-279/Domain: transmembrane #status predicted <TMN>  
F:280-461/Domain: intracellular #status predicted <INT>  
F:171.193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.2%; Score 119; DB 1; Length 461;  
Best Local Similarity 26.3%; Pred. No. 0.023;  
Matches 41; Conservative 14; Mismatches 63; Indels 38; Gaps 8;  
  
QY 34 CGPG---RLLLGTGDARC-----CRVHTTRCCRDYPGEECCSEW-- 71  
DB 57 CSPGQAHKVFCTKTSDTVCDSCEDSTVQLNMWVPECLSCGSRCSDDQVQACTREQNR 116  
  
QY 72 -CMCQVPEFHC-----GDPCCCTCRHHPCPPGGVQSOGKFSGFCIDCASGTFSG-- 122  
DB 117 ICTC-RPGWYCALSKQEGRCRLCAPLR--KCRPGFVARPGTETSDVVCCKPCAPGTFSTNT 173  
  
QY 123 GHEGHCKPWTCTQFGFLTVFPGNKTHNAVCPGSP 158  
DB 174 SSTDICRPHOICN----VVAIPGNASMDAVCTSTSP 205

RESULT 13  
B38634  
tumor necrosis factor receptor type 2 precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Jul-1999  
C:Accession: B38634; A40254; S54816  
R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,  
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto  
A:Reference number: A38634; MUID:91187885  
A:Accession: B38634  
A:Molecule type: mRNA  
A:Residues: 1-474 <LEW>  
A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828



C:Keywords: growth factor receptor; transmembrane protein  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-271/Product: OX40 antigen #status predicted <MAT>  
F:211-235/Domain: transmembrane #status predicted <TM>

Query Match 15.4%; Score 151; DB 2; Length 271;  
Best Local Similarity 28.5%; Pred. No. 5.2e-05;  
Matches 47; Conservative 12; Mismatches 62; Indels 44; Gaps 8;  
QY 26 QRPTGGPGCGRLLLG--TGTDAACRVTHT-----RCRD--YPGECCSEWD----- 71  
DB 6 QQPT-----AFLLLGLSLGVTVKLVNKVDYTPSGHKCCRCQPGHGVSRCDHTRTDV 58  
QY 72 CMCVQPEFHCG----DPC--CTTCRHH-----PCPGQGVQSGQKFSF 108  
DB 59 CHPCPEGFYNEAVNYDTCKQCTQCNHRSGSELKQNCPTPTEDTVCCQCRPGTPPQDSSHL 118  
QY 109 GRCQIDCASGTSGGHEGCKPWTCTQRTGFLTVFGNKTTHAVC 153  
DB 119 GVDVCPPEPFHSPGSGNQACKPWTNCTLSGKQIRHPASNSLDTVC 163

RESULT 6  
JC5559  
Lectin-B - Virginian pokeweed  
C:Species: Phytolacca americana (Virginian pokeweed)  
C:Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 17-Mar-2000  
C:Accession: JC5559  
R:Yamaguchi, K.; Yurino, N.; Kino, M.; Ishiguro, M.; Funatsu, G.  
Biosci. Biotechnol. Biochem. 61, 690-698, 1997  
A:Title: The amino acid sequence of mitogenic lectin-B from the roots of pokeweed (Phytolacca americana)  
A:Reference number: JC5559; MUID:97290889  
A:Accession: JC5559  
A:Molecule type: protein  
A:Experimental source: root  
C:Comment: This protein is a lectin specific for N-acetylglucosamine-containing saccharides  
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; plant lectin  
C:Keywords: glycoprotein  
F:96.139/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.2%; Score 139; DB 2; Length 295;  
Best Local Similarity 28.8%; Pred. No. 0.00047;  
Matches 36; Conservative 18; Mismatches 41; Indels 30; Gaps 8;  
QY 20 CALSLGQRTGGP-----GGCGRLLLGTGTDAACRVTHTTRCCRDYPG-----EECC 67  
DB 133 CGVDFGNRTCPNDLCCSEWGCGETEGYCGECQSQC---NHQRCGKDFAGRTCLNDLCC 189  
QY 68 SEWDCMCVQPEFHCGDPCCTTCRHHPCCPGQGVQSGKFSFGQ-C---IDCASGTFSGG 123  
DB 190 SEWG-WCGSSEAHCGQGSNCYNRC-----GR-NFGFRTCPNELCCSSGCGCS 238  
QY 124 HEGHC 128  
DB 239 NDAHC 243

RESULT 7  
A46476  
B cell-associated surface molecule CD40, long splice form - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Nov-2000  
C:Accession: A46476; A46515  
R:Torres, R.M.; Clark, E.A.  
J. Immunol. 148, 620-626, 1992  
A:Title: Differential increase of an alternatively polyadenylated mRNA species of murine B cell-associated surface molecule CD40, long splice form  
A:Reference number: A46476; MUID:92105763  
A:Accession: A46476  
A:Status: preliminary  
A:Molecule type: mRNA

A:Residues: 1-305 <TOR>  
A:Cross-references: GB:M83312; NID:g1553058  
A:Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:P:75207)  
A:Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0  
R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockay  
J. Immunol. 149, 3921-3926, 1992  
A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.  
A:Reference number: A46515; MUID:93094586  
A:Accession: A46515  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-287, LV' <GR>  
A:Cross-references: GB:M83312; NID:g1553058; PIDN:ANB08705.1; PID:g1553059; GB:M94126  
A:Experimental source: BALB/c, liver  
A:Note: sequence extracted from NCBI backbone (NCBI:P:120357)  
C:Comment: For an alternative splice form, see PIR:A46515.  
C:Comment: For an alternative splice form, see PIR:A46476.  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: alternative splicing; transmembrane protein  
F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 13.8%; Score 135.5; DB 2; Length 305;  
Best Local Similarity 26.1%; Pred. No. 0.00091;  
Matches 49; Conservative 10; Mismatches 74; Indels 55; Gaps 8;  
QY 13 LCGLI--ALLCALSLGQRTGGPGCGRLLLGTGTDAAC----- 50  
DB 7 LCALWGCLLTAHLGQCVT---CSDQYLV-----HDGCCDLQCPGSRKLTSHCTALEKTQ 58  
QY 51 -----RVHTTRCCRDYPG-----EECCSEWDCMCVQPE-FHCGDPCCTT 88  
DB 59 CHPCDSGEFSAQNNREIRHQHRRCEPNQGLRVKKEGTAEEDTCTCKEGQHCTSKDCEA 118  
QY 89 C-RHHPCPPCGVQSGKFSFGFCIDCASGTFSGGHE--CHCKPWTCTQFGFLTVFP 145  
DB 119 CAQHTPCIPGFGVMEMATEETDTVCHPCPVGFFNQSLFEKCYPTWTSCEKLNLEVLQ 178  
QY 146 NKTHNAV 153  
DB 179 TSQTNVIC 186

RESULT 8  
MMRTS  
Laminin beta-2 chain precursor - rat  
A:Alternate names: laminin chain B3; S-laminin  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 10-Dec-1999  
C:Accession: S03539  
R:Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.  
Nature 338, 229-234, 1989  
A:Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neocortex  
A:Reference number: S03539; MUID:89159410  
A:Accession: S03539  
A:Molecule type: mRNA  
A:Residues: 1-1801 <HUN>  
A:Cross-references: EMBL:X16563; NID:g57250; PIDN:CAA34561.1; PID:g57251  
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C:Function:  
A:Description: Interact with cells and with other basement membrane proteins to promote cell-cell adhesion  
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C:Keywords: basement membrane; calcium binding; cell binding; coll; extracellular matrix  
F:1-35/Domain: signal sequence #status predicted <SIG>  
F:36-1801/Product: laminin beta-2 chain #status predicted <MAT>  
F:36-285/Domain: VI <DOM6>  
F:286-555/Domain: V <DOM5>  
F:286-347/Domain: laminin-type EGF-like homology <LE01>  
F:350-410/Domain: laminin-type EGF-like homology <LE02>  
F:413-470/Domain: laminin-type EGF-like homology <LE03>  
F:473-522/Domain: laminin-type EGF-like homology <LE04>  
F:525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F:556-784/Domain: IV <DOM4>

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Qy   121 --SGHGHGCHKPWTDCQTGFGLTVFPGNKTHNAVVCVPGSPAPBPL 163
      :|:| | | | | | | | | | | | | | | | | | | | | | | | | |
Db   176 QNTSSPSARCOPHTRCENOGIVEAAPGTQSDTTC---KNPLEPL 217

RESULT 10
I48854
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: I48854
R:Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A>Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A:Reference number: I48854; MUID:95178848
A:Accession: I48854
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-459 <RES>
A:Cross-references: EMBL:X76401; NID:q433830; PIDN:CAA53981.1; PID:q433831
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
F:151-188/Domain: NGF receptor repeat homology <NGF>

Query Match          12.3%; Score 120.5; DB 2; Length 459;
Best Local Similarity 30.3%; Pred. No. 0.017;
Matches 37; Conservative 11; Mismatches 57; Indels 17; Gaps 6;

Qy   48 RCRVHTTRCGRDYPRGCCSEWD---CMCVQPF-----HCGDPCCTTC-RHIPCPGGQ 98
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db   77 RTCLSCSSSCTDQVETRACTKQNRYCAGEAGRYCALKTSHGS--CRQCMRLSKCGFGF 134

Qy   99 GVQSOGNFSGFCQICDASGFESG--GHEGHCKPWTDCTQGFGLTVFPGNKTHNAVCPVG 156
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db   135 GVASSRAPGNVLCKACAPGTFSTTSSTDVCRPHRICS----ILAIPGNASTDAVCAPE 190

Qy   157 SP 158
      ||
Db   191 SP 192

RESULT 11
S53869
laminin beta-2 chain precursor (version 2) - human
N:Alternate names: s-laminin
C:Species: Homo sapiens (man)
C>Date: 27-Oct-1995 #sequence_revision 23-Feb-1996 #text_change 24-Sep-1998
C:Accession: S53869
R:Iivanainen, A.; Vuolteenaho, R.; Sainio, K.; Eddy, R.; Sariola, H.; Tr
Matrix Biol. 14, 489-497, 1994
A>Title: The human laminin beta-2 chain (S-laminin); structure, expression in fetal t
A:Reference number: S53869
A:Accession: S53869
A:Molecule type: mRNA
A:Residues: 1-1798 <II>
C:Genetics:
A:Gene: GDB:LAMB2
A:Cross-references: GDB:l32363; OMIM:150325
A:Map position: 3p21.3-p21.2
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C:Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-1798/Product: laminin beta-2 chain #status predicted <MAT>
F:283-344/Domain: laminin-type EGF-like homology <LEO1>
F:347-407/Domain: laminin-type EGF-like homology <LEO2>
F:410-467/Domain: laminin-type EGF-like homology <LEO3>
F:470-519/Domain: laminin-type EGF-like homology <LEO4>
F:522-552/Domain: laminin-type EGF-like homology #status atypical <LEO5>
F:783-828/Domain: laminin-type EGF-like homology <LEO6>
F:831-874/Domain: laminin-type EGF-like homology <LEO7>
F:877-924/Domain: laminin-type EGF-like homology <LEO8>
F:927-983/Domain: laminin-type EGF-like homology <LEO9>

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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	162	16.5	272	2	I48700	gene ox40 protein	
2	162	16.5	277	2	I37552	OX40 homolog - hum	
3	160.5	16.4	255	2	I38426	lymphocyte activat	
4	153	15.6	256	2	B32393	T-cell antigen 4-1	
5	151	15.4	271	2	S13783	OX40 antigen precu	
6	139	14.2	295	2	JC5559	lectin-B - Virgini	
7	135.5	13.8	305	2	A46476	B cell-associated	
8	134.5	13.7	1801	1	MMPTS	laminin beta-2 cha	
9	121	12.4	435	2	I54182	tumor necrosis fac	
10	120.5	12.3	459	2	I48854	gene murine tumour	
11	119.5	12.2	1798	2	S53869	laminin beta-2 cha	
12	119	12.2	461	1	A35356	tumor necrosis fac	
13	119	12.2	474	2	B38634	tumor necrosis fac	
14	118.5	12.1	277	2	A60771	B-cell activation	
15	115.5	11.8	1371	2	A3837	insulin-like growt	
16	114.5	11.7	329	2	A48805	insulin-like growt	
17	112.5	11.5	1797	2	A55677	laminin beta-2 cha	
18	112	11.4	152	2	T18975	hypothetical prote	
19	111	11.3	1111	2	T26972	hypothetical prote	
20	110.5	11.3	1687	2	T30176	EGF repeat transme	
21	110.5	11.3	2907	2	A57278	fibillin-2 precu	
22	109.5	11.2	164	2	T24272	hypothetical prote	
23	109.5	11.2	2531	2	A46019	Notch-1 protein -	
24	109	11.1	1574	2	T13954	MEGF6 protein - ra	
25	109	11.1	3635	2	T10053	laminin alpha 5 ch	
26	106.5	10.9	2918	2	A54105	fibillin-2 precu	
27	105	10.7	188	2	T15651	hypothetical prote	
28	105	10.7	1172	1	TSHP2	thrombospondin 2 p	
29	102.5	10.5	956	1	A46016	thrombospondin 3 -	

C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000  
C;Accession: I37552  
R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat  
Eur. J. Immunol. 24, 677-683, 1994  
A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment  
A;Reference number: I37552; MUID:94170844  
A;Accession: I37552  
A;Status: preliminary; translated from GB/EMBL/DDBBJ  
A;Molecule type: mRNA  
A;Residues: 1-277 <RES>  
A;Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958  
C;Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match            16.5%; Score 162; DB 2; Length 277;  
Best Local Similarity 29.7%; Pred. No. 7.4e-06;  
Matches 51; Conservative 11; Mismatches 92; Indels 18; Gaps 5;

QY 5 GAMGAFRALGLALLCALSLG-----QRPTGGPGCGPGRLLLTGTGDARCCRVHT 54  
| | | | | | | | | | : | : | : | : | : | : |  
DB 4 GARLRGPCAALLLLGLLSTVTGLHCVGDTYPSNRDRCHECR--PCNGMVSRCSRSQN 61  
| | | | | | | | | | : | : | : | : | : | : |  
QY 55 TRCCRDYPG--EECCSEWDCM-CVQPEFHCD---PCITTCRRHHPPCPGGVGQSQGKFSF 108  
| | | | | | | | | | : | : | : | : | : | : |  
DB 62 TVCRPCGGFYNDVVYSKKPKCTWCNLRSERKQLTATQDTVCRCRAGTQPLDSYKP 121  
| | | | | | | | | | : | : | : | : | : | : |  
QY 109 GFQCICDASGFSGHGCHCKPWTDCTQFGELTVFPGNKTHNAVCPGPSPPA 160  
| | | | | | | | | | : | : | : | : | : | : |  
DB 122 GVDCAPCPGHFSPGDNQACKPWTNCTLAGKHTLOPASNSDAICEDRPDP 173  
| | | | | | | | | | : | : | : | : | : | : |

RESULT 3  
I38426  
lymphocyte activation-induced receptor ILA precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 01-Dec-2000  
C;Accession: I38426; JT0752  
R;Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; R  
Eur. J. Immunol. 24, 2219-2227, 1994  
A;Title: Molecular and biological characterization of human 4-1BB and its ligand.  
A;Reference number: I38426; MUID:94374434  
A;Accession: I38426  
A;Status: preliminary; translated from GB/EMBL/DDBBJ  
A;Molecule type: mRNA  
A;Residues: 1-255 <RES>  
A;Cross-references: EMBL:U03397; NID:g571320; PIDN:AAA53133.1; PID:g571321  
R;Schwarz, H.; Tuckwell, J.; Lotz, M.  
Gene 134, 295-298, 1993  
A;Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne  
A;Reference number: JT0752; MUID:94085794  
A;Accession: JT0752  
A;Molecule type: mRNA  
A;Residues: 1-106,'R',108-255 <SCH>  
C;Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-neuro  
C;Comment: This receptor recognizes soluble, cell-surface bound or extracellular matrix  
C;Superfamily: CD27 antigen; NGF receptor repeat homology  
C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein  
F;1-17/Domain: signal sequence #status predicted <SIG>  
F;18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <NAT>  
F;187-213/Domain: transmembrane #status predicted <TM>  
F;138,149/Binding site: carbohydate (Asn) (covalent) #status predicted  
F;234,235/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predict  
F;242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match            16.4%; Score 160.5; DB 2; Length 255;  
Best Local Similarity 30.9%; Pred. No. 9.2e-06;  
Matches 47; Conservative 12; Mismatches 52; Indels 41; Gaps 9;

QY 34 CGPGRLLLTGTADARCCRVHTTRCCRDYPG-----EECCS-----EWDCCMCVQPEFFHCGRP 84  
| | | | | | | | | | : | : | : | : | : | : |  
DB 48 CPPNFSSAGG--QRTCDI-----CRCKGVFTRKCSSTSNAECD----TPGFHLGLA 97  
| | | | | | | | | | : | : | : | : | : | : |

Qy 85 CTTCTRHHPGPPGGVQSOGKFSFGFCIDCASTFSGHGHCKPMTDCTQFGFLVFP 144  
I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :  
Db 98 GCSMC - EODCKQGQELTKKG -----CKDKCFGTFTNDQKRIGICRPWTNCSLDGSKVLVN 149

Qy 145 GNKTHNAVCPG-----SPPA---EP 162  
I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :  
Db 150 GTKERDVVGPSPADLSPGASSVTTPAPAREP 181

RESULT 4  
B32393  
T-cell antigen 4-1BB precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 21-Jul-2000  
C:Accession: B32393; I48879  
R:Kwon, B.S.; Weissman, S.M.  
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989  
A>Title: cDNA sequence of two inducible T-cell genes.  
A:Reference number: A32393; MUID:89184547  
A:Accession: B32393  
A:Molecule type: mRNA  
A:Residues: 1-256 <KWQ>  
A:Cross-references: GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122  
R:Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.  
J. Immunol. 152, 2256-2262, 1994  
A>Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1BB  
A:Reference number: I48879; MUID:941179805  
A:Accession: I48879  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-256 <RES>  
A:Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178  
C:Genetics:  
A:Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: transmembrane protein  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-256/Product: 4-1BB protein #status predicted <MAT>

Query Match 15.6%; Score 153; DB 2; Length 256;  
Best Local Similarity 31.5%; Pred. No. 3.5e-05;  
Matches 40; Conservative 17; Mismatches 52; Indels 18; Gaps 7;

Qy 34 CGPGLR-LLGHTGDARCRVHTTRCCRDYGECECSEW---DCMVCQPERFHCGPCQTTC 89  
I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :  
Db 47 CPPTFFSISGQPNCNTRV----CAGYFRFKFCSTSHNAECIE-GFHCLGPQCSTRC 101

Qy 90 RHHPCPPGQVSOGKFSFGFCIDCASTFSGGH-BGHCKPMTDCTQFGFLVFPGNKT 148  
I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :  
Db 102 -EKDCRPQEQLTKG-----CKTCSLIGTFNDQNGTGVCPRPWNTNCSLDGRSVLKGTTE 153

Qy 149 HNAVCP 155  
I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :  
Db 154 KDVVCGP 160

RESULT 5  
SI2783  
Ox40 antigen precursor -. rat  
N:Alternate names: nerve growth factor receptor homolog  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 05-Nov-1999  
C:Accession: SI2783; S08036  
R:Mallett, S.; Fossum, S.; Barclay, A.N.  
EMBO J. 9, 1063-1068, 1990  
A>Title: Characterization of the MRC Ox40 antigen of activated CD4 positive T lymphocytes  
A:Reference number: SI2783; MUID:90214614  
A:Accession: SI2783  
A:Molecule type: mRNA  
A:Residues: 1-271 <MAL>  
A:Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831  
C:Superfamily: CD27 antigen; NGF receptor repeat homology

FT DOMAIN 831 876 LAMININ EGF-LIKE 7.  
FT DOMAIN 877 986 LAMININ EGF-LIKE 8.  
FT DOMAIN 927 985 LAMININ EGF-LIKE 9.  
FT DOMAIN 986 1037 LAMININ EGF-LIKE 10.  
FT DOMAIN 1038 1094 LAMININ EGF-LIKE 11.  
FT DOMAIN 1095 1142 LAMININ EGF-LIKE 12.  
FT DOMAIN 1143 1189 LAMININ EGF-LIKE 13.  
FT DOMAIN 1190 1409 DOMAIN 11.  
FT DOMAIN 1410 1442 DOMAIN ALPHA.  
FT DOMAIN 1443 1798 DOMAIN I.  
FT DOMAIN 1253 1319 COILED COIL (POTENTIAL).  
FT DOMAIN 1472 1526 COILED COIL (POTENTIAL).  
FT DOMAIN 1577 1790 COILED COIL (POTENTIAL).  
FT DISULFID 283 292 BY SIMILARITY.  
FT DISULFID 285 310 BY SIMILARITY.  
FT DISULFID 312 321 BY SIMILARITY.  
FT DISULFID 324 344 BY SIMILARITY.  
FT DISULFID 347 356 BY SIMILARITY.  
FT DISULFID 349 374 BY SIMILARITY.  
FT DISULFID 377 386 BY SIMILARITY.  
FT DISULFID 389 407 BY SIMILARITY.  
FT DISULFID 410 423 BY SIMILARITY.  
FT DISULFID 412 438 BY SIMILARITY.  
FT DISULFID 440 449 BY SIMILARITY.  
FT DISULFID 452 467 BY SIMILARITY.  
FT DISULFID 470 484 BY SIMILARITY.  
FT DISULFID 472 491 BY SIMILARITY.  
FT DISULFID 493 502 BY SIMILARITY.  
FT DISULFID 505 519 BY SIMILARITY.  
FT DISULFID 783 795 BY SIMILARITY.  
FT DISULFID 785 802 BY SIMILARITY.  
FT DISULFID 804 813 BY SIMILARITY.  
FT DISULFID 816 828 BY SIMILARITY.  
FT DISULFID 831 843 BY SIMILARITY.  
FT DISULFID 833 850 BY SIMILARITY.  
FT DISULFID 852 861 BY SIMILARITY.  
FT DISULFID 864 874 BY SIMILARITY.  
FT DISULFID 877 886 BY SIMILARITY.  
FT DISULFID 879 893 BY SIMILARITY.  
FT DISULFID 896 905 BY SIMILARITY.  
FT DISULFID 908 924 BY SIMILARITY.  
FT DISULFID 927 943 BY SIMILARITY.  
FT DISULFID 929 954 BY SIMILARITY.  
FT DISULFID 956 965 BY SIMILARITY.  
FT DISULFID 968 983 BY SIMILARITY.  
FT DISULFID 986 1000 BY SIMILARITY.  
FT DISULFID 988 1007 BY SIMILARITY.  
FT DISULFID 1010 1019 BY SIMILARITY.  
FT DISULFID 1022 1035 BY SIMILARITY.  
FT DISULFID 1095 1107 BY SIMILARITY.  
FT DISULFID 1097 1114 BY SIMILARITY.  
FT DISULFID 1116 1125 BY SIMILARITY.  
FT DISULFID 1128 1140 BY SIMILARITY.  
FT DISULFID 1143 1155 BY SIMILARITY.  
FT DISULFID 1145 1162 BY SIMILARITY.  
FT DISULFID 1164 1173 BY SIMILARITY.  
FT DISULFID 1176 1187 BY SIMILARITY.  
FT DISULFID 1190 1190 INTERCHAIN (PROBABLE).  
FT DISULFID 1193 1193 INTERCHAIN (PROBABLE).  
FT DISULFID 1797 1797 INTERCHAIN (PROBABLE).  
FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1085 1085 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1249 1249 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1308 1308 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1348 1348 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1499 1499 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 914 914 R -> G (IN REF. 2).  
FT CONFLICT 1179 1179 G -> A (IN REF. 2).  
FT SEQUENCE 1798 AA; 196079 MW; 9555CF5B24850CB7 CRC64;

Query Match 11.4%; Score 111.5; DB 1; Length 1798;

Best Local Similarity 23.2%; Pred. No. 0.018;  
Matches 55; Conservative 10; Mismatches 65; Indels 107; Gaps 13;  
QY 8 GAFRALC----GLALLCALSLGQR-----PTGGPGCGGPRLLLTCTDARC-----CVCNGHAD 884  
Db 837 GALSLECKTSGQCLCRGTGATGLRCDRCQRCQWGFPSCRP-----  
QY 50 -CRVHTTRC--CRDYPGECCSEWDCMCVQPEFFHCGD--PCTTCRHHPCPPGQGVQ--- 101  
Db 885 ECNHTGTACLCGRDHTGGEHCEH-----CI-AGFHRDRLPYGGQCRPCPCPEGPGSQRHF 939  
QY 102 ----SQKFS-----FGQCIDCASGTF-----  
Db 940 ATSCHQDEYSQOIYVCHCRAGYTGRLRCEACAFGHEGDPSPRGRCQLCECSGNIDPMDPDA 999  
QY 121 -----SGGHEGHCCKPWTDTCTQGFLLTVFPGNKTNAVC--VPGSPPAE 161  
Db 1000 CDPTGGQCLRLHHTEGPHCAHCRP-----GFHGQAAROSCHRCTCNLLGTNPQQ 1049

Search completed: September 4, 2001, 16:15:27  
Job time: 1139 sec





RT with its receptor CD40.";  
 RL Protein Sci. 7:1124-1135(1998).  
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.  
 CC -1- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD40 entry; htm".  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL: X60592; CAA43045.1; -  
 DR PIR: S04460; S04460.  
 DR FDB: ICDF; 01-APR-97.  
 DR MIM: 109535; -  
 DR InterPro: IPR001368; -  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 4.  
 DR Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;  
 KW 3D-structure.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 277 CD40L RECEPTOR.  
 FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 194 215 POTENTIAL.  
 FT DOMAIN 216 277 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 187 4 X TNFR-CYS.  
 FT REPEAT 25 60 TNFR-CYS 1.  
 FT REPEAT 61 103 TNFR-CYS 2.  
 FT REPEAT 104 144 TNFR-CYS 3.  
 FT REPEAT 145 187 TNFR-CYS 4.  
 FT DISULFID 26 37  
 FT DISULFID 38 51  
 FT DISULFID 41 59  
 FT DISULFID 62 77  
 FT DISULFID 83 103  
 FT DISULFID 105 119  
 FT DISULFID 111 116  
 FT DISULFID 125 143  
 FT CARBOHYD 153 153 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 180 180 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 277 AA: 30619 MW: 36776 EC2C4A5680 CRC64;  
 Query Match 12.1%; Score 118.5; DB 1; Length 277;  
 Best Local Similarity 27.7%; Pred. No. 0.0011;  
 Matches 36; Conservative 10; Mismatches 73; Indels 11; Gaps 5;  
 QY 34 CGPGRLLGTGTDAACRCVHTTRCCRDYDG-----EECCSEDCMCVQPE-FHCDDPQCTT 88  
 DB 62 CGSEFLDTWNRTHC---HQHYCDPNLGRVQOKTSETDTICTCEGWHCTSEACES 118  
 QY 89 C-RHHFCPPCGQVQSGKSFQFCQDCASGTFSGGHEG--HCKPWTDCQFGELTVFPG 145  
 DB 119 CVLHRSCTPGVGVKQIATGVSDTICEPCVPGFFSNVSSAFKCHPWTSCETKDLVQVQAG 178  
 QY 146 NKTHNAVCPV 155  
 DB 179 TNKTDVVCVP 188  
 RESULT 14  
 IGIR\_RAT  
 ID IGIR\_RAT STANDARD; PRT: 1370 AA.  
 AC P24062;  
 DT 01-NAR-1992 (Rel. 21, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR (EC 2.7.1.112).  
 GN IGFI.  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=95277910; PubMed=7758167;  
 RA Du J., Delafontaine P.;  
 RT "Inhibition of vascular smooth muscle cell growth through antisense  
 RL transcription of a rat insulin-like growth factor I receptor cDNA.";  
 RN Circ. Res. 76:963-972(1995).  
 CC [2]  
 RP SEQUENCE OF 1-364 FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RX MEDLINE=90017496; PubMed=2477843;  
 RA Werner H., Woloschak M., Adamo M., Shen-Orr Z., Roberts C.T. Jr.,  
 RA Leroith D.;  
 RT "Developmental regulation of the rat insulin-like growth factor I  
 RL receptor gene.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 86:7451-7455(1989).  
 CC [3]  
 RP SEQUENCE OF 913-1017 FROM N.A.  
 RX MEDLINE=92412145; PubMed=1530648;  
 RA Kurachi H., Jobo K., Ohta M., Kawasaki T., Itoh N.;  
 RT "A new member of the insulin receptor family, insulin  
 RL receptor-related receptor, is expressed preferentially in the  
 RL kidney.";  
 CC Biochem. Biophys. Res. Commun. 187:934-939(1992).  
 CC -1- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)  
 CC WITH A HIGH AFFINITY AND IGF II WITH A LOWER AFFINITY. IT HAS A  
 CC TYROSINE-PROTEIN KINASE ACTIVITY.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +  
 CC PROTEIN TYROSINE PHOSPHATE.  
 CC -1- SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE  
 CC BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-  
 CC BINDING DOMAIN, WHILE THE BETA CHAIN CARRIES THE KINASE DOMAIN.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-  
 CC PROTEIN KINASES.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -----  
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 CC -----  
 CC EMBL: L29232; AAA41392.1; -  
 DR EMBL: M27293; AAA41384.1; -  
 DR PIR: A33837; A33837.  
 DR HSP: P06213; 11RK.  
 DR InterPro: IPR000494; -  
 DR InterPro: IPR000719; -  
 DR InterPro: IPR001245; -  
 DR InterPro: IPR001777; -  
 DR InterPro: IPR002011; -  
 DR InterPro: IPR002174; -  
 DR Pfam: PF00757; Furin-like; 1.  
 DR Pfam: PF01030; Recep\_L\_domain; 2.  
 DR Pfam: PF00041; fn3; 2.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS00239; RECEPTOR\_TYR\_KIN\_II; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR Transferase; Tyrosine-protein kinase; Receptor; Transmembrane;  
 KW

KW Glycoprotein; ATP-binding; Phosphorylation; Repeat; Signal.  
FT SIGNAL 1 30  
FT CHAIN 31 740  
FT CHAIN 742 1370  
FT DOMAIN 742 936  
FT TRANSMEM 937 960  
FT DOMAIN 961 1370  
FT DOMAIN 608 829  
FT DOMAIN 830 929  
FT DOMAIN 1000 1275  
FT NP\_BIND 1006 1014  
FT BINDING 1034 1034  
FT ACT\_SITE 1136 1136  
FT MOD\_RES 1166 1166  
FT CARBOHYD 51 51  
FT CARBOHYD 102 102  
FT CARBOHYD 135 135  
FT CARBOHYD 245 245  
FT CARBOHYD 314 314  
FT CARBOHYD 418 418  
FT CARBOHYD 439 439  
FT CARBOHYD 535 535  
FT CARBOHYD 608 608  
FT CARBOHYD 623 623  
FT CARBOHYD 641 641  
FT CARBOHYD 748 748  
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FT CARBOHYD 901 901  
FT CARBOHYD 914 914  
FT CONFLICT 985 986  
SQ SEQUENCE 1370 AA; 155395 MW; A5946897A41CB145 CRC64;

Query Match 11.8%; Score 115.5; DB 1; Length 1370;

Best Local Similarity 27.1%; Pred. No. 0.0066;

Matches 57; Conservative 22; Mismatches 52; Indels 79; Gaps 20;

Qy 8 GAFA-----LCGLA-----LLCAL-----LQRPCTGPGCG-----PGR-----L 40  
Db 139 GAIRTEKNADLCYLTIDWSLIDAVSNYIVGNKPP--KEGDLCPGTLEKPMCKXTT 196  
Qy 41 LGTGTDAACRHHVTRC---CRDYPGECCSEWDCMCVQPEHCGDPC-----CTTC 89  
Db 197 INNEYNYKWT--TNRCKQKMPSCVCGKRACTE--NNECCHEPE--CLGSCHTPDDNTTCVAC 251  
Qy 90 RHH-----PCPPGQGVQSGKFSEF-GFQCID---CAS-----GTFSGG---HEGHCK 129  
Db 252 RHYVYKGVCPACPP-----GTVRFEGWRCVDRDFCANIPNAESSDSGDFVIHDGEC- 303  
Qy 130 PWTDTQTFGLTVFPGNKTHNAVCPVGSPP 159  
Db 304 -MQECPG-GFIR-----NSTQSMYICPCGP 327

RESULT 15

LMB2\_HUMAN STANDARD; PRT; 1798 AA.  
ID LMB2\_HUMAN  
AC P55268; Q16321;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ).  
GN LMB2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95213013; PubMed=7698745;

RA Wewer U.M., Gerecke D.R., Durkin M.E., Kurtz K.S., Mattei M.-G.,  
RT Champlaud M.F., Burgeson R.E., Albrechtsen R.;  
FT "Human beta 2 chain of laminin (formerly S chain): cDNA cloning,  
RL chromosomal localization, and expression in carcinomas.";  
RN Genomics 24:243-252(1994).  
RX SEQUENCE FROM N.A.  
RP MEDLINE=95316263; PubMed=7795887;  
RA Ilvanainen A., Vuolteenaho R., Sainio K., Eddy R., Shows T.B.,  
RT Sariola H., Tryggvason K.;  
FT "The human laminin beta 2 chain (S-laminin): structure, expression in  
RL fetal tissues and chromosomal assignment of the LAMB2 gene.";  
CC Matrix Biol. 14:489-497(1995).  
CC IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, AND ORGANIZATION OF  
CC CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING  
CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.  
CC -! SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE  
CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND  
CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE  
CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.  
CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4  
CC (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).  
CC -! SUBCELLULAR LOCATION: EXTRACELLULAR.  
CC -! TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR  
CC COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC  
CC CLEFT OF THE NEUROMUSCULAR JUNCTION.  
CC -! DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT  
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.  
CC -! DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.  
CC -! SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).  
CC -! SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.  
CC -! SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL; 268155; CAA92279.1; .  
DR EMBL; 268156; CAA92279.1; JOINED.  
DR EMBL; X79683; CAA56130.1; .  
DR EMBL; S77512; AAB34682.2; .  
DR HSP; P02468; IKLO.  
DR MIM; 150325; .  
DR InterPro; IPR000561; .  
DR InterPro; IPR001886; .  
DR InterPro; IPR002049; .  
DR Pfam; PF00053; laminin\_EGF; 13.  
DR Pfam; PF00055; laminin\_Nterm; 1.  
DR PRINTS; PR00011; EGF\_LAMININ.  
DR PROSITE; PS00022; EGF\_1; 10.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 12.  
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
FT SIGNAL 1 32  
FT CHAIN 33 1798  
FT DOMAIN 33 280  
FT DOMAIN 281 552  
FT DOMAIN 283 346  
FT DOMAIN 347 409  
FT DOMAIN 410 469  
FT DOMAIN 470 521  
FT DOMAIN 522 552  
FT DOMAIN 553 781  
FT DOMAIN 782 1190  
FT DOMAIN 783 830  
FT DOMAIN 830 830  
FT LAMININ EGF-LIKE 1.  
FT LAMININ EGF-LIKE 2.  
FT LAMININ EGF-LIKE 3.  
FT LAMININ EGF-LIKE 4.  
FT LAMININ EGF-LIKE 5 (INCOMPLETE).  
FT 8 X LAMININ EGF-LIKE REPEATS (DOMAIN  
FT III).  
FT LAMININ EGF-LIKE 6.







```
DR Pfam: PF00020; TNFR_C6: 4.  
DR PROSITE; PS00652; TNFR_NGFR_1; 1.  
DR PROSITE; PS0050; TNFR_NGFR_2; 1.  
KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 >269  
FT DOMAIN 20 193  
FT TRANSMEM 20 193  
FT DOMAIN 194 215  
FT DOMAIN 216 >269  
FT DOMAIN 25 187  
FT REPEAT 25 60  
FT REPEAT 61 103  
FT REPEAT 104 144  
FT REPEAT 145 187  
FT CARBOHYD 153 153  
FT CARBOHYD 180 180  
FT NON_TER 269 269  
SQ SEQUENCE 269 AA; 29983 MW; 746903F30F95F387 CRC64;  
  
Query Match 12.5%; Score 122.5; DB 1; Length 269;  
Best Local Similarity 28.7%; Pred. No. 0.00049;  
Matches 37; Conservative 9; Mismatches 70; Indels 13; Gaps 5;  
  
QY 34 CGPRLLLGTGTDARCCRVHTRCRDYPGECCSEWD-----CMCVQPEFHCGDPCCT 87  
DB 62 CGKGEFTSTNRKYC---HEHRYCNPNLRLRIQSEGLTNTDTCVCEVGO-HCTSHTC 117  
QY 88 TCRHHP-CPPCGGVQSQGKSFQFCIDCASGTFSSGHEG--HCKPWTDCQFGFLTVFP 144  
DB 118 SCTPHSLCPGFGVKQIATGLLTVCEPCLGFFSNVSAFEKCHRWTSCKRKGGLVQHV 177  
QY 145 GNKTHNAVY 153  
DB 178 GTNKTDVVC 186  
  
RESULT 10  
TNRC_HUMAN STANDARD; PRT; 435 AA.  
ID P36941;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR  
DE 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).  
GN LTR OR TNFR OR TNFR3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=93252381; PubMed=8486360;  
RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;  
RT "Construction and evaluation of a hncDNA library of human l2p  
transcribed sequences derived from a somatic cell hybrid.";  
RL Genomics 16:214-218(1993).  
RN [2]  
RP FUNCTION.  
RX MEDLINE=94225209; PubMed=8171323;  
RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,  
RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;  
RT "A lymphotoxin-beta-specific receptor."  
RL Science 264:707-710(1994).  
CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN  
CC IMMUNE DEVELOPMENT.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
CC  
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CC or send an email to license@isb-sib.ch).  
CC  
CC EMBL; L04270; AAA36757.1; -.  
DR HSSP; P25942; ICDF.  
DR MIM; 600979; -.  
DR InterPro; IPR001368; -.  
DR Pfam; PF00020; TNFR_C6: 4.  
DR PROSITE; PS00652; TNFR_NGFR_1; 2.  
DR PROSITE; PS0050; TNFR_NGFR_2; 3.  
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 30  
FT CHAIN 31 435  
FT DOMAIN 31 227  
FT TRANSMEM 228 248  
FT DOMAIN 249 435  
FT DOMAIN 42 211  
FT REPEAT 42 81  
FT REPEAT 82 124  
FT REPEAT 125 168  
FT REPEAT 169 211  
FT DISULFID 43 58  
FT DISULFID 59 72  
FT DISULFID 62 80  
FT DISULFID 83 98  
FT DISULFID 101 116  
FT DISULFID 104 124  
FT DISULFID 126 132  
FT DISULFID 139 148  
FT DISULFID 142 167  
FT DISULFID 170 185  
FT CARBOHYD 40 40  
FT CARBOHYD 177 177  
SQ SEQUENCE 435 AA; 46709 MW; 62462656022F656F CRC64;  
  
Query Match 12.4%; Score 121; DB 1; Length 435;  
Best Local Similarity 26.1%; Pred. No. 0.00094;  
Matches 43; Conservative 12; Mismatches 66; Indels 44; Gaps 10;  
  
QY 34 CGPRLLLGTGTDARCCRVHTRC-----CRDYPGEE---C 66  
DB 62 CPP-----GTYSVSAKSRIRDTVCATCAENSYNEHNNYLTICQLCRCPDPMVMSLEELAP 116  
QY 67 CS--EWDCMCVQPEFHCGDPC--CTTCR-HHPCPPGQGVQSQGKFSFG-FCIDCASGTF 120  
DB 117 TSKRRITQCR-C-QPGMFCAAWALECTHCELLSDCPPGTEAELEKDEVGKGNHCVPCKAGHF 175  
QY 121 --SGGHEGHCPEWTDCQFGFLTVFPKNTNAVCPVPGSPPAEPL 163  
DB 176 QNTSSPSARCQPHTRCENOGLEVAAPGTAQSDTTC---KNPLEPL 217  
  
RESULT 11  
TNR2_HUMAN STANDARD; PRT; 461 AA.  
ID P20333;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR  
DE BINDING PROTEIN 2) (TNFII) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).  
GN TNFRSF1B OR TNFR2 OR TNFR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90260639; PubMed=2160731;
```







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RN [3]
RP REVISION TO 107.
RA Schwarz H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95347766; PubMed=7622190;
RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,
RT "Characterization of human homologue of 4-1BB and its ligand.";
RL Immunol. Lett. 45:67-73(1995).
CC -1- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY
CC ACTIVE DURING T CELL ACTIVATION.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T
CC CELLS.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd137.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U03397; AAA53133.1; -.
DR EMBL; LI2964; AA62478.2; -.
DR HSP; P19438; 1EXT.
DR MIM; 602250; -.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_C6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 1.
DR Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
KW SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 255 4-1BB LIGAND RECEPTOR.
FT DOMAIN 18 186 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 187 213 POTENTIAL.
FT DOMAIN 214 255 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 47 159 3 X TNFR-CYS.
FT REPEAT 47 86 TNFR-CYS 1.
FT REPEAT 87 118 TNFR-CYS 2.
FT REPEAT 119 159 TNFR-CYS 3.
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 255 AA; 27899 MW; F3A563FE5EF00460 CRC64;
SQ

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Query Match 16.4%; Score 160.5; DB 1; Length 255;

Best Local Similarity 30.9%; Pred. No. 2.4e-07;

Matches 47; Conservative 12; Mismatches 52; Indels 41; Gaps 9;

QY 34 CGPGLLLGTGDARCCRVHTTRCCRDYDQ-----ECCS-----ENDCMCVQPEFHCGDP 84

Db 48 CPNSSFSSAGG--QRTCDI-----CRQCKGVFTRKCSSTSNACDC---TFGFHCLGA 97

QY 85 CCTCRHHPCPGQVQSGKFSFGQCIDCASGTSGGHEGCKPWTCTQFGFLTVFP 144

Db 98 GCSMC-EQDCKQKQELTKG-----CKDCCFGTNDQKRGICRPWNCSLDGKSLVN 149

QY 145 GNKTHNACVPG-----SPPA---EP 162

Db 150 GTRKDVWCGSPADLSPGASSVTPAPAPREP 181

RESULT 4

ID 41BB\_MOUSE

AC P20334; STANDARD; PRT; 256 AA.

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DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB).
GN TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=89184547; PubMed=2784565;
RA Kwon B.S., Weissman S.M.;
RT "cDNA sequences of two inducible T-cell genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=94179805; PubMed=8133039;
RA Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;
RT "Genomic organization and chromosomal localization of the T-cell
RT antigen 4-1BB.";
RL J. Immunol. 152:2256-2262(1994).
RN [3]
RP CHARACTERIZATION, AND SEQUENCE OF 25-29.
RX MEDLINE=93139510; PubMed=7678621;
RA Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kim K.K., Pickard R.T.,
RA Kwon B.S.;
RT "Inducible T cell antigen 4-1BB. Analysis of expression and
RT function.";
RL J. Immunol. 150:771-781(1993).
CC -1- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY
CC ACTIVE DURING T CELL ACTIVATION.
CC -1- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.
CC -1- ASSOCIATES WITH P56-LCK.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.
CC -1- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC -----
DR EMBL; J04492; AAA40167.1; -.
DR EMBL; U02567; AAA93113.1; -.
DR PIR; B32393; B32393.
DR HSP; P25942; ICDF.
DR MGD; MGI:1101059; Tnfrsf9.
DR InterPro: IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; FALSE_NEG.
DR Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
KW SIGNAL 1 24
FT CHAIN 25 256 4-1BB LIGAND RECEPTOR.
FT DOMAIN 25 187 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 188 208 POTENTIAL.
FT DOMAIN 209 256 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 17 159 4 X TNFR-CYS.
FT REPEAT 17 45 TNFR-CYS 1.
FT REPEAT 46 85 TNFR-CYS 2.
FT REPEAT 86 117 TNFR-CYS 3.
FT REPEAT 118 159 TNFR-CYS 4.
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 256 AA; 27598 MW; 93A10D03C60813C4 CRC64;
SQ

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	Query Match	15.68;	Score 153;	DB 1; Length 256;
	Best Local Similarity	31.5%;	Pred. No. 1.le-06;	
	Matches	40;	Conservative	7;
			Mismatches 52;	Indels 18; Gaps
QY	34 CGPGRLL-LLGRTGDARCCRVHTTRCCRDYPGEECCSEW---- <td>:</td> <td>:</td> <td>:</td>	:	:	:
Dd	47 CPPSTFSISIGQPNCNCRV-----CAGYFRFKFCSSTHNAECEIE-GFHCLGPQCITRC 101	:	:	:
QY	90 RHHPCPPGQVSQSOKSFSGFCIDCASCTSSGGH-EGHCKRPWTDDCTQFGFLTVFPFNKT 148	:	:	:
Dd	102 -EKDCRPGQLTKQS-----CKTCSLGTENDQNGTGVCRPWINGNSLDGRSLVKLTGTTE 153	:	:	:
QY	149 HNAVCV 155	:	:	:
Dd	154 KDVVCGP 160	:	:	:
RESULT	5			
ID	OX40_RAT	STANDARD;	PRT;	271 AA.
AC	P15725;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).			
GN	TNFRSP4 OR TNXPIL OR OX40.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Rattus.			
OX	NCHI_TaxID=10116;			
NP	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=T-cell;			
RX	MEDLINE=90214614; PubMed=2157591;			
RA	Mallett S., Fossum S., Barclay A.N.;			
RT	"Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes -- a molecule related to nerve growth factor receptor.";			
RL	EMBO J. 9:1063-1068(1990).			
CC	- - FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.			
CC	- - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	- - TISSUE SPECIFICITY: ACTIVATED T-CELLS			
CC	- - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
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DR	EWBL: X17037; CAA34897.1; -			
DR	PIR: S08036; S08036.			
DR	PIR: S12783; S12783.			
DR	HSSP: P25942; ICDF.			
DR	InterPro: IPR001368; -			
DR	Pfam: PF00020; TNFR_c6; 3			
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.			
DR	PROSITE; PS50050; TNFR_NGFR_2; 2.			
KW	Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;			
KW	Signal.			
FT	SIGNAL	1	19	POTENTIAL.
FT	CHAIN	20	271	OX40L RECEPTOR.
FT	DOMAIN	20	210	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	211	235	POTENTIAL.
FT	DOMAIN	236	271	CYTOPASMIC (POTENTIAL).
FT	DOMAIN	25	164	4 X TNFR-CYS.
FT	REPEAT	25	60	TNFR-CYS 1.
FT	REPEAT	61	102	TNFR-CYS 2.
FT	REPEAT	103	123	TNFR-CYS 3 (INCOMPLETE).
FT	REPEAT	124	164	TNFR-CYS 4.
FT	CARBOHYD	143	143	N-LINKED (GLCNAC...) (POTENTIAL).
SQ	SEQUENCE	271 AA;	238995 MW;	C06465136B16E821 CRC64;

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:15:26 ; Search time 43.78 Seconds  
(without alignments)  
128.321 Million cell updates/sec

Title: us-09-512-363-2\_copy\_1\_164

Perfect score: 979

Sequence: 1 MAQHGAMGAFRALCGLALC.....GNKTHNAVCPGSPAPPLG 164

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	162	16.5	272	1	OX40_MOUSE
2	162	16.5	277	1	OX40_HUMAN
3	160.5	16.4	255	1	41BB_HUMAN
4	153	15.6	256	1	41BB_MOUSE
5	151	15.4	271	1	OX40_RAT
6	135.5	13.8	289	1	CD40_MOUSE
7	134.5	13.7	1801	1	CD40_MOUSE
8	127.5	13.0	1799	1	CD40_MOUSE
9	122.5	12.5	269	1	CD40_BOVIN
10	121	12.4	435	1	TNRC_HUMAN
11	121	12.4	461	1	TNRC_MOUSE
12	119	12.2	474	1	TNRC_MOUSE
13	118.5	12.1	277	1	CD40_HUMAN
14	115.5	11.8	1370	1	IGIR_RAT
15	111.5	11.4	1798	1	LMB2_HUMAN
16	110.5	11.3	2907	1	FBN2_MOUSE
17	109.5	11.2	2531	1	NTC1_MOUSE
18	109	11.1	3635	1	LMA5_MOUSE
19	108.5	11.1	1373	1	IGIR_MOUSE
20	106.5	10.9	2911	1	FBN2_HUMAN
21	105	10.7	1172	1	TSP2_HUMAN
22	104.5	10.7	684	1	FBL1_CHICK
23	102.5	10.5	956	1	TSP3_MOUSE
24	102	10.4	186	1	AG13_WHEAT
25	101.5	10.4	1367	1	IGIR_HUMAN
26	101.5	10.4	2318	1	NTC3_MOUSE
27	101	10.3	4543	1	LRP1_CHICK
28	100.5	10.3	2531	1	NTC1_RAT
29	100	10.2	581	1	IRR_RAT
30	100	10.2	1106	1	STC_DROME
31	99.5	10.2	169	1	KRUA_HUMAN
32	99.5	10.2	227	1	AGL_ORYZA
33	99.5	10.2	2569	1	LMA3_MOUSE

RESULT 1

ID	OX40_MOUSE	STANDARD;	PRT;	272 AA.
AC	P47741			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).			
GN	TNFRSF4 OR TXGP1 OR OX40.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BA1B/C;			
RX	MEDLINE=94044750; PubMed=8228223;			
RA	Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J.,			
RA	Claassen E., Noelle R.J., Fell H.;			
RT	"Cloning of mouse OX40: a T cell activation marker that may mediate			
RT	T-B cell interactions.";			
RL	J. Immunol. 151:5261-5271(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95255413; PubMed=7737295;			
RA	Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,			
RA	Barclay A.N.;			
RT	"Gene structure and chromosomal localization of the mouse homologue			
RT	of rat OX40 protein.";			
RL	Eur. J. Immunol. 25:926-930(1995).			
CC	-!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.			
CC	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; Z21674; CAA79772.1; -			
DR	EMBL; X85214; CAA59476.1; -			
DR	HSSP; P25942; ICDF.			
DR	MGI; M104512; Tnfrsf4.			
DR	InterPro; IPR001368; -			
DR	Pfam; PF00020; TNFR_C6; 3.			
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.			
DR	PROSITE; PS50050; TNFR_NGFR_2; 2.			
KW	Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;			
KW	Signal.			
FT	SIGNAL	1	19	POTENTIAL.
FT	CHAIN	20	272	OX40L RECEPTOR.
FT	DOMAIN	20	211	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	212	236	POTENTIAL.

ALIGNMENTS

DR	EMBL; S76792; AAB33944.1; ALT_INIT.	
DR	HSSP; P25942; ICDF.	
DR	MIM; 600315; .	
DR	InterPro; IPR001368; .	
DR	Pfam; PF00020; TNFR_C6; 3.	
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.	
DR	PROSITE; PS00050; TNFR_NGFR_2; 2.	
KW	Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;	
KW	Signal.	
FT	SIGNAL	1 28
FT	CHAIN	29 277
FT	DOMAIN	29 214
FT	TRANSMEM	215 235
FT	DOMAIN	236 277
FT	DOMAIN	30 169
FT	REPEAT	30 65
FT	REPEAT	66 107
FT	REPEAT	108 126
FT	REPEAT	127 167
FT	CARBOHYD	146 146
FT	CARBOHYD	160 160
SQ	SEQUENCE	277 AA; 29340 MW; 49F15525941550BF CRC64;

  

Query Match	16.5%;	Score 162;	DB 1;	Length 277;
Best Local Similarity	29.7%;	Pred. No. 1.9e-07;		
Matches	51;	Conservative	11;	Mismatches 92; Indels 18; Gaps

  

QY	5	GAMGAFRALGLIALICALSLG-----QRTGGGCGPGRLLLTGTDA	CRVHT 54
DB	4	GARRLGRGPCAALLLLGLGLSTVTLGHCVGDTGPSNDRCCHECR--PGNGMVSRGSR	SRQN 61
QY	55	TRCCRDYPG--ECCSEWDCM-CVQPEFHCGD---PCCTTCRRHPCPCGQGV	QSOGKFSF 10
DB	62	TVCRPCGPGFTNDVVSSRCPKPCTWNCNLSRSGERKQLCTATQD	TVCRCRAGTQPLDSYK 12
QY	109	GFCQIDCASGTFSGGHEGCHKPWTDCDTQFGELTVPPGNKTHNAV	CVGPSPPA 150
DB	122	GVDCAPCPGPHFSPCDNQACKPWINCTLAGKHTLQPASNSSDAICED	RDPPA 173

  

RESULT	3	
ID	41BB_HUMAN	STANDARD; PRT; 255 AA.
AC	Q07011;	
DT	01-FEB-1995 (Rel. 31, Created)	
DT	01-FEB-1995 (Rel. 31, Last sequence update)	
DT	01-OCT-2000 (Rel. 40, Last annotation update)	
DE	4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB HOMOLOG)	
DE	(T-CELL ANTIGEN ILA) (CD137 ANTIGEN).	
GN	TNFRSF9 OR ILA.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
OX	[1]	
PP	SEQUENCE FROM N.A.	
RC	TISSUE=Blood;	
RC	MEDLINE=94374434; PubMed=8088337;	
RA	Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J.,	
RA	Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;	
RT	"Molecular and biological characterization of human 4-1BB and its	
RT	ligand."	
RL	Eur. J. Immunol. 24:2219-2227(1994).	
RL	[2]	
RN	SEQUENCE FROM N.A.	
RC	TISSUE=Blood;	
RC	MEDLINE=94085794; PubMed=8262389;	
RA	Schwarz H., Tuckwell J., Lotz M.;	
RT	"A receptor induced by lymphocyte activation (ILA): a new member of	
RT	the human nerve-growth-factor/tumor-necrosis-factor receptor	
RT	family."	
RL	Gene 134:295-298(1993).	



A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of its role in the regulation of tumor necrosis factor production and release  
A:Reference number: A36007; MUID:90349572  
A:Accession: A36007  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>  
A:Cross-references: GB:M35857; NID:9339751; PID:9339752  
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M. J. Biol. Chem. 265, 20131-20138, 1990  
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors  
A:Reference number: A23666; MUID:91056048  
A:Accession: A23666  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 23-40; 65-69; 136-141; 300-306 <LOE>  
R:Engelmann, H.; Novick, D.; Wallach, D. J. Biol. Chem. 265, 1531-1536, 1990  
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence for their role in the regulation of tumor necrosis factor production and release  
A:Reference number: A35010; MUID:90110215  
A:Accession: B35010  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 27-31 <ENG>  
R:Kuhnert, P.; Kemper, O.; Wallach, D. Gene 150, 381-386, 1994  
A:Title: Cloning, sequencing and partial functional characterization of the 5' region of the human tumor necrosis factor receptor type 2  
A:Reference number: I38094; MUID:95121934  
A:Accession: I38094  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-37 <RES>  
A:Cross-references: EMBL:X80021; NID:9666044; PID:CAA56324.1; PID:g825701  
C:Genetics:  
A:Gene: GDB:TNFR2  
A:Cross-references: GDB:125914; OMIM:191191  
A:Map position: lp36.2-1p36.2  
A:Introns: 26/3  
A:Note: the list of introns is incomplete  
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>  
F:40-76/Domain: NGF receptor repeat homology <NG1>  
F:78-119/Domain: NGF receptor repeat homology <NG2>  
F:120-162/Domain: NGF receptor repeat homology <NG3>  
F:164-201/Domain: NGF receptor repeat homology <NG4>  
F:262-279/Domain: transmembrane #status predicted <TMN>  
F:280-461/Domain: intracellular #status predicted <INT>  
F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.9%; Score 117; DB 1; Length 461;  
Best Local Similarity 30.4%; Pred. No. 0.0089;  
Matches 35; Conservative 11; Mismatches 51; Indels 18; Gaps 6;  
QY 10 TRCCRDYEGEECCSEMD---CMCVPERHC-----GDPCCCTCRHHPCPPCGVQSQK 60  
Db 98 SKCSDDQVETACTREQNRICTC-RPGWYCALSKGEGRLCAPLR--KCRPGFGVARGPT 154  
QY 61 FSFGQCIDCASGTPSG--GHEGHCKPWTDCQFGFLTVFPNGKTHNAVCVPGSP 113  
Db 155 ETSDDVCKPCAPGTFSTNTSSDIDCRPHQICN----VVAIPGNASMDVCTSTSP 205

RESULT 12  
S53869  
laminin beta-2 chain precursor (version 2) - human  
N:Alternate names: s-laminin  
C:Species: Homo sapiens (man)  
C:Date: 27-Oct-1995 #sequence\_revision 23-Feb-1996 #text\_change 24-Sep-1998  
C:Accession: S53869  
R:Iivanainen, A.; Vuolteenaho, R.; Sainio, K.; Eddy, R.; Shows, T.B.; Sariola, H.; Tryggvason, K. J. Biol. Chem. 269, 489-497, 1994

A:Title: The human laminin beta-2 chain (S-laminin): structure, expression in fetal tissues and its role in the regulation of tumor necrosis factor production and release  
A:Reference number: S53869  
A:Accession: S53869  
A:Molecule type: mRNA  
A:Residues: 1-1798 <LI>  
C:Genetics:  
A:Gene: GDB:LAMB2  
A:Cross-references: GDB:132363; OMIM:150325  
A:Map position: 3p21.3-3p21.2  
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C:Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer  
F:1-32/Domain: signal sequence #status predicted <SIG>  
F:33-1798/Product: laminin beta-2 chain #status predicted <MAT>  
F:283-344/Domain: laminin-type EGF-like homology <LE01>  
F:347-407/Domain: laminin-type EGF-like homology <LE02>  
F:410-467/Domain: laminin-type EGF-like homology <LE03>  
F:470-519/Domain: laminin-type EGF-like homology <LE04>  
F:522-552/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F:783-828/Domain: laminin-type EGF-like homology <LE06>  
F:831-874/Domain: laminin-type EGF-like homology <LE07>  
F:877-924/Domain: laminin-type EGF-like homology <LE08>  
F:927-983/Domain: laminin-type EGF-like homology <LE09>  
F:986-1035/Domain: laminin-type EGF-like homology <LE10>  
F:1038-1092/Domain: laminin-type EGF-like homology <LE11>  
F:1095-1140/Domain: laminin-type EGF-like homology <LE12>  
F:1143-1187/Domain: laminin-type EGF-like homology <LE13>

Query Match 15.2%; Score 112; DB 2; Length 1798;  
Best Local Similarity 24.9%; Pred. No. 0.058;  
Matches 44; Conservative 8; Mismatches 47; Indels 78; Gaps 10;  
QY 5 CRVHTTRC--CRDPYEGEECCSEMDCMCVQEPFHCQDPCCT---TCRHHPCPPCGVQ--- 56  
Db 886 CNTHTGACLCGRDHTGGEHCER---CI-AGFH-GDPLPYGQCRPCPCPGSGQRHF 939  
QY 57 ----SOGKES-----FGQCIDCASGTF----- 75  
Db 940 ATSCHQDEYSQQIVCHRCAGYTGURCEACAPGHGDSRPGRCQLCESGNIDPMPDA 999  
QY 76 -----SGHEGHCKPWTDCQFGFLTVFPNGKTHNAVVC-VPGSPPAE 116  
Db 1000 CDPHTGQCLRLHHTGPHCAHCKP-----GFHGQAARQSHRCTNLLGTNPQQ 1049

RESULT 13  
I54182  
tumor necrosis factor receptor 2-related protein - human  
C:Species: Homo sapiens (man)  
C:Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 17-Mar-2000  
C:Accession: I54182  
R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P. Genomics 16, 214-218, 1993  
A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequences  
A:Reference number: I54182; MUID:93252381  
A:Accession: I54182  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-435 <RES>  
A:Cross-references: GB:I04270; NID:g339761; PID:AAA36757.1; PID:g339762  
C:Genetics:  
A:Gene: GDB:UTBR  
A:Cross-references: GDB:1230195; OMIM:600979  
A:Map position: 12p13.3-12p13.1  
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 15.1%; Score 111.5; DB 2; Length 435;  
Best Local Similarity 25.7%; Pred. No. 0.024;  
Matches 39; Conservative 12; Mismatches 62; Indels 39; Gaps 9;  
QY 2 ARCCRVHTTRC-----CRDPGEE-----CCS--EWDCMCVQP 32  
Db 155 ETSDDVCKPCAPGTFSTNTSSDIDCRPHQICN----VVAIPGNASMDVCTSTSP 205

Search completed: September 4, 2001, 16:12:13  
Job time: 1110 sec



Query Match 20.2%; Score 149; DB 2; Length 271;  
Best Local Similarity 28.9%; Pred. No. 1.4e-05;  
Matches 37; Conservative 10; Mismatches 51; Indels 30; Gaps 5;

QY 11 RCRDR-YGEECCSEWD-----CMCQVQPFHCG-----DPC--CTTCRRHH----- 47  
Db 36 KCRRECQPGHGMVSRCDHTRDTVCHPCEPGFYNEAVNYDTCKQCTQCNRHSGSELKQNT 95  
QY 48 -----PCPPGGQGVQSGKFSFGFCIDCASGTFSGGHEGCHKPWTCTQFGFLTVPFG 100  
Db 96 PTEDTVQCRRPGTQPRQDSSHKLGVDVCPFGPHFSGNQACRPWTNCTLSGKQIRHPA 155  
QY 101 NKTHNAVC 108  
Db 156 SNSLDTVC 163

RESULT 6  
JC5559  
lectin-B - Virginian pokeweed  
C:Species: Phytolacca americana (Virginian pokeweed)  
C:Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 17-Mar-2000  
C:Accession: JC5559  
R:Yamaguchi, K.; Yurino, N.; Kino, M.; Ishiguro, M.; Funatsu, G.  
Biosci. Biotechnol. Biochem. 61, 690-698, 1997  
A:Title: The amino acid sequence of mitogenic lectin-B from the roots of pokeweed (Phytolacca americana)  
A:Reference number: JC5559; MUID:97290889  
A:Accession: JC5559  
A:Molecule type: protein  
A:Residues: 1-295 <YAM>  
A:Experimental source: root  
C:Comment: This protein is a lectin specific for N-acetylglucosamine-containing saccharides  
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p  
C:Keywords: glycoprotein  
F:96.139/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.2%; Score 127; DB 2; Length 295;  
Best Local Similarity 34.1%; Pred. No. 0.00097;  
Matches 28; Conservative 14; Mismatches 20; Indels 20; Gaps 6;

QY 11 RCRDRYPG-----EECCSEMDCMVQPEFHCGDPCCTTCRRHHPGPPGGVQSGKFSFGF 65  
Db 173 RGGKDFAGRTCLNDLCCSEWG-WCGSSEAHCQGCGQSCNRYNC-----GR-NFGF 221  
QY 66 Q-C---IDCASGTFSGGHEGHC 83  
Db 222 RTCPNELCCSSGGWCGSNDAC 243

RESULT 7  
A46476  
B cell-associated surface molecule CD40, long splice form - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Nov-2000  
C:Accession: A46476; A46515  
R:Torres, R.M.; Clark, E.A.  
J. Immunol. 149, 620-626, 1992  
A:Title: Differential increase of an alternatively polyadenylated mRNA species of murine CD40  
A:Reference number: A46476; MUID:92105763  
A:Accession: A46476  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-305 <TOR>  
A:Cross-references: GB:M83312; NID:gl553058  
A:Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)  
R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, J.  
J. Immunol. 149, 3921-3926, 1992  
A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.  
A:Reference number: A46515; MUID:93094586

A:Accession: B38634  
A:Molecule type: mRNA  
A:Residues: 1-474 <LE0>  
A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828  
R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk  
Mol. Cell. Biol. 11, 3020-3026, 1991  
A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for  
A:Reference number: A40254; MUID:91246168  
A:Accession: A40254  
A:Molecule type: mRNA  
A:Residues: 1-474 <GO>  
A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828  
R:Kisssnerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.  
submitted to the EMBL Data Library, May 1995  
A:Description: Characterization of the promoter region of the murine p75-TNF receptor.  
A:Reference number: S54816  
A:Accession: S54816  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-22 <KIS>  
A:Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044  
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
C:Keywords: cytokine receptor; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>  
F:40-77/Domain: NGF receptor repeat homology <NG1>  
F:79-120/Domain: NGF receptor repeat homology <NG2>  
F:166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 16.1%; Score 119; DB 2; Length 474;  
Best Local Similarity 31.0%; Pred. No. 0.0062;  
Matches 36; Conservative 8; Mismatches 54; Indels 18; Gaps 5;

Qy 1 DARCVRHTTRCCRDYGECCSEWDCMCVQPERHCGDPCCTC-RHHPCPPGGVQSG 59  
Db 107 EIRACTKQKNVCAACAGRYCAL-----KTHSGS--CRQCMRLSKCGPGFGVASSR 155

Qy 60 KFSFGFCIDCAGTFSG--GHEGHCCKPMTDCTQFGFLTPPGNKTNNAVCPGSP 113  
Db 156 APNGVLKACAPCTFSDTSSDVCPRHICS----ILAIPGNASTDAVCAPESP 207

RESULT 10  
MMRTS  
laminin beta-2 chain precursor - rat  
N:Alternate names: laminin chain B3; S-laminin  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 10-Dec-1999  
R:Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.  
Nature 338, 229-234, 1989  
A:Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neuro  
A:Reference number: S03539; MUID:89159410  
A:Accession: S03539  
A:Molecule type: mRNA  
A:Residues: 1-1801 <HUN>  
A:Cross-references: EMBL:X16563; NID:g57250; PIDN:CAA34561.1; PID:g57251  
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C:Function:  
A:Description: Interact with cells and with other basement membrane proteins to promote  
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
F:1-35/Domain: signal sequence #status predicted <SIG>  
F:36-1801/Product: laminin beta-2 chain #status predicted <MAT>  
F:36-285/Domain: VI <DOM6>  
F:286-555/Domain: V <DOM5>  
F:286-347/Domain: laminin-type EGF-like homology <LE01>  
F:350-410/Domain: laminin-type EGF-like homology <LE02>  
F:413-470/Domain: laminin-type EGF-like homology <LE03>  
F:473-522/Domain: laminin-type EGF-like homology <LE04>  
F:525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F:556-784/Domain: laminin-type IV <DOM4>

F:786-831/Domain: laminin-type EGF-like homology <LE06>  
F:788-1196/Domain: III <DOM3>  
F:834-877/Domain: laminin-type EGF-like homology <LE07>  
F:880-927/Domain: laminin-type EGF-like homology <LE08>  
F:930-986/Domain: laminin-type EGF-like homology <LE09>  
F:989-1038/Domain: laminin-type EGF-like homology <LE10>  
F:1041-1095/Domain: laminin-type EGF-like homology <LE11>  
F:1098-1143/Domain: laminin-type EGF-like homology <LE12>  
F:1146-1190/Domain: laminin-type EGF-like homology <LE13>  
F:1197-1412/Domain: II <DOM2>  
F:1197-1412/Region: heptad repeats  
F:1413-1445/Domain: alpha <ALP>  
F:1446-1801/Region: heptad repeats  
F:1446-1801/Domain: I <DOM1>  
F:45-50/Disulfide bonds: #status predicted  
F:251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #statu  
F:1193,1196,1800/Disulfide bonds: interchain #status predicted

Query Match 16.0%; Score 118; DB 1; Length 1801;  
Best Local Similarity 26.0%; Pred. No. 0.019;  
Matches 46; Conservative 5; Mismatches 44; Indels 82; Gaps 10;

Qy 5 CRVHTTRC--CRDYGEECCSEWDCMCVQPERHCGDPCCT---TCRHHPCPPGGVQSG 59  
Db 889 CDAHTGACLCGRDYGGEHCEH-----CI-AGFH-GDRLPYGGQCRPCPCPEPG--SOR 940  
Qy 60 KFS-----FGFCIDCAGTFSG-----FGHQAARQSCRCCTCNLLGTDP 1050

Db 941 HFATSCHRDGYSSQIVCHCRAGYTGRLCEACAPGHGDPKPGRCQCECSGNIDPTDP 1000

Qy 76 -----SGHGHCKPMTDCTQFGFLTPPGNKTNNAVCPGSP 114  
Db 1001 GACDPHTGCLRLHHTGPHGCHCKP-----GFHQAARQSCRCCTCNLLGTDP 1050

RESULT 11  
A35356  
tumor necrosis factor receptor 2 precursor [validated] - human  
N:Alternate names: 75k tumor necrosis factor receptor; TNF receptor type 2  
C:Species: Homo sapiens (man)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 08-Dec-2000  
C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094  
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower,  
Science 248, 1019-1023, 1990  
A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular a  
A:Reference number: A35356; MUID:90260639  
A:Accession: A35356  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-461 <SMI>  
A:Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186  
R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squir  
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990  
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally oc  
A:Reference number: A36475; MUID:91045991  
A:Accession: A36475  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-195; R, 197-461 <KOH>  
A:Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758  
R:Dembik, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus,  
Cytokine 2, 231-237, 1990  
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular  
A:Reference number: A48416; MUID:91370690  
A:Accession: A48416  
A>Status: preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 23-461 <DEM>  
A:Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649  
A:Note: sequence extracted from NCBI backbone (NCBI:63368, NCBIP:63371)  
R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990

GenCore version 4.5

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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:12:12 ; Search time 80.15 Seconds  
(without alignments)  
113.098 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_46\_164

Perfect score: 737

Sequence: 1 DARRCVHTRCCRDYPGEE.....GNKTHNAVCPGPPAPPLG 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_68.\*

1: p1r1.\*

2: p1r2.\*

3: p1r3.\*

4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159.5	21.6	255	2	I38426
2	158	21.4	272	2	I48700
3	150	20.4	277	2	I37532
4	149.5	20.3	256	2	B32393
5	149	20.2	271	2	S12783
6	127	17.2	295	2	JC5559
7	123	16.7	305	2	A46476
8	120.5	16.4	459	2	I48854
9	119	16.1	474	2	B38634
10	118	16.0	1801	1	MMRTS
11	117	15.9	461	1	A35356
12	112	15.2	1798	2	S53869
13	111.5	15.1	435	2	I54182
14	111	15.1	277	2	A50711
15	110	14.9	1371	2	A33837
16	109	14.8	329	2	A48805
17	108	14.7	1574	2	T13954
18	103	14.0	1797	2	A55677
19	99	13.4	1367	1	IGHUR1
20	94	12.8	152	2	T18975
21	93	12.6	3635	2	T10053
22	92	12.5	416	1	JN0006
23	92	12.5	1172	1	T5HUP2
24	92	12.5	1820	2	A55494
25	91.5	12.4	1106	2	T13938
26	91.5	12.4	2318	2	A45306
27	91	12.3	956	1	A46016
28	90.5	12.3	1106	2	T44598
29	90.5	12.3	2150	2	T32497

## ALIGNMENTS

## RESULT 1

I38426

Lymphocyte activation-induced receptor ILA precursor - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 01-Dec-2000

C:Accession: I38426; JT0752

R:Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.

Eur. J. Immunol. 24, 2219-2227, 1994

A:Title: Molecular and biological characterization of human 4-1BB and its ligand.

A:Reference number: I38426; MUID:94374434

A:Accession: I38426

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-255 &lt;RES&gt;

A:Cross-references: EMBL:U03397; NID:g571320; PIDN:AAA53133.1; PID:g571321

R:Schwarz, H.; Tuckwell, J.; Lotz, M.

Gene 134, 295-298, 1993

A:Title: A receptor induced by lymphocyte activation (ILA): a new member of the human

A:Reference number: JT0752; MUID:94085794

A:Accession: JT0752

A:Molecule type: mRNA

A:Residues: 1-106,'R',108-255 &lt;SCH&gt;

C:Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-ne

C:Comment: This receptor recognizes soluble, cell-surface bound or extracellular mat

C:Superfamily: CD27 antigen; Ngf receptor repeat homology

C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein

F:1-17/Domain: signal sequence #status predicted &lt;SIG&gt;

F:18-255/Product: lymphocyte activation-induced receptor ILA #status predicted &lt;MAT&gt;

F:187-213/Domain: transmembrane #status predicted &lt;TM&gt;

F:138,149/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:234,235/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status pred

F:242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status pred

Query Match

Best Local Similarity 21.6%; Score 159.5; DB 2; Length 255;

Matches 44; Conservative 12; Mismatches 43; Indels 39; Gaps 8;

QY	3	RCRCVHTTRCCRDYPG	-----ECCS-----	EWDCMCVQPEFHGCDPCCTTCRHHPCPPGQ	53
DB	60	RYCDI	-----CROCKGVFRTRKESSTSNACDC---	TPGFHCLGACSMC-EDQCKQGQ	110
QY	54	GVQSQKFSFGFCIDCASGTGSGHGGHCKPMTDCTQFGFLTVFPGNKTHNAVCPG--	111		
DB	111	ELTKKG	-----CKDCCFGTFENDQKRGICRPWTNCSLDGKSVLVNCTKRDVVCGSP	163	
QY	112	-----SPPA---	EP	117	
DB	164	DLSPGASSVTPPAPAREP	181		
RESULT	2				

Insulin receptor-r  
insulin receptor-r  
fibrillin-2 precu  
hypothetical prote  
thrombospondin 3 p  
laminin beta-1 cha  
notch3 protein - h  
fibrillin-2 precu  
Notch homolog prot  
crumbs protein - f  
Notch-1 protein -  
hypothetical prote  
disintegrin-like m  
hypothetical prote  
thrombospondin 2 p  
notch4 - mouse

30 90 12.2 540 2 B47417  
31 90 12.2 1268 2 B36502  
32 90 12.2 2907 2 A57278  
33 89 12.1 164 2 T24272  
34 89 12.1 956 2 A57121  
35 89 12.1 1786 1 MMHUB1  
36 89 12.1 2321 2 S78549  
37 89 12.1 2918 2 A54105  
38 88.5 12.0 2352 2 T30201  
39 88 11.9 2139 2 A35672  
40 88 11.9 2531 2 A46019  
41 87.5 11.9 259 2 T21011  
42 87.5 11.9 814 2 G02390  
43 87.5 11.9 1111 2 T26972  
44 87.5 11.9 1172 2 A42587  
45 87.5 11.9 1964 2 T09059

I48700  
gene ox40 protein - mouse  
N:Alternate names: OX40 antigen  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 11-Jan-2000  
C:Accession: I48700; I48334; S34377  
R:Calderhead, D.M.; Buhlmann, J.E.; van den Bortwegh, A.J.; Claassen, E.; Noelle, R.J.; J. Immunol. 151, 5261-5271, 1993  
A:Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell interaction  
A:Reference number: I48700; MUID:94044750  
A:Accession: I48700  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-272 <RES>  
A:Cross-references: EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g312828  
R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N. Eur. J. Immunol. 25, 926-930, 1995  
A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40  
A:Reference number: I48334; MUID:95255413  
A:Accession: I48334  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-14,'G',16-272 <RE2>  
A:Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819  
C:Genetics:  
A:Gene: ox40  
A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1  
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 21.4%; Score 158; DB 2; Length 272;  
Best Local Similarity 27.4%; Pred. No. 2.5e-06;  
Matches 40; Conservative 11; Mismatches 45; Indels 50; Gaps 6;  
QY 5 CRVHT-----TRCRRD-YPG-----EECCSEWDCMCVQPEFFHCGDPC----- 40  
Db 27 CVKHTPSGHKKCCRECPQGHGWSRCDHTDTC-----HPCETGYNEAVNYDTCK 78  
QY 41 -CTTCRRHP-----CPPGGVQSGKFSFGFCIDCASGTFSGGHEGH 82  
Db 79 OCTQCNRHSSELKQNCPTQDTVCRCPGTPRODSGYKLGVDVCPCHPFGPNQA 138  
QY 83 CKPWTDCTQFGFLTVFNGKTHNAV 108  
Db 139 CKPWTNCTLSGKQTRHPASDSDAVC 164

RESULT 3  
I37552  
OX40 homolog - human  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000  
C:Accession: I37552  
R:Latza, U.; Durrkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat Eur. J. Immunol. 24, 677-683, 1994  
A:Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment  
A:Reference number: I37552; MUID:94170844  
A:Accession: I37552  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-277 <RES>  
A:Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958  
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 20.4%; Score 150; DB 2; Length 277;  
Best Local Similarity 30.8%; Pred. No. 1.2e-05;  
Matches 41; Conservative 11; Mismatches 53; Indels 28; Gaps 7;  
QY 11 RCCRD-YPG-----EECCSEWDCMC--VQPEFH-----CGDPC--CTTC-----RHHPCP 50  
Db 41 RCCECRPGNGMVSRCSSRONTVCRPGPGFYNDVVSCKPKCPCTWCNLRSGSERKQLCT 100

I48700  
gene ox40 protein - mouse  
N:Alternate names: OX40 antigen  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 11-Jan-2000  
C:Accession: I48700; I48334; S34377  
R:Calderhead, D.M.; Buhlmann, J.E.; van den Bortwegh, A.J.; Claassen, E.; Noelle, R.J.; J. Immunol. 151, 5261-5271, 1993  
A:Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell interaction  
A:Reference number: I48700; MUID:94044750  
A:Accession: I48700  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-272 <RES>  
A:Cross-references: EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g312828  
R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N. Eur. J. Immunol. 25, 926-930, 1995  
A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40  
A:Reference number: I48334; MUID:95255413  
A:Accession: I48334  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-14,'G',16-272 <RE2>  
A:Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819  
C:Genetics:  
A:Gene: ox40  
A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1  
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 21.4%; Score 158; DB 2; Length 272;  
Best Local Similarity 27.4%; Pred. No. 2.5e-06;  
Matches 40; Conservative 11; Mismatches 45; Indels 50; Gaps 6;  
QY 5 CRVHT-----TRCRRD-YPG-----EECCSEWDCMCVQPEFFHCGDPC----- 40  
Db 27 CVKHTPSGHKKCCRECPQGHGWSRCDHTDTC-----HPCETGYNEAVNYDTCK 78  
QY 41 -CTTCRRHP-----CPPGGVQSGKFSFGFCIDCASGTFSGGHEGH 82  
Db 79 OCTQCNRHSSELKQNCPTQDTVCRCPGTPRODSGYKLGVDVCPCHPFGPNQA 138  
QY 83 CKPWTDCTQFGFLTVFNGKTHNAV 108  
Db 139 CKPWTNCTLSGKQTRHPASDSDAVC 164

RESULT 3  
I37552  
OX40 homolog - human  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000  
C:Accession: I37552  
R:Latza, U.; Durrkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat Eur. J. Immunol. 24, 677-683, 1994  
A:Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment  
A:Reference number: I37552; MUID:94170844  
A:Accession: I37552  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-277 <RES>  
A:Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958  
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 20.4%; Score 150; DB 2; Length 277;  
Best Local Similarity 30.8%; Pred. No. 1.2e-05;  
Matches 41; Conservative 11; Mismatches 53; Indels 28; Gaps 7;  
QY 11 RCCRD-YPG-----EECCSEWDCMC--VQPEFH-----CGDPC--CTTC-----RHHPCP 50  
Db 41 RCCECRPGNGMVSRCSSRONTVCRPGPGFYNDVVSCKPKCPCTWCNLRSGSERKQLCT 100

QY 51 PGQ-----GVQSQKFSFGFCIDCASGTFSGGHEGHCKPWTDTCTQFGFLTVFPNGK 102  
Db 101 ATQDTVCRCRAGTQPLDSYKPGVDCAPCPGPHFSPGDNQACKPWTNCTLAGKHTLPASN 160  
QY 103 THNAVCPGSPPA 115  
Db 161 SSDAICEDRDPPA 173

RESULT 4  
B32393  
T-cell antigen 4-1BB precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 21-Jul-2000  
C:Accession: B32393; I48879  
R:Kwon, B.S.; Weissman, S.M. Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989  
A:Title: cDNA sequence of two inducible T-cell genes.  
A:Reference number: A32393; MUID:89184547  
A:Accession: B32393  
A:Molecule type: mRNA  
A:Residues: 1-256 <KWO>  
A:Cross-references: GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122  
R:Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.F. J. Immunol. 152, 2256-2262, 1994  
A:Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1B  
A:Reference number: I48879; MUID:94179805  
A:Accession: I48879  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-256 <RES>  
A:Cross-references: EMBL:U02567; NID:g117783; PIDN:AAA93113.1; PID:g409178  
C:Genetics:  
A:Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: transmembrane protein  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-256/Product: 4-1BB protein #status predicted <MAT>

Query Match 20.3%; Score 149.5; DB 2; Length 256;  
Best Local Similarity 33.6%; Pred. No. 1.2e-05;  
Matches 37; Conservative 15; Mismatches 41; Indels 17; Gaps 6;  
QY 5 CRVHTTCCRDYPGEECGSEW---DCMCVQPEFFHCGDPCCTTCRHHPCPPGQGVQSGKRF 61  
Db 64 CRV---CAGYFRPKKFCSSSTHNAECIE-GFCHLGQCTRC-EKDCRPGQLTKQG--- 115  
QY 62 SFGFCIDCASGTFSGGH-EGHCKPWTDTCTQFGFLTVFPNGKTHNAVCP 110  
Db 116 -----CKTCSLGTENDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGP 160

RESULT 5  
SI2783  
OX40 antigen precursor - rat  
N:Alternate names: nerve growth factor receptor homolog  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 05-Nov-1999  
C:Accession: SI2783; S08036  
R:Mallett, S.; Fossum, S.; Barclay, A.N. EMBO J. 9, 1063-1068, 1990  
A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphoc  
A:Reference number: SI2783; MUID:90214614  
A:Accession: SI2783  
A:Molecule type: mRNA  
A:Residues: 1-271 <MAL>  
A:Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: growth factor receptor; transmembrane protein  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-271/Product: OX40 antigen #status predicted <MAT>  
F:211-235/Domain: transmembrane #status predicted <TMM>







QY 33 EFHCGDPC--CTTCR-HHPGPPGVOSQKFSFG-FQCIDCASGTF--SGHGHCKPWP 86  
 DB 129 GMFCAAWALECTHCELLSDCPGTEALKEVKGNNHCVPCKAGHFTQNTSSPSARCQPH 188  
 QY 87 TDCTQFGFLVFPCKNTHNAVCPGSPPAEPL 118  
 DB 189 TRCENQGLVEAAGTAQSDTTC---KNPLEPL 217

RESULT 12  
 CD40\_HUMAN STANDARD; PRT; 277 AA.  
 ID CD40\_HUMAN  
 AC P25942;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)  
 DE (TUMOR NECROSIS FACTOR RECEPTOR 5).  
 GN TNFRSF5 OR CD40.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89356608; PubMed=2475341;  
 RA Stamenkovic I., Clark E.A., Seed B.;  
 RT "A B-lymphocyte activation molecule related to the nerve growth  
 factor receptor and induced by cytokines in carcinomas";  
 RL ENBO J. 8:1403-1410(1989).  
 RN [2]  
 RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.  
 RX MEDLINE=97189482; PubMed=9037712;  
 RA Bajorath J., Aruffo A.;  
 RT "Construction and analysis of a detailed three-dimensional model of  
 the ligand binding domain of the human B cell receptor CD40.";  
 RL Proteins 27:59-70(1997).  
 RN [3]  
 RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.  
 RX MEDLINE=98266353; PubMed=9605317;  
 RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,  
 RA Zheng Z., Naismith J.H., Thomas D.;  
 RT "The role of polar interactions in the molecular recognition of CD40L  
 with its receptor CD40.";  
 RL Protein Sci. 7:1124-1135(1998).  
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X60592; CAA43045.1; -;  
 DR PIR; S04460; S04460.  
 DR PDB; 1CDF; 01-APR-97.  
 DR MIM; 109535; -;  
 DR InterPro: IPR001368; -;  
 DR Pfam; PF000020; TNFR\_C6; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 4.  
 KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;  
 KW 3D-structure. 1 19  
 FT SIGNAL 20 277 POTENTIAL.  
 FT CHAIN CD40L RECEPTOR.

FT DOMAIN 20 193  
 FT TRANSMEM 194 215  
 FT DOMAIN 216 277  
 FT DOMAIN 25 187  
 FT REPEAT 25 60  
 FT REPEAT 61 103  
 FT REPEAT 104 144  
 FT REPEAT 145 187  
 FT DISULFID 26 37  
 FT DISULFID 38 51  
 FT DISULFID 41 59  
 FT DISULFID 62 77  
 FT DISULFID 83 103  
 FT DISULFID 105 119  
 FT DISULFID 111 116  
 FT DISULFID 125 143  
 FT CARBOHYD 153 153  
 FT CARBOHYD 180 180  
 SQ SEQUENCE 277 AA; 30619 MW; BC8776EC2C4A5680 CRC64;  
 N-LINKED (GLCNAC... ) (POTENTIAL).  
 N-LINKED (GLCNAC... ) (POTENTIAL).  
 Query Match 15.1%; Score 111; DB 1; Length 277;  
 Best Local Similarity 31.5%; Pred. No. 0.0019;  
 Matches 29; Conservative 6; Mismatches 53; Indels 4; Gaps 3;  
 QY 23 SEWDCMCVQPE-FHCGDPCCTTC-RHHPCPPGVOSQKFSFGFQCIDCASGTFSGGHE 80  
 DB 97 SETDTICTCEGWHCTSEACSVLHRSCTPGVSKQIATGVSDTICEPCPVGFFSNVSS 156  
 QY 81 G--HCKPWTDTCTQFGFLVFPCKNTHNAVCP 110  
 DB 157 AFEKCHPWTSCETKDLVVQQAGTKNTKTVVCGP 188

RESULT 13  
 IG1R\_RAT  
 ID IG1R\_RAT STANDARD; PRT; 1370 AA.  
 AC P24062;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR (EC 2.7.1.112).  
 GN IG1R.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=95277910; PubMed=7758167;  
 RA Du J., Delafontaine P.;  
 RT "Inhibition of vascular smooth muscle cell growth through antisense  
 transcription of a rat insulin-like growth factor I receptor cDNA.";  
 RL Circ. Res. 76:963-972(1995).  
 RN [2]  
 RP SEQUENCE OF 1-364 FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RX MEDLINE=90017496; PubMed=2477843;  
 RA Werner H., Woloschak M., Adamo M., Shen-Orr Z., Roberts C.T. Jr.,  
 RA Leroith D.;  
 RT "Developmental regulation of the rat insulin-like growth factor I  
 receptor gene";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:7451-7455(1989).  
 RN [3]  
 RP SEQUENCE OF 913-1017 FROM N.A.  
 RX MEDLINE=92412145; PubMed=1530648;  
 RA Kurachi H., Jobo K., Ohta M., Kawasaki T., Itoh N.;  
 RT "A new member of the insulin receptor family, insulin  
 receptor-related receptor, is expressed preferentially in the  
 kidney.";  
 RL Biochem. Biophys. Res. Commun. 187:934-939(1992).  
 CC -1- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)



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FT DISULFID 443 452 BY SIMILARITY.
FT DISULFID 455 470 BY SIMILARITY.
FT DISULFID 473 487 BY SIMILARITY.
FT DISULFID 475 494 BY SIMILARITY.
FT DISULFID 496 505 BY SIMILARITY.
FT DISULFID 508 522 BY SIMILARITY.
FT DISULFID 784 796 BY SIMILARITY.
FT DISULFID 786 803 BY SIMILARITY.
FT DISULFID 805 814 BY SIMILARITY.
FT DISULFID 817 829 BY SIMILARITY.
FT DISULFID 832 844 BY SIMILARITY.
FT DISULFID 834 851 BY SIMILARITY.
FT DISULFID 853 862 BY SIMILARITY.
FT DISULFID 865 875 BY SIMILARITY.
FT DISULFID 878 887 BY SIMILARITY.
FT DISULFID 880 894 BY SIMILARITY.
FT DISULFID 897 906 BY SIMILARITY.
FT DISULFID 909 925 BY SIMILARITY.
FT DISULFID 928 944 BY SIMILARITY.
FT DISULFID 930 955 BY SIMILARITY.
FT DISULFID 957 966 BY SIMILARITY.
FT DISULFID 969 984 BY SIMILARITY.
FT DISULFID 987 1001 BY SIMILARITY.
FT DISULFID 989 1008 BY SIMILARITY.
FT DISULFID 1011 1020 BY SIMILARITY.
FT DISULFID 1023 1036 BY SIMILARITY.
FT DISULFID 1096 1108 BY SIMILARITY.
FT DISULFID 1098 1115 BY SIMILARITY.
FT DISULFID 1117 1126 BY SIMILARITY.
FT DISULFID 1129 1141 BY SIMILARITY.
FT DISULFID 1144 1156 BY SIMILARITY.
FT DISULFID 1146 1163 BY SIMILARITY.
FT DISULFID 1165 1174 BY SIMILARITY.
FT DISULFID 1177 1188 BY SIMILARITY.
FT DISULFID 1191 1191 INTERCHAIN (PROBABLE).
FT DISULFID 1194 1194 INTERCHAIN (PROBABLE).
FT DISULFID 1798 1798 INTERCHAIN (PROBABLE).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1086 1086 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1250 1250 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1309 1309 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1349 1349 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1500 1500 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1799 AA; 196352 MW; 1F28967A67AEDE33 CRC64;

Query Match . 15.3%; Score 113; DB 1; Length 1799;
Best Local Similarity 25.4%; Pred. No. 0.0054;
Matches 45; Conservative 6; Mismatches 44; Indels 82; Gaps 10;

QY 5 CRVHTTRC--CRDYPGEECCSMDCMVOPFHGDPDCT---TCRHHPCPGQGVQSG 59
DB 887 CDTHTGACLGCRDYGTHGECER----CI-AGFH-GDPLPYGGQCRPCPCPGPG--SQR 938
QY 60 KFS-----FGQCIDCASGTF----- 75
DB 939 HFATSHRDGYSQQIVCHCRAGYTLGRCEACAPGPGDPSPKGGRCQCECSGNDPMDP 998
QY 76 -----SGHGHGCHKPWTDCQFGFLTVFPGNKTHNAVC-VPGSP 114
DB 999 DACDPHTGQCLRLHNTGEPHCGYCKP-----GFHGQAARQSHRCRCNLLGTDP 1048

RESULT 11
TNRC_HUMAN STANDARD; PRT; 435 AA.
AC P36941.
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
DE 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).

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GN LTBR OR TNFR OR TNFRSF3.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93252381; PubMed=8486360;
RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT "Construction and evaluation of a hncDNA library of human 12p
RL transcribed sequences derived from a somatic cell hybrid.";
RN [2]
RP FUNCTION.
RX MEDLINE=94225209; PubMed=8171323;
RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-beta-specific receptor.";
RL Science 264:707-710(1994).
CC -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC -----
DR EMBL; L04270; AAA36757.1; -.
DR HSP; P25942; LCDF.
DR MIM; 600979; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 435 LYMPHOTOXIN-BETA RECEPTOR.
FT DOMAIN 31 227 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 228 248 POTENTIAL.
FT DOMAIN 42 211 CYTOPLASMIC (POTENTIAL).
FT REPEAT 42 81 4 X TNFR-CYS.
FT REPEAT 82 124 TNFR-CYS 1.
FT REPEAT 125 168 TNFR-CYS 2.
FT REPEAT 169 211 TNFR-CYS 3.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 104 124 BY SIMILARITY.
FT DISULFID 126 132 BY SIMILARITY.
FT DISULFID 139 148 BY SIMILARITY.
FT DISULFID 142 167 BY SIMILARITY.
FT DISULFID 170 185 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 435 AA; 46709 MW; 624626E6022F656F CRC64;

Query Match 15.1%; Score 111.5; DB 1; Length 435;
Best Local Similarity 25.7%; Pred. No. 0.0025;
Matches 39; Conservative 12; Mismatches 62; Indels 39; Gaps 9;

QY 2 ARCCRVHTTRC-----CRDYPGEE-----CCS---EWDCMCVQP 32
DB 70 AKCSIRDVTCAENSYNEHWNLYTICQLCRPCDPVMGLEETAPCTSKRKTCRC-QP 128

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FT	CARBOHYD	1088	1088	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1252	1252	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1311	1311	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1351	1351	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1502	1502	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1801	1801	N-LINKED (GLCNAC. . .)	(POTENTIAL).
SEQ	SEQUENCE	1801	AA; 196473 MW; 97AEF32F831FA75	CRC64;	

Query Match 16.0%; Score 118; DB 1; Length 1801;  
 Best Local Similarity 26.0%; Pred. No. 0.0019;  
 Matches 46; Conservative 5; Mismatches 44; Indels 82; Gaps

QY	5	CRVHTTRC--CRDYPGECSCWDCMCVOPHCGDPCCT---	TCRHHPCPPGGVGSQ 59
DB	889	CDARTGACGLCRDYTGEHCER-----CI-AGFH-GDPLPYGGOCRPCPCGPGC--	SQR 940
QY	60	KFS-----	FFQCICDASGTF----- 75
DB	941	HFTYCHRDGYSQIIVCHCRAGYGLRCACAPGHGDPSPGGRQCQCEGNIPTDP	1000
QY	76	-----SGHGEGHCKPMTDCTQCFGLTVFPGNKTNNAVC--	VPGSPP 114
DB	1001	GACDPHTGQCLRLHHTGPHGCHKP-----	GFHQGAARQSCHRTCNLGTD 1050

RESULT 10

LMB2_MOUSE	STANDARD;	PRT; 1799	AA.
ID	LMB2_MOUSE	061292;	
AC	061292;	062182;	
DT	01-NOV-1997	(Rel. 35, Created)	
DT	01-NOV-1997	(Rel. 35, Last sequence update)	
DT	15-JUL-1999	(Rel. 38, Last annotation update)	
DE	LAMININ BETA-2 CHAIN PRECURSOR.		
GN	LAMB2 OR S-LAM OR LAMS.		
OS	Mus musculus (Mouse)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
ON	[1]		
RP	SEQUENCE FROM N.A.		
RC	SPRAIN=129/J;		
RC	MEDLINE=96278760; PubMed=8662701;		
RX	Durkin M.E., Gautam M., Loeschel S., Sanes J.R., Merlie J.P.,		
RA	Albrechtsen R., Wewer U.M.;		
RT	"Structural organization of the human and mouse laminin beta2 chain		
RT	genes, and alternative splicing at the 5' end of the human		
RT	transcript.";		
RL	J. Biol. Chem. 271:13407-13416(1996).		
RN	[2]		
RP	SEQUENCE OF 348-428 FROM N.A.		
RC	TISSUE=Lung;		
RC	MEDLINE=94319092; PubMed=8043959;		
RX	Aberdam D., Galliano M.F., Mattei M.-G., Ortonne J.P., Meneguzzi G.;		
RA	"S-laminin gene (lams) maps to F1 band of mouse chromosome 9.";		
RT	Mamm. Genome 5:393-394(1994).		
RL	[3]		
RN	FUNCTION.		
RP	SPRAIN=129/J;		
RC	MEDLINE=95191650; PubMed=7885444;		
RX	Noakes P.G., Gautam M., Mudd J., Sanes J.R., Merlie J.P.;		
RA	"Aberrant differentiation of neuromuscular junctions in mice lacking		
RT	s-laminin/laminin beta 2.";		
RT	Nature 374:258-262(1995).		
RL	[3]		
CC	-1- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR. LAMININ		
CC	IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF		
CC	CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING		
CC	WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.		
CC	-1- FUNCTION: LAMININ-3 (S-LAMININ) REGULATES THE FORMATION OF MOTOR		
CC	NERVE TERMINALS.		
CC	-1- SUBUNIT. LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE		
CC	DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND		
CC	TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE		
CC	COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.		

**THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4 (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).**

-I- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT MEMBRANES (MAJOR COMPONENT).

-I- TISSUE SPECIFICITY: NEUROMUSCULAR SYNAPSE AND KIDNEY GLOMERULUS.

-I- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

-I- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.

-I- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).

-I- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.

-I- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.

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EMBL; U43541; AAC53535.1; -.  
EMBL; U42624; AAC53535.1; JOINED.  
EMBL; X75928; CAA53532.1; -.  
HSSP; P02468; IKLO.  
MGD; MGI:99916; Lamb2.  
InterPro; IPRO00561; -.  
InterPro; IPRO01886; -.  
InterPro; IPRO02049; -.  
Pfam; PF00053; laminin\_EGF\_13.  
Pfam; PF00055; laminin\_Nterm; 1.  
PRINTS; PR00011; EGFLAMIN.  
PROSITE; PS00022; EGF\_1; 10.  
PROSITE; PS01186; EGF\_2; 2.  
PROSITE; PS01248; LAMININ\_TYPE\_EGF; 12.  
**KW Glycoprotein;** Basement membrane; Extracellular matrix; Coiled coil;  
**Laminin EGF-like domain;** Cell adhesion; Repeat; Signal.  
**SIGNAL** 1 35  
FT CHAIN 36 1799 POTENTIAL.  
FT DOMAIN 36 283 LAMININ N-TERMINAL (DOMAIN VI).  
FT DOMAIN 284 555 4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN V).  
FT DOMAIN 286 349 LAMININ EGF-LIKE 1.  
FT DOMAIN 350 412 LAMININ EGF-LIKE 2.  
FT DOMAIN 413 472 LAMININ EGF-LIKE 3.  
FT DOMAIN 473 524 LAMININ EGF-LIKE 4.  
FT DOMAIN 525 555 LAMININ EGF-LIKE 5 (INCOMPLETE).  
FT DOMAIN 556 782 LAMININ DOMAIN IV.  
FT DOMAIN 783 1191 8 X LAMININ EGF-LIKE REPEATS (DOMAIN III).  
FT DOMAIN 784 831 LAMININ EGF-LIKE 6.  
FT DOMAIN 832 877 LAMININ EGF-LIKE 7.  
FT DOMAIN 878 927 LAMININ EGF-LIKE 8.  
FT DOMAIN 928 986 LAMININ EGF-LIKE 9.  
FT DOMAIN 987 1038 LAMININ EGF-LIKE 10.  
FT DOMAIN 1039 1095 LAMININ EGF-LIKE 11.  
FT DOMAIN 1096 1143 LAMININ EGF-LIKE 12.  
FT DOMAIN 1144 1190 LAMININ EGF-LIKE 13.  
FT DOMAIN 1191 1410 DOMAIN II.  
FT DOMAIN 1411 1443 DOMAIN ALPHA.  
FT DOMAIN 1444 1799 DOMAIN I.  
FT DOMAIN 1257 1304 COILED COIL (POTENTIAL).  
FT DOMAIN 1473 1527 COILED COIL (POTENTIAL).  
FT DOMAIN 1577 1791 COILED COIL (POTENTIAL).  
FT DISULFID 286 295 BY SIMILARITY.  
FT DISULFID 318 324 BY SIMILARITY.  
FT DISULFID 327 347 BY SIMILARITY.  
FT DISULFID 350 359 BY SIMILARITY.  
FT DISULFID 352 377 BY SIMILARITY.  
FT DISULFID 380 389 BY SIMILARITY.  
FT DISULFID 392 410 BY SIMILARITY.  
FT DISULFID 413 426 BY SIMILARITY.  
FT DISULFID 415 441 BY SIMILARITY.





DR PIR: A23666; A23666.  
 DR PDB: 1CA9; 12-APR-99.  
 DR MIM: 191191; .  
 DR InterPro: IPR001368; .  
 DR DR Pfam: PF00020; TNFR\_NGFR\_1; 2.  
 DR DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR DR PROSITE: PS00652; TNFR\_NGFR\_2; 4.  
 DR PROSITE: PS00650; TNFR\_NGFR\_2; 4.  
 DR Receptor; transmembrane; Glycoprotein; Repeat; Signal;  
 KW Phosphorylation; Pharmaceutical; 3D-structure.  
 FT SIGNAL 1 22  
 FT CHAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.  
 FT DOMAIN 23 257 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 258 287 POTENTIAL.  
 FT DOMAIN 288 461 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 39 76 4 X TNFR-CYS.  
 FT REPEAT 39 76 TNFR-CYS 1.  
 FT REPEAT 77 118 TNFR-CYS 2.  
 FT REPEAT 119 162 TNFR-CYS 3.  
 FT REPEAT 163 201 TNFR-CYS 4.  
 FT DISULFID 40 53 BY SIMILARITY.  
 FT DISULFID 54 67 BY SIMILARITY.  
 FT DISULFID 57 75 BY SIMILARITY.  
 FT DISULFID 78 93 BY SIMILARITY.  
 FT DISULFID 96 110 BY SIMILARITY.  
 FT DISULFID 100 118 BY SIMILARITY.  
 FT DISULFID 120 126 BY SIMILARITY.  
 FT DISULFID 134 143 BY SIMILARITY.  
 FT DISULFID 137 161 BY SIMILARITY.  
 FT DISULFID 164 179 BY SIMILARITY.  
 FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 141 141 R -> P (IN REF. 4).  
 FT CONFLICT 196 196 R -> M (IN REF. 1 AND 3).  
 FT CONFLICT 363 363 A -> T (IN REF. 4).  
 SQ SEQUENCE 461 AA; 48316 MW; 603580ECD67636F CRC64;

Query Match 16.1%; Score 119; DB 1; Length 461;  
 Best Local Similarity 30.4%; Pred. No. 0.00055;  
 Matches 35; Conservative 11; Mismatches 51; Indels 18; Gaps 6;

QY 10 TRCDYRPGECSEWD--CMVQPEFHC-----GDPCTTCRHHPGPPGQVQSGK 60  
 DB 98 SRGSSDQVETQACTREONRICTC-RPGWYKALSKQECRLCAPLR--KCRPGFGVARPGT 154  
 QY 61 FSGFCIDCASCFTSG--GHEGCKRWTDCTQGFVTVPFKNTHNAVCPGSP 113  
 DB 155 ETSDDVCKPCAPGTSTSTSDICRPHQICN----VVAIPGNASRDVACTSTSP 205

RESULT 8  
 TNR2\_MOUSE STANDARD; PRT; 474 AA.  
 AC P25119; P97893;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).  
 GN TNFRSF1B OR TNFR2 OR TNFR-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91187885; PubMed=1849278;  
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,  
 RA Wong G.H., Chen E.Y., Goeddel D.V.;  
 RT "Cloning and expression of cDNAs for two distinct murine tumor  
 RT necrosis factor receptors demonstrate one receptor is species  
 RT specific.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834 (1991).  
 RN [2]

SEQUENCE FROM N.A.  
 MEDLINE=91246168; PubMed=1645445;  
 Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,  
 Copeland N.G., Jenkins N.A., Smith C.A.;  
 "Molecular cloning and expression of the type 1 and type 2 murine  
 receptors for tumor necrosis factor.";  
 Mol. Cell. Biol. 11:3020-3026 (1991).  
 [3]  
 RN SEQUENCE OF 1-26 FROM N.A.  
 RC STRAIN=NOD;  
 RA Jacob C.O., Liu J.;  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RC TISSUE=Liver;  
 RA Kissnerghis M., Fellows R., Feldmann M., Chernajovsky Y.;  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 CC -|- FUNCTION: RECEPTOR FOR TNF-ALPHA.  
 CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
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 EMBL: M60469; AAA39752.1; .  
 EMBL: M59378; AAA40463.1; .  
 EMBL: U39488; AAA85021.1; .  
 EMBL: X87128; CAA60618.1; .  
 PIR: B38634; B38634.  
 HSP: P19438; IJNF.  
 MGD: MGI:1314883; Tnfrsf1b.  
 InterPro: IPR001368; .  
 Pfam: PF00020; TNFR\_C6; 4.  
 PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 PROSITE: PS00650; TNFR\_NGFR\_2; 3.  
 Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
 SIGNAL 1 22  
 CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.  
 DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).  
 TRANSMEM 259 288 POTENTIAL.  
 DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).  
 DOMAIN 39 203 4 X TNFR-CYS.  
 REPEAT 39 77 TNFR-CYS 1.  
 REPEAT 78 119 TNFR-CYS 2.  
 REPEAT 120 164 TNFR-CYS 3.  
 REPEAT 165 203 TNFR-CYS 4.  
 DISULFID 40 54 BY SIMILARITY.  
 DISULFID 55 68 BY SIMILARITY.  
 DISULFID 58 76 BY SIMILARITY.  
 DISULFID 79 94 BY SIMILARITY.  
 DISULFID 97 111 BY SIMILARITY.  
 DISULFID 101 119 BY SIMILARITY.  
 DISULFID 121 127 BY SIMILARITY.  
 DISULFID 136 145 BY SIMILARITY.  
 DISULFID 139 163 BY SIMILARITY.  
 DISULFID 166 181 BY SIMILARITY.  
 CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 474 AA; 50319 MW; 462AE398C4D6563 CRC64;

Query Match 16.1%; Score 119; DB 1; Length 474;  
 Best Local Similarity 31.0%; Pred. No. 0.00056;  
 Matches 36; Conservative 8; Mismatches 54; Indels 18; Gaps 5;

QY 1 DARCCRVHTTRCCRDYRPGECSEWDCMVQPEFHCGRPCCTTC-RHHPGPPGQVQSGK 59  
 DB 107 EIRACTRQQRNVKACEAGRYCAL-----KTHSGS--CRQCRLSKCGPGFGVASSR 155

```

Query Match          20.3%; Score 149.5; DB 1; Length 256;
Best Local Similarity 33.6%; Pred. No. 6.5e-07;
Matches 37; Conservative 15; Mismatches 41; Indels 17; Gaps 6;

QY 5 CRVHTTRCCRDYCECCSEW---DCMCVQPERHCQDPCCCTTCRHHCPGQGVOSQKF 61
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 64 CRV-----CAGYFRFKFCSTHNAECIE-GFHCIGPQCTRC-EKDCRPQELTKOG-- 115
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 62 SFGQCIDCASGTFSGGH-BGHCKPWTDCDTQFGELTVFPNGKTNACVCP 110
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 116 ----CKTCSLGTENDQNGTGVCRPTWNCSLDGRSVLKTGTTERDVCVP 160
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

RESULT 5
OX40_RAT STANDARD; PRT; 271 AA.
ID OX40_RAT STANDARD; PRT; 271 AA.
AC P15725;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).
GN TNFRSF4 OR TXGP1L OR OX40.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=101116;
RX [1]
SEQUENCE FROM N.A.
RC TISSUE-T-cell.
RX MEDLINE=90214614; PubMed=2157591;
RA Mallett S., Fossom S., Barclay A.N.;
RT "Characterization of the MRC OX40 antigen of activated CD4 positive T
RL lymphocytes -- a molecule related to nerve growth factor receptor.";
EMBO J. 9:1063-1068(1990).
CC 1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC 1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC 1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
CC 1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
-----
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EMBL; X17037; CAA34897.1; --
DR PIR; S08036; S08036.
DR PIR; S12783; S12783.
DR HSSP; P25942; ICDF.
DR InterPro; IPR001368; --
DR Pfam; PF00020; TNFR_c6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW Signal.
FT SIGNAL.
FT CHAIN 1 19 POTENTIAL.
FT CHAIN 20 271 OX40L RECEPTOR.
FT DOMAIN 20 210 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 211 235 POTENTIAL.
FT DOMAIN 236 271 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 164 4 X TNFR-CYS.
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 102 TNFR-CYS 2.
FT REPEAT 103 123 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 124 164 TNFR-CYS 4.
FT CARBOHYD 143 143 N-LINKED (GLCNAC... ) (POTENTIAL).
FT SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;

Query Match          20.2%; Score 149; DB 1; Length 271;
Best Local Similarity 28.9%; Pred. No. 7.5e-07;

```



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2001, 16:15:23 ; Search time 43.78 Seconds  
(without alignments)  
93.111 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_46\_164

Perfect score: 737

Sequence: 1 DACCRRVHTTRCCRDYPGE.....GNKTHNAVCPGSPAPLEPLG 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	159.5	21.6	255	1 41BB_HUMAN	Q07011 homo sapien
2	158	21.4	272	1 0X40_MOUSE	P47741 mus musculus
3	150	20.4	277	1 0X40_HUMAN	P43489 homo sapien
4	149.5	20.3	256	1 41BB_MOUSE	P20334 mus musculus
5	149	20.2	271	1 0X40_RAT	P15725 rattus norv
6	123	16.7	289	1 CD40_MOUSE	P27512 mus musculus
7	119	16.1	461	1 TNR2_HUMAN	P20333 homo sapien
8	119	16.1	474	1 TNR2_MOUSE	P25119 mus musculus
9	118	16.0	1801	1 LMB2_RAT	P15800 rattus norv
10	113	15.3	1799	1 LMB2_MOUSE	O61292 mus musculus
11	111.5	15.1	435	1 TNR2_HUMAN	P36941 homo sapien
12	111	15.1	277	1 CD40_HUMAN	P25942 homo sapien
13	110	14.9	1370	1 IG1R_RAT	P24062 rattus norv
14	109	14.8	269	1 CD40_BOVIN	P28203 bos taurus
15	104	14.1	1798	1 LMB2_HUMAN	P55268 homo sapien
16	103	14.0	1373	1 IG1R_MOUSE	O60751 mus musculus
17	99	13.4	1367	1 IG1R_HUMAN	P08069 homo sapien
18	93	12.6	3635	1 LMA5_MOUSE	O61001 mus musculus
19	92	12.5	416	1 NGFR_CHICK	P18519 gallus gall
20	92	12.5	1172	1 TSP2_HUMAN	P35442 homo sapien
21	91.5	12.4	1106	1 SPC_DROME	P40798 drosophila
22	91.5	12.4	2318	1 NTC3_MOUSE	O61982 mus musculus
23	91	12.3	956	1 TSP3_MOUSE	Q05895 mus musculus
24	90	12.2	581	1 IRR_RAT	O64716 rattus norv
25	90	12.2	1297	1 IRR_HUMAN	P14616 homo sapien
26	90	12.2	2907	1 FEN2_MOUSE	O61555 mus musculus
27	89	12.1	116	1 MCS_HUMAN	P49901 homo sapien
28	89	12.1	956	1 TSP3_HUMAN	P49746 homo sapien
29	89	12.1	1786	1 LMB1_HUMAN	P07942 homo sapien
30	89	12.1	2911	1 FBN2_HUMAN	P35556 homo sapien
31	88.5	12.0	2569	1 LMA3_MOUSE	O61789 mus musculus
32	88	11.9	810	1 NELL1_HUMAN	Q92832 homo sapien
33	88	11.9	2139	1 CRB_DROME	P10040 drosophila

#### RESULT 1

ID	41BB_HUMAN	STANDARD;	PRT;	255 AA.
AC	Q07011;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB HOMOLOG)			
DE	(T-CELL ANTIGEN ILA) (CD137 ANTIGEN).			
GN	TNFRSF9 OR ILA.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Blood;			
RX	MEDLINE=94374434; PubMed=8088337;			
RA	Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J.,			
RA	Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;			
RT	"Molecular and biological characterization of human 4-1BB and its			
RT	ligand."			
RL	Eur. J. Immunol. 24:2219-2227(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Blood;			
RX	MEDLINE=94085794; PubMed=8262389;			
RA	Schwarz H., Tuckwell J., Lotz M.;			
RT	"A receptor induced by lymphocyte activation (ILA): a new member of			
RT	the human nerve-growth-factor/tumor-necrosis-factor receptor			
RT	family."			
RN	[3]			
RP	REVISION TO 107.			
RA	Schwarz H.;			
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Blood;			
RX	MEDLINE=95347766; PubMed=7622190;			
RA	Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,			
RA	Kwon B.S.;			
RT	"Characterization of human homologue of 4-1BB and its ligand."			
RT	Immunol. Lett. 45:67-73(1995).			
CC	- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY			
CC	ACTIVE DURING T CELL ACTIVATION.			
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T			
CC	CELLS.			
CC	- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
CC	- DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry.			
CC	WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw137.htm".			
CC	-----			
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34	88	11.9	2531	1	NTCL_MOUSE	Q01705 mus musculus
35	87.5	11.9	867	1	SSPO_BOVIN	P98167 bos taurus
36	87.5	11.9	1172	1	TSP2_MOUSE	Q03350 mus musculus
37	87.5	11.9	1964	1	NTC4_MOUSE	P31695 mus musculus
38	87	11.8	415	1	TNRC_MOUSE	P50284 mus musculus
39	87	11.8	961	1	TSPA_HUMAN	P35443 homo sapien
40	87	11.8	1394	1	TGFB_HUMAN	P22084 homo sapien
41	87	11.8	1786	1	LMB1_MOUSE	Q02459 mus musculus
42	86	11.7	169	1	KRUA_HUMAN	P26371 homo sapien
43	86	11.7	1170	1	TSP2_BOVIN	Q95116 bos taurus
44	86	11.7	1173	1	TSPL_XENLA	P35448 xenopus lae
45	86	11.7	1210	1	EGFR_MOUSE	Q01279 mus musculus

#### ALIGNMENTS



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CC EMBL; U03397; AAA53133.1; -;  
 DR EMBL; L12964; AAA62478.2; -;  
 DR HSSP; P19438; 1EXT.  
 DR MIM; 602250; -;  
 DR InterPro; IPR001368; -;  
 DR Pfam; PF00020; TNFR\_C6; 2;  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1;  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 1;  
 KW Receptor; Glycoprotein; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 17  
 FT CHAIN 18 255  
 FT DOMAIN 18 186  
 FT TRANSMEM 187 213  
 FT DOMAIN 214 255  
 FT REPEAT 47 159  
 FT REPEAT 87 118  
 FT REPEAT 119 159  
 FT CARBOHYD 138 138  
 FT CARBOHYD 149 149  
 SQ SEQUENCE 255 AA; 27899 MW; F3A563FE5EF00460 CRC64;

Query Match 21.6%; Score 159.5; DB 1; Length 255;  
 Best Local Similarity 31.9%; Pred. No. 8.2e-08;  
 Matches 44; Conservative 12; Mismatches 43; Indels 39; Gaps 8;  
 QY 3 RCRVHTTRTCRDYPG-----EECCS-----EWDCMCVQPEFHCGDPCCTTCRHHPCPPGQ 53  
 Db 60 RTCDI-----CRCKGVFTYRKESSTNSAECDC---TPGFHCLGAGCSMC-EQDCKQGG 110  
 QY 54 GVQSQKSFQFCIDCASFTSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCPVG-- 111  
 Db 111 ELTKKG-----CKDCFGTFNDKRGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPA 163  
 QY 112 -----SPPA---BP 117  
 Db 164 DLSPGASSVTPPAPAREP 181

RESULT 2  
 OX40\_MOUSE STANDARD; PRT; 272 AA.  
 AC P47741;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).  
 GN TNFRSF4 OR TXGP1 OR OX40.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C;  
 RA Caldarhead D.M., Buhlmann J.E., van den Eertwegh A.J.,  
 RA Claassen E., Noelle R.J., Fell H.;  
 RT "Cloning of mouse OX40: a T cell activation marker that may mediate  
 RT T-B cell interactions."  
 RL J. Immunol. 151:5261-5271(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95255413; PubMed=7737295;  
 RA Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,  
 RA Barclay A.N.;  
 RT "Gene structure and chromosomal localization of the mouse homologue

RT of rat OX40 protein.";  
 RL Eur. J. Immunol. 25:926-930(1995).  
 CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -----  
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CC EMBL; Z21674; CAA79772.1; -;  
 DR EMBL; X85214; CAA59476.1; -;  
 DR HSSP; P25942; 1CDF.  
 DR MGD; MGI:104512; Tnfrsf4.  
 DR InterPro; IPR001368; -;  
 DR Pfam; PF00020; TNFR\_C6; 3;  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3;  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 2;  
 KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
 KW Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 272  
 FT DOMAIN 20 211  
 FT TRANSMEM 212 236  
 FT DOMAIN 237 272  
 FT DOMAIN 26 165  
 FT REPEAT 26 61  
 FT REPEAT 62 103  
 FT REPEAT 104 124  
 FT REPEAT 125 165  
 FT CARBOHYD 144 144  
 FT CONFLICT 15 15  
 SQ SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;

Query Match 21.4%; Score 158; DB 1; Length 272;  
 Best Local Similarity 27.4%; Pred. No. 1.2e-07;  
 Matches 40; Conservative 11; Mismatches 45; Indels 50; Gaps 6;  
 QY 5 CRVHT---TRCCRD-YPG-----EECCSEWDCMCVQPEFHCGDPC----- 40  
 Db 27 CVKHTYPSGHKCCRECQPGHGMVSRCDHTDRLC-----HPCETGFYNEAVNYDTCK 78  
 QY 41 -CTTCRHHP-----CPPGQVQSGKFSFGFCIDCASGTFSGHEGH 82  
 Db 79 QCTQCNRHRSSELKQNCCTPTQDVTVCRCRPGTQPRQDSGYKLGVCVCPGPPHFGSPGNNOA 138  
 QY 83 CKPWTDCTQFGFLTVFPGNKTHNAV 108  
 Db 139 CKPWNTCTLSGKQTRHPASDSDAVC 164

RESULT 3  
 OX40\_HUMAN STANDARD; PRT; 277 AA.  
 AC P43489; Q13663;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY  
 DE ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).  
 GN TNFRSF4 OR TXGP1L.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94170844; PubMed=7510240;



```

QY 1 GGGPRLLLGTGDARCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRRHH 60
    |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 61 GGGG-----GGCGCCCR-----PRCC-----CCRPKCCCTCCTCCTCCTCCTC-- 104
    |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 61 PCPPGGVQSGKFSFGFCIDCASS 86
    |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 105 PCCCGCG-----GGCGCCGGG 122
    |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

RESULT 12
S53869
laminin beta-2 chain precursor (version 2) - human
N:Alternate names: s-laminin
C:Species: Homo sapiens (man)
C:Date: 27-Oct-1995 #sequence_revision 23-Feb-1996 #text_change 24-Sep-1998
C:Accession: S53869
R:Ilivanainen, A.; Vuolteenaho, R.; Sainio, K.; Eddy, R.; Shows, T.B.; Sariola, H.; Tryggvason, M.;
Matrix Biol. 14, 489-497, 1994
A:Title: The human laminin beta-2 chain (S-laminin): structure, expression in fetal tissue
A:Reference number: S53869
A:Accession: S53869
A:Molecule type: mRNA
A:Residues: 1-1798 <IIV>
C:Genetics:
A:Gene: GDB:LAMB2
A:Cross-references: GDB:132363; OMIM:150325
A:Map position: 3p21.3-3p21.2
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C:Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-1798/Product: laminin beta-2 chain #status predicted <MAT>
F:283-344/Domain: laminin-type EGF-like homology <LE801>
F:347-467/Domain: laminin-type EGF-like homology <LE802>
F:410-467/Domain: laminin-type EGF-like homology <LE803>
F:470-519/Domain: laminin-type EGF-like homology <LE804>
F:522-532/Domain: laminin-type EGF-like homology #status atypical <LE805>
F:783-828/Domain: laminin-type EGF-like homology <LE806>
F:831-874/Domain: laminin-type EGF-like homology <LE807>
F:877-924/Domain: laminin-type EGF-like homology <LE808>
F:927-983/Domain: laminin-type EGF-like homology <LE809>
F:986-1035/Domain: laminin-type EGF-like homology <LE10>
F:1038-1092/Domain: laminin-type EGF-like homology <LE11>
F:1095-1140/Domain: laminin-type EGF-like homology <LE12>
F:1143-1187/Domain: laminin-type EGF-like homology <LE13>

Query Match 14.8%; Score 111.5; DB 2; Length 1798;
Best Local Similarity 25.0%; Pred. No. 0.059;
Matches 42; Conservative 5; Mismatches 44; Indels 77; Gaps 9;

QY 18 CRVHTTRC--CRDYPGEECCSEWDCMCVQPEFHCGDPCCT---TCRHHPCPPGQGVQ--- 69
    |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 886 CMTHTGACLGCRDHTGGEHCE-----CI-AGRH-GDPLPYGGQRCPCPCPGPSQRHF 939
    |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 70 ----SQGKFS-----FGFCIDCAGTF----- 88
    |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 940 ATSCHQDEYSQIVCHCRAGYTGRLCEACAPGHGDPSPRGRCQCEGNDPMDPDA 999
    |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 89 -----SSGHEGHCKPWTDTCTQFGFTLVFPGNKTHNAV 121
    |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 1000 CDPHTGQCLRLRHTEGPHCAHCKP-----GFHGQAARQSCHRCTC 1040
    |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

RESULT 13
A35356
tumor necrosis factor receptor 2 precursor [validated] - human
N:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K.
Science 248, 1019-1023, 1990
A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular and

```

```

A:Reference number: A35356; MUID:90260639
A:Accession: A35356
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <SMI>
A:Cross-references: GB:M32315; NID:gl89185; PIDN:AAAS9929.1; PID:gl89186
R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squir
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally oc
A:Reference number: A36475; MUID:91045991
A:Accession: A36475
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-195, 'R', 197-461 <KOH>
A:Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus,
CytoKine 2, 231-237, 1990
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular
A:Reference number: A48416; MUID:91370690
A:Accession: A48416
A:Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 23-461 <DEM>
A:Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
A:Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIP:63371)
R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demons
A:Reference number: A36007; MUID:90349572
A:Accession: A36007
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>
A:Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus,
J. Biol. Chem. 265, 20131-20138, 1990
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor
A:Reference number: A23666; MUID:91056048
A:Accession: A23666
A:Status: preliminary
A:Molecule type: protein
A:Residues: 23-40; 65-69; 136-141; 300-306 <LOB>
R:Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Eviden
A:Reference number: A35010; MUID:90110215
A:Accession: B35010
A:Status: preliminary
A:Molecule type: protein
A:Residues: 27-31 <ENG>
R:Kuhnert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
A:Title: Cloning, sequencing and partial functional characterization of the 5' region
A:Reference number: I38094; MUID:95121934
A:Accession: I38094
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-37 <RES>
A:Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
C:Genetics:
A:Gene: GDB:TNFR2
A:Cross-references: GDB:125914; OMIM:191191
A:Map position: lp36.2-lp36.2
A:Introns: 26/3
A:Note: the list of introns is incomplete
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F:40-76/Domain: NGF receptor repeat homology <NG1>
F:78-119/Domain: NGF receptor repeat homology <NG2>
F:120-162/Domain: NGF receptor repeat homology <NG3>
F:164-201/Domain: NGF receptor repeat homology <NG4>

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F:2488-2523/Domain: EGF homology <EGF>

Query Match      14.0%; Score 105.5; DB 2; Length 2907;
Best Local Similarity 26.8%; Pred. No. 0.25;
Matches 33; Conservative 11; Mismatches 40; Indels 39; Gaps 8;

QY  2 CGPGRLLLTGTDAKCC-----RVHTTRCCRDYPGEECCSEWDCMCVQPEFHCG 50
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
677 CPPG---LAVGVDRVCVDTTHMRSTCYGEIKKGVCVRPFPGAVTKSE--CCCANPDYGFG 731
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  51 DPCTTTCRHHPCPPGQGVQSGKSFSGF-----QC-ID---CASG---TFSGGHE 93
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
732 EPC-----QPCPAKNSAEFHGLCSGIGITVDGRDINECALDPDICANGICENLRGTyr 785
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  94 GNC 96
Db   : |
      786 CNC 788

Search completed: September 4, 2001, 16:12:13
Job time: 1110 sec

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A:Molecule type: mRNA

A:Residues: 1-277 <RES>

A:Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958

C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 19.3%; Score 145.5; DB 2; Length 277;  
Best Local Similarity 31.0%; Pred. No. 2.7e-05;  
Matches 39; Conservative 10; Mismatches 66; Indels 11; Gaps 4;

QY 2 CGPGRLLLTGTGDARCCRVHTTRCCRDYPG---EECCSEWDCM-CVQPEFHCGD---PCCTT 55

Db 46 CRP-----GNGMVSKRSRQNTVCRPGEGFNDVVVSSRPCKPCTWCNLSRSGERKQLCT 100

QY 56 TCRHHPCPPGGVQSGKFSFGQICDASGTFSGGHEGCHKPWTCTQFGFLTVPPGNK 115

Db 101 ATQDTVCRACGTQPLDSYKPGVDCAPCPPGHFSPCDNCAKRPWTNCTLAGKHTLPASN 160

QY 116 THNAVC 121

Db 161 SSDAIC 166

RESULT 6

JC5559

Lectin-B - Virginian pokeweed

C:Species: Phytolacca americana (Virginian pokeweed)

C:Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 17-Mar-2000

C:Accession: JC5559

R:Yamaguchi, K.; Yurino, N.; Kino, M.; Ishiguro, M.; Funatsu, G.

Biosci. Biotechnol. Biochem. 61, 690-698, 1997

A:Title: The amino acid sequence of mitogenic lectin-B from the roots of pokeweed (Phytolacca americana)

A:Reference number: JC5559; MUID:97290889

A:Accession: JC5559

A:Molecule type: protein

A:Residues: 1-295 <YAM>

A:Experimental source: root

C:Comment: This protein is a lectin specific for N-acetylglucosamine-containing saccharide

C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; ph

C:Keywords: glycoprotein

F:96,139/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.4%; Score 138.5; DB 2; Length 295;

Best Local Similarity 31.7%; Pred. No. 0.00011;

Matches 33; Conservative 17; Mismatches 31; Indels 23; Gaps 7;

QY 2 CGPGRLLLTGTGDARCCRVHTTRCCRDYPG---EECCSEWDCM-CVQPEFHCGDPCCTT 56

Db 154 CGITEGYCGEGCQSQC---NHQRCQKDFAGRTCLNDLCCSENG-WCGSSEAHCGQCSQN 209

QY 57 CRHHPCPPGGVQSGKFSFGQ-C---IDCASGTFSGGHEGHC 96

Db 210 CNYNRC-----GR-NFGFRTCPNELCCSSGGMGCSNDAC 243

RESULT 7

A46476

B cell-associated surface molecule CD40, long splice form - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Nov-2000

C:Accession: A46476; A46515

R:Torres, R.M.; Clark, E.A.

J. Immunol. 148, 620-626, 1992

A:Title: Differential increase of an alternatively polyadenylated mRNA species of murine

A:Reference number: A46476; MUID:92105763

A:Accession: A46476

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-305 <TOR>

A:Cross-references: GB:M83312; NID:g1553058

A:Note: sequence extracted from NCBI backbone (NCBI:75206, NCBIP:75207)

A:Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0

R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockay  
J. Immunol. 149, 3921-3926, 1992

A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.

A:Reference number: A46515; MUID:93094586

A:Accession: A46515

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-287, 'IV' <GR>

A:Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126

A:Experimental source: BALB/C, liver

A:Note: sequence extracted from NCBI backbone (NCBI:120357)

C:Comment: For an alternative splice form, see PIR:A46515.

C:Superfamily: CD27 antigen; NGF receptor repeat homology

C:Keywords: alternative splicing; transmembrane protein

F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 16.9%; Score 127.5; DB 2; Length 305;

Best Local Similarity 28.9%; Pred. No. 0.00089;

Matches 37; Conservative 8; Mismatches 72; Indels 11; Gaps 5;

QY 2 CGPGRLLLTGTGDARCCRVHTTRCCRDYPG---EECCSEWDCM-CVQPE-FHCGDPCCTT 56

Db 62 CDSGEFSAOWNREIRC---HQHRCPEPNQGLRVKKEGTAEISDTVCTCKEGQHCSTKDEA 118

QY 57 C-RHHPCPPGGVQSGKFSFGQICDASGTFSGGHE--GHCKPWTCTQFGFLTVPPG 113

Db 119 CAQHTPCIPGFGVEMWEMATETDTVCHPCVPVGFSSNOSLFKCYPMWTSCECDKNLEVLQKG 178

QY 114 NKTHNAVC 121

Db 179 TSOTNVIC 186

RESULT 8

MMRTS

Laminin beta-2 chain precursor - rat

N:Alternate names: laminin chain B3; S-laminin

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 10-Dec-1999

C:Accession: S03539

R:Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.

Nature 338, 229-234, 1989

A:Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the ne

A:Reference number: S03539; MUID:89159410

A:Accession: S03539

A:Molecule type: mRNA

A:Residues: 1-1801 <HUN>

A:Cross-references: EMBL:X16563; NID:g57250; PIDN:CAA34561.1; PID:g57251

C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type lamin

C:Function:

A:Description: Interact with cells and with other basement membrane proteins to promo

C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology

C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellu

F:36-1801/Product: laminin beta-2 chain #status predicted <SIG>

F:36-285/Domain: VI <DOM6>

F:286-555/Domain: V <DOM5>

F:286-347/Domain: laminin-type EGF-like homology <LEO1>

F:350-410/Domain: laminin-type EGF-like homology <LEO2>

F:413-470/Domain: laminin-type EGF-like homology <LEO3>

F:473-522/Domain: laminin-type EGF-like homology <LEO4>

F:525-555/Domain: laminin-type EGF-like homology #status atypical <LEO5>

F:556-784/Domain: IV <DOM4>

F:786-831/Domain: laminin-type EGF-like homology <LEO6>

F:788-1196/Domain: III <DOM3>

F:834-877/Domain: laminin-type EGF-like homology <LEO7>

F:880-927/Domain: laminin-type EGF-like homology <LEO8>

F:930-986/Domain: laminin-type EGF-like homology <LEO9>

F:989-1038/Domain: laminin-type EGF-like homology <LEO10>

F:1041-1095/Domain: laminin-type EGF-like homology <LEO11>

F:1098-1143/Domain: laminin-type EGF-like homology <LEO12>

F;1146-1190/Domain: laminin-type EGF-like homology <LE13>

F;1197-1412/Domain: II <DOM2>

F;1197-1412/Region: heptad repeats

F;1413-1445/Domain: alpha <ALP>

F;1446-1801/Region: heptad repeats

F;1446-1801/Domain: I <DOM1>

F;45-50/Disulfide bonds: #status predicted

F;251,371,1088,1252,1311,1351,1503/Binding site: carbohydrate (Asn) (covalent) #status F

F;1193,1196,1800/Disulfide bonds: interchain #status predicted

Query Match 15.6%; Score 117.5; DB 1; Length 1801;  
Best Local Similarity 25.9%; Pred. No. 0.019;  
Matches 44; Conservative 3; Mismatches 42; Indels 81; Gaps 9;

QY 18 CRVHTTRC--CRDYPGEGECSEWDCMCVQPEFHCGDPCCT---TCRHPCPPGGQVQSQG 72

Db 889 CDATGACGLGRDTGGEHCR-----CI-AGFH-GDPLPYGGQCRPCPCPEGPG--SQR 940

QY 73 KFS-----FGQCIDCASGTF----- 88

Db 941 HFATSCHRDGYSQIVCHRCAGYTGRLRCEACAPGHGDPSPKPGRCQCEGNDIPTDP 1000

QY 89 -----SGGHEGCHKPWTCTQFGFLTVPFGKTHNAVC 121

Db 1001 GACDPHTGQCLRLHHTGPHGCHKP-----GFHGQAARQSCHRC 1043

RESULT 9

A60771

B-cell activation protein CD40 precursor - human

N;Alternate names: B-cell surface antigen Bp50

C;Species: Homo sapiens (man)

C;Date: 03-Jun-1993 #sequence\_revision 03-Feb-1994 #text\_change 21-Jul-2000

C;Accession: S04460; A60771

R;Stamenkovic, I.; Clark, E.A.; Seed, B.

EMBO J. 8, 1403-1410, 1989

A;Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor

A;Reference number: S04460; MUID:89356608

A;Accession: S04460

A;Molecule type: mRNA

A;Residues: 1-277 <STA>

R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.;

J. Immunol. 142, 562-567, 1989

A;Title: Biochemical characteristics and partial amino acid sequence of the receptor-like

A;Reference number: A60771; MUID:89093941

A;Accession: A60771

A;Molecule type: protein

A;Residues: 21-50 <BRA>

A;Experimental source: Burkitt lymphoma cell line Raji

C;Genetics:

A;Gene: GDB:CD40

A;Cross-references: GDB:215268; OMIM:109535

A;Map position: 20q12-20q13.2

C;Superfamily: CD27 antigen; NGF receptor repeat homology

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-27/Product: B-cell activation protein CD40 #status experimental <MAT>

F;21-193/Domain: extracellular #status predicted <EXT>

F;194-215/Domain: transmembrane #status predicted <TM>

F;216-277/Domain: intracellular #status predicted <CYT>

F;153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.2%; Score 114.5; DB 2; Length 277;

Best Local Similarity 27.3%; Pred. No. 0.0099;

Matches 35; Conservative 10; Mismatches 72; Indels 11; Gaps 5;

QY 2 CGPRLLLGTGTARCRVHTTRCCRDYPG-----EECCSEWDCMCVQPE-FHCGDPCCTT 56

Db 62 CGESEFLDTWNRETHC---HQHKYCDNLGLRVQOKGTSETDTTICTCEGWHCTSEACES 118

QY 57 C-RHHPCPPGGQVQSQGKFSFGFCQICDSCASGTFSGGHEG--HCKPWTDCTQFGFLTVPFG 113

Db 119 CVLHRSCSPGFGVKQIATGVSDTICEPCPVGVGFSNVSSAFKCHPWTSCETKDLVVQAG 178

QY 114 NKTHNAVC 121

Db 179 TNKTDVVC 186

RESULT 10

I54182

tumor necrosis factor receptor 2-related protein - human

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 17-Mar-2000

C;Accession: I54182

R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.

Genomics 16, 214-218, 1993

A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed seq

A;Reference number: I54182; MUID:93252381

A;Accession: I54182

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-435 <RES>

A;Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762

C;Genetics:

A;Gene: GDB:LTBR

A;Cross-references: GDB:1230195; OMIM:600979

A;Map position: 12p13.3-12p13.1

C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match

Best Local Similarity 14.9%; Score 112.5; DB 2; Length 435;

Matches 39; Conservative 12; Mismatches 63; Indels 41; Gaps 9;

QY 2 CGPRLLLGTGTARCRVHTTRC-----CRDYPGEE----C 34

Db 62 CPP-----GTVSARKSRIRDTVCATCAENSNEHWNLTTCQLCRPCDPVPMGLEEIAPC 116

QY 35 CS--EWDCMCVQPEFHCGDPC--CTTCR-HHPCPPGGQVQSQGKFSFG--FQCIDCASGTF 88

Db 117 TSKRKTQGR-CQPMFCAAWALECTHCELLSDCPGCTAELEKDEVGKGNHCVPCKAGHF 175

QY 89 --SGGHEGCHKPWTCTQFGFLTVPFGKTHNAVC 121

Db 176 QNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC 210

RESULT 11

T18975

hypothetical protein C06A1.6 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C;Accession: T18975

R;McMurray, A.

submitted to the EMBL Data Library, June 1995

A;Reference number: Z19054

A;Accession: T18975

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-152 <WIL>

A;Cross-references: EMBL:Z49886; PIDN:CAA90055.1; GSPDB:GN00020; CESP:C06A1.6

A;Experimental source: clone C06A1

C;Genetics:

A;Gene: CESP:C06A1.6

A;Map position: 2

A;Introns: 22/3

Query Match

Best Local Similarity 14.9%; Score 112; DB 2; Length 152;

Matches 30; Conservative 0; Mismatches 32; Indels 24; Gaps 5;



C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 01-Dec-2000  
 C;Accession: I38426; JT0752  
 R;Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; R  
 Eur. J. Immunol. 24, 2219-2227, 1994  
 A;Title: Molecular and biological characterization of human 4-1BB and its ligand.  
 A;Reference number: I38426; MUID:94374434  
 A;Accession: I38426  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-255 <RES>  
 A;Cross-references: EMBL:U03397; NID:g571320; PIDN:AAA5313.1; PID:g571321  
 Gene 134, 295-298, 1993  
 R;Schwarz, H.; Tuckwell, J.; Lotz, M.  
 A;Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne  
 A;Reference number: JT0752; MUID:94085794  
 A;Accession: JT0752  
 A;Molecule type: mRNA  
 A;Residues: 1-106, R', 108-255 <SCH>  
 C;Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necro  
 C;Superfamily: CD27 antigen; NGF receptor repeat homology  
 C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein  
 F;1-17/Domain: signal sequence #status predicted <SIG>  
 F;18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT>  
 F;187-213/Domain: transmembrane #status predicted <TM>  
 F;138,149/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F;234,235/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predict  
 F;242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 20.3%; Score 152.5; DB 2; Length 255;  
 Best Local Similarity 31.8%; Pred. No. 6.8e-06;  
 Matches 41; Conservative 11; Mismatches 50; Indels 27; Gaps 7;

QY 2 CGPGRLLGGTGDARCCRVHTTCCRDYPG-----EBCCS-----EWCVCVQPEFHCGDP 52  
 Db 48 CPPNSFSSAGG--QRTCDI-----CROCKGVFRKRCSTSNACDC---TPGFHCLGA 97

QY 53 CCTTCRHHPPGQGVQSGKFSFGFCIDCASGTFSGGHEGCKPWTCTQFGFLTVFP 112  
 Db 98 GCSMC-EQDCKQGELTKG-----CKDCCFCFTNDQKRGICRPWTNCLSDGSKVLVN 149

QY 113 GNKTHNAV 121  
 Db 150 GTRERDVVC 158

RESULT 3  
 S12783  
 OX40 antigen precursor - rat  
 N;Alternate names: nerve growth factor receptor homolog  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 05-Nov-1999  
 C;Accession: S12783; S08036  
 R;Mallett, S.; Fossum, S.; Barclay, A.N.  
 EMBO J. 9, 1063-1068, 1990  
 A;Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte  
 A;Reference number: S12783; MUID:90214614  
 A;Accession: S12783  
 A;Molecule type: mRNA  
 A;Residues: 1-271 <NAL>  
 A;Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831  
 C;Superfamily: CD27 antigen; NGF receptor repeat homology  
 C;Keywords: growth factor receptor; transmembrane protein  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-271/Product: OX40 antigen #status predicted <MAT>  
 F;211-235/Domain: transmembrane #status predicted <TM>

Query Match 19.9%; Score 149.5; DB 2; Length 271;  
 Best Local Similarity 28.9%; Pred. No. 1.3e-05;  
 Matches 44; Conservative 11; Mismatches 60; Indels 37; Gaps 7;

QY 7 LLLG--TGTDAKCCRVHTT-----RCCRD-YPGEECCSEWD-----CMCVQPEFHCG-- 50  
 Db 12 LLLGLSLGVTVKLCVNDYTPSGHKCCRECPQGHGWSRCDHTRDTVCHPCPEPGYNEAV 71  
 QY 51 --DPC--CTTCRRH-----PCPPGQGVQSGKFSFGFCIDCASGTF 89  
 Db 72 NYDTCKQCTQCNRHSRSGSELKONCTPTEDTVQCRRGTQPRQDSSHKLGVDCVCPGPHFS 131

QY 90 GGHEGCKPWTCTQFGFLTVFPGNKTHNAV 121  
 Db 132 PGSNQACKPWTNCTLSGKQIRHPASNSLDTVC 163

RESULT 4  
 B32393  
 T-cell antigen 4-1BB precursor - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 21-Jul-2000  
 C;Accession: B32393; I48879  
 R;Kwon, B.S.; Weissman, S.M.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989  
 A;Title: cDNA sequence of two inducible T-cell genes.  
 A;Reference number: A32393; MUID:89184547  
 A;Accession: B32393  
 A;Molecule type: mRNA  
 A;Residues: 1-256 <KWO>  
 A;Cross-references: GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122  
 R;Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.  
 J. Immunol. 152, 2256-2262, 1994  
 A;Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1B  
 A;Reference number: I48879; MUID:94179805  
 A;Accession: I48879  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-256 <RES>  
 A;Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178  
 C;Genetics:  
 A;Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1  
 C;Superfamily: CD27 antigen; NGF receptor repeat homology  
 C;Keywords: transmembrane protein  
 F;1-23/Domain: signal sequence #status predicted <SIG>  
 F;24-256/Product: 4-1BB protein #status predicted <MAT>

Query Match 19.8%; Score 149; DB 2; Length 256;  
 Best Local Similarity 31.2%; Pred. No. 1.3e-05;  
 Matches 39; Conservative 17; Mismatches 51; Indels 18; Gaps 7;

QY 2 CGPGRLLGGTGDARCCRVHTTCCRDYPGEECCSEW---DCMCVQPEFHCGDCPCTTC 57  
 Db 47 CPPSTFSSIGGPNCICRV---CAGYFRFKFCSSTHNAECEIE-GFHLGSPQCTRC 101

QY 58 RHHPCCPGQGVQSGKFSFGFCIDCASGTFSGGH-EGHCKPWTCTQFGFLTVFPGNKT 116  
 Db 102 -EKDCRPGQELTKG-----CKTCSLGTFDNQNGTGVCRPWTNCLSDGRSVLTGTTE 153

QY 117 HNAV 121  
 Db 154 KDVC 158

RESULT 5  
 I37552  
 OX40 homolog - human  
 C;Species: Homo sapiens (man)  
 C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000  
 C;Accession: I37552  
 R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fo  
 Eur. J. Immunol. 24, 677-683, 1994  
 A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignmen  
 A;Reference number: I37552; MUID:94170844  
 A;Accession: I37552  
 A;Status: preliminary; translated from GB/EMBL/DBJ



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FT DOMAIN 851 890 EGF-LIKE 13, CALCIUM-BINDING.
FT DOMAIN 954 895 EGF-LIKE 14, CALCIUM-BINDING.
FT REPEAT 996 1071 TGFBP 3.
FT DOMAIN 1072 1113 EGF-LIKE 15, CALCIUM-BINDING.
FT DOMAIN 1114 1156 EGF-LIKE 16, CALCIUM-BINDING.
FT DOMAIN 1157 1198 EGF-LIKE 17, CALCIUM-BINDING.
FT DOMAIN 1199 1240 EGF-LIKE 18, CALCIUM-BINDING.
FT DOMAIN 1241 1281 EGF-LIKE 19, CALCIUM-BINDING.
FT DOMAIN 1282 1323 EGF-LIKE 20, CALCIUM-BINDING.
FT DOMAIN 1324 1365 EGF-LIKE 21, CALCIUM-BINDING.
FT DOMAIN 1366 1406 EGF-LIKE 22, CALCIUM-BINDING.
FT DOMAIN 1407 1447 EGF-LIKE 23, CALCIUM-BINDING.
FT DOMAIN 1448 1489 EGF-LIKE 24, CALCIUM-BINDING.
FT DOMAIN 1490 1530 EGF-LIKE 25, CALCIUM-BINDING.
FT DOMAIN 1531 1571 EGF-LIKE 26, CALCIUM-BINDING.
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FT DOMAIN 1691 1732 EGF-LIKE 28, CALCIUM-BINDING.
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FT DOMAIN 1807 1848 EGF-LIKE 29, CALCIUM-BINDING.
FT DOMAIN 1849 1890 EGF-LIKE 30, CALCIUM-BINDING.
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FT REPEAT 2097 2169 TGFBP 6.
FT DOMAIN 2170 2211 EGF-LIKE 36, CALCIUM-BINDING.
FT DOMAIN 2212 2251 EGF-LIKE 37, CALCIUM-BINDING.
FT DOMAIN 2252 2292 EGF-LIKE 38, CALCIUM-BINDING.
FT DOMAIN 2293 2336 EGF-LIKE 39, CALCIUM-BINDING.
FT DOMAIN 2337 2378 EGF-LIKE 40, CALCIUM-BINDING.
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Query Match 13.7%; Score 103.5; DB 1; Length 2911;

Best Local Similarity 26.8%; Pred. No. 0.044;

Matches 33; Conservative 11; Mismatches 40; Indels 39; Gaps 8;

Qy 2 CGPGRLLLGTTDARCC-----RVHTTRCCRDYPGECCSEWDCMCVQPEFHCG 50

Db 683 CPGG---LAVGMDGRVCVDTHMRSTCYGGIKKGVCPPEPQAVTKSE--CCCANPDYGF 737

Qy 51 DPCCTTCRHHPCPPGQGVQSOGKFSFGF-----QC-ID---CASG---TFSGGHE 93

Db 738 EPC-----QPCPAKNSAEFHGLCSGSGVITVDGRDINECALDPDICANGICENLRGSTR 791

Qy 94 GNC 96

Db 792 CNC 794

Search completed: September 4, 2001, 16:15:24  
Job time: 1136 sec

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DR	Pfam; PF00683; TB; 9.	FT	DISULFID	280	292	BY SIMILARITY.
DR	PRINTS; PR00010; EGFBLD.	FT	DISULFID	287	301	BY SIMILARITY.
DR	PROSITE; PS00010; ASX_HYDROXYL; 43.	FT	DISULFID	303	316	BY SIMILARITY.
DR	PROSITE; PS00022; EGF_1; 2.	FT	DISULFID	322	334	BY SIMILARITY.
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Query Match 14.0%; Score 105.5; DB 1; Length 2907;  
 Best Local Similarity 26.8%; Pred. No. 0.029;  
 Matches 33; Conservative 11; Mismatches 40; Indels 39; Gaps 8;

QY	2	CGCGRLLGTGDARCC-----RVHTTCCRDYPCGEECCSEWDCMCVQPEFHCG	50
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QY	51	DPCTCTCRHHPCPPGQGVQSGKSFSGF-----QC-ID---CASG---TFSGGHE	93
DB	732	EPC-----QPCPAKNSAEFHGLSSGIGITVDGRDINECALDPPCANGCINLRGT	785
QY	94	GHC 96	
DB	786	CNC 788	

RESULT 14

LMB2_HUMAN	STANDARD;	PRT;	1798	AA.
ID	LMB2_HUMAN			
AC	P52268; Q16321;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	DE LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ).			
GN	LAMB2.			
OS	homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=95213013; PubMed=7698745;			
RA	Wewer U.M., Gerecke D.R., Durkin M.E., Kurtz K.S., Mattei M.-G.,			
RA	Champlaud M.F., Burgeson R.E., Albrechtsen R.;			
RT	"Human beta 2 chain of laminin (formerly S chain): cDNA cloning,			
RT	chromosomal localization, and expression in carcinomas.";			
RL	Genomics 24:243-252(1994).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=95316263; PubMed=7795887;			
RA	Iivanainen A., Vuolteenaho R., Sainio K., Eddy R., Shows T.B.,			
RA	Sariola H., Tryggvason K.;			
RT	"The human laminin beta 2 chain (S-laminin): structure, expression in			
RT	fetal tissues and chromosomal assignment of the LAMB2 gene.";			
RL	Matrix Biol. 14:489-497(1995).			
CC	-1- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ			
CC	IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF			
CC	CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING			
CC	WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.			
CC	-1- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE			
CC	DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND			
CC	TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE			
CC	COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.			
CC	THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4			
CC	(S-MEROSIN), AND LAMININ-7 (KS-LAMININ).			
CC	-1- SUBCELLULAR LOCATION: EXTRACELLULAR.			
CC	-1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR			
CC	COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC			
CC	CLEFT OF THE NEUROMUSCULAR JUNCTION.			
CC	-1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT			
CC	WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.			
CC	-1- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.			
CC	-1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).			
CC	-1- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.			
CC	-1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.			









CHARACTERIZATION.  
 MEDLINE=93016040; PubMed=1328224;  
 Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,  
 Lipari M.T., Goeddel D.V.;  
 "Biochemical properties of the 75-kDa tumor necrosis factor receptor.  
 Characterization of ligand binding, internalization, and receptor  
 phosphorylation.";  
 J. Biol. Chem. 267:21172-21178(1992).  
 [8]  
 X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.  
 MEDLINE=99221490; PubMed=10206649;  
 Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;  
 "Structural basis for self-association and receptor recognition of  
 human TRAF2.";  
 Nature 398:533-538(1999).  
 -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND  
 APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.  
 -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 -!- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW  
 LEVEL ON THREONINE RESIDUES.  
 -!- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND  
 WYETH-AVERST). USED TO TREAT MODERATE TO SEVERE RHEUMATOID  
 ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING  
 PORTION OF TNFR2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO  
 TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.  
 -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 -!- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;  
 WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm".  
 -!- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;  
 WWW="http://www.enbrelinfo.com/".  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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 EMBL; M32315; AAA59929.1; -  
 EMBL; M35857; AAA63262.1; -  
 EMBL; U52165; AAC50622.1; -  
 EMBL; U52156; AAC50622.1; JOINED.  
 EMBL; U52157; AAC50622.1; JOINED.  
 EMBL; U52158; AAC50622.1; JOINED.  
 EMBL; U52159; AAC50622.1; JOINED.  
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 EMBL; U52163; AAC50622.1; JOINED.  
 EMBL; U52164; AAC50622.1; JOINED.  
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 PIR; A36007; A36007.  
 PIR; A36475; A36475.  
 PIR; B35010; B35010.  
 PIR; A23666; A23666.  
 PDB; 1CA9; 12-APR-99.  
 MIM; 191191; -  
 InterPro; IPR001368; -  
 Pfam; PF00020; TNFR\_C6; 4.  
 PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 PROSITE; PS50050; TNFR\_NGFR\_2; 4.  
 Receptor; Transmembrane; Glycoprotein; Repeat; Signal;  
 Phosphorylation; Pharmaceutical; 3D-structure.  
 SIGNAL  
 1 22 TUMOR NECROSIS FACTOR RECEPTOR 2.  
 CHAIN 23 461 EXTRACELLULAR (POTENTIAL).  
 DOMAIN 23 257  
 TRANSMEM 258 287 POTENTIAL.  
 FT DOMAIN 288 461 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 39 201 4 X TNFR-CYS.  
 FT REPEAT 77 76 TNFR-CYS 1.  
 FT REPEAT 37 118 TNFR-CYS 2.

FT REPEAT 119 162 TNFR-CYS 3.  
 FT REPEAT 163 201 TNFR-CYS 4.  
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 FT DISULFID 137 161 BY SIMILARITY.  
 FT DISULFID 164 179 BY SIMILARITY.  
 FT CARBOHYD 171 171 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 193 193 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CONFLICT 141 141 R -> P (IN REF. 4).  
 FT CONFLICT 196 196 R -> M (IN REF. 1 AND 3).  
 FT CONFLICT 363 363 A -> T (IN REF. 4).  
 SQ SEQUENCE 461 AA; 48316 MW; 603B580ECD67636F CRC64;  
 Query Match 15.0%; Score 113; DB 1; Length 461;  
 Best Local Similarity 25.8%; Pred. No. 0.0016;  
 Matches 39; Conservative 14; Mismatches 60; Indels 38; Gaps 8;  
 QY 2 CGPG---RLLGTTGDARC-----CRVHTRCRDYPGECCSEWD-- 39  
 DB 57 CSPQGHARVFKTSKSTVCDSCEDSTYTLWNWVPECLSCGSSDQVETQACTREQNR 116  
 QY 40 -CMCVQPEFHC-----GDPCCCTCRHHPCPPGGVQSGKFSFGFCIDCASGTFSG-- 90  
 DB 117 ICTC-RGWIYCALSKQECRLCAPLR--KCRPGFVARPGTETSDVCKPCAPGFSNWT 173  
 QY 91 GHEGHCPRWTDCTQFGFLTFPPGNKTHNAV 121  
 DB 174 SSTDCRPHQICN---VVAIPGNASRDVAV 200  
 RESULT 11  
 TNRC HUMAN STANDARD; PRT; 435 AA.  
 AC P36941;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR  
 DE 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).  
 GN LTBR OR TNFR OR TNFRSF3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=93252381; PubMed=8486360;  
 RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;  
 RT "Construction and evaluation of a hncDNA library of human lrp  
 RT transcribed sequences derived from a somatic cell hybrid.";  
 RL Genomics 16:214-218(1993).  
 RN [2]  
 RP FUNCTION.  
 RX MEDLINE=94225209; PubMed=8171323;  
 RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,  
 RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;  
 RT "A lymphotoxin-beta-specific receptor.";  
 RL Science 264:707-710(1994).  
 CC -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN  
 CC IMMUNE DEVELOPMENT.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -----  
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DR	PROSITE; PS00652; TNFR_NGFR_1; 1.	
DR	PROSITE; PS50050; TNFR_NGFR_2; 1.	
KW	Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.	
FT	SIGNAL 1 19 POTENTIAL.	
FT	CHAIN 20 >269 CD40L RECEPTOR.	
FT	DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 194 215 POTENTIAL.	
FT	DOMAIN 216 >269 CYTOPLASMIC (POTENTIAL).	
FT	DOMAIN 25 187 4 X TNFR-CYS.	
FT	REPEAT 25 160 TNFR-CYS 1.	
FT	REPEAT 61 103 TNFR-CYS 2.	
FT	REPEAT 104 144 TNFR-CYS 3.	
FT	REPEAT 145 187 TNFR-CYS 4.	
FT	CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	NON_TER 269 269	
SQ	SEQUENCE 269 AA; 29983 MW; 746903F30F95F387 CRC64;	
	Query Match 16.3%; Score 122.5; DB 1; Length 269;	
	Best Local Similarity 28.7%; Pred. No. 0.00015;	
	Matches 37; Conservative 9; Mismatches 70; Indels 13; Gaps	
Qy	2 CGPGRLLLTGTDAICRCRVHTTCRRDYGEECCSEWD-----CMCVQPERHCGDCPCT 55	
	:	
Db	62 CGKGEFLSTWNRKYC---HEHRYCPNPLGLRIQSESTLNTDTICVCEGO-HCTSHSTCE 117	
Qy	56 TCRHHP-CPPGQGVQSGKRFSEFGFCIDCASGTFSGGHSG--HCKPWTDCQTFGLTVFP 112	
	:   :	
Db	118 SCTPHSLCLGFGVKQIATGLLDTVCEPCLGPFSSVSAFEKCHRWTSCEKRGGLVEQHV 177	
Qy	113 GNKTHNAV 121	
	:	
Db	178 GTNKTDVVC 186	
RESULT	8	
LMB2_RAT		
ID	LMB2_RAT STANDARD; PRT; 1801 AA.	
AC	P15800;	
DT	01-APR-1990 (Rel. 14, Created)	
DT	01-APR-1990 (Rel. 14, Last sequence update)	
DT	15-JUL-1999 (Rel. 38, Last annotation update)	
DE	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3).	
GN	LAMB2.	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
OX	NCBI_TaxID=10116;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Liver;	
RX	MEDLINE=89159410; PubMed=2922051;	
RA	Hunter D.D., Shah V., Merlie J.P., Sanes J.R.;	
RT	"A laminin-like adhesive protein concentrated in the synaptic cleft	
RT	of the neuromuscular junction.";	
RL	Nature 338:229-234(1989).	
CC	-1- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR. LAMININ	
CC	IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF	
CC	CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT.	
CC	WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.	
CC	-1- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE	
CC	DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND	
CC	TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE	
CC	COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.	
CC	THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4	
CC	(S-MEROSIN), AND LAMININ-7 (KS-LAMININ).	
CC	-1- SUBCELLULAR LOCATION: EXTRACELLULAR.	
CC	-1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR	
CC	COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC	
CC	CLEFT OF THE NEUROMUSCULAR JUNCTION.	
CC	-1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT	
CC	WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.	

[illegible]

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RA Mallett S., Fossum S., Barclay A.N.;
RT "Characterization of the MRC OX40 antigen of activated CD4 positive T
RT lymphocytes -- a molecule related to nerve growth factor receptor.";
RL EMOB J. 9:1063-1068(1990).
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC -----
DR EMBL: X17037; CAA34897.1; -.
DR PIR: S08036; S08036.
DR PIR: S12783; S12783.
DR HSP: P25942; ICDF.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_C6; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW Signal.
FT SIGNAL 1 19
FT CHAIN 20 271
FT DOMAIN 20 210
FT TRANSMEM 211 235
FT DOMAIN 236 271
FT DOMAIN 25 164
FT REPEAT 25 60
FT REPEAT 61 102
FT REPEAT 103 123
FT REPEAT 124 164
FT CARBOHYD 143 143
FT SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;

Query Match 19.9%; Score 149.5; DB 1; Length 271;
Best Local Similarity 28.9%; Pred. No. 5.3e-07;
Matches 4; Conservative 11; Mismatches 60; Indels 37; Gaps 7;

QY 7 LLLG--TCTDARCCRVHTT-----RCRD--YPGECCSEWD-----CMCVOPEFHCG-- 50
DB 12 LLLGLSLGVTLKNCVKTDFSGHKCCRCQPGHGMVSRCDHTRDTVCHPCPEGGYNEAV 71
QY 51 --DPC--CTTCRHH-----PCPPGQGVQSGKFSFGFCIDCASGTFSS 89
DB 72 NYDTCKOCTQCNHRSGSELKQNCPTEDTVQCPRGTPQRPQDSSHKLGVDCVPCPPGHFS 131
QY 90 CGHEGHCKPWTDCTQFGFLTVFPGNKTHNAV 121
DB 132 PCSNQACKPWTNCTLSGKQIRHPASNSLDTVC 163

RESULT 4
41BB_MOUSE STANDARD; PRT; 256 AA.
ID 41BB_MOUSE
AC P20334;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 4-LBB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-LBB).
GN TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
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RX MEDLINE-89184547; PubMed-2784565;
RA Kwon B.S., Weissman S.M.;
RT "cDNA sequences of two inducible T-cell genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE-94179805; PubMed-8133039;
RA Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;
RT "Genomic organization and chromosomal localization of the T-cell
RT antigen 4-LBB.";
RL J. Immunol. 152:2256-2262(1994).
RN [3]
RP CHARACTERIZATION, AND SEQUENCE OF 25-29.
RX MEDLINE-93139510; PubMed-7678621;
RA Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kim K.K., Pickard R.T.,
RA Kwon B.S.;
RT "Inducible T cell antigen 4-LBB. Analysis of expression and
RT function.";
RL J. Immunol. 150:771-781(1993).
CC -1- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-LBB. POSSIBLY
CC ACTIVE DURING T CELL ACTIVATION.
CC -1- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.
CC -1- ASSOCIATES WITH P56-LCK.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.
CC -1- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J04492; AAA40167.1; -.
DR EMBL: U02567; AAA93113.1; -.
DR PIR: B32393; B32393.
DR HSP: P25942; ICDF.
DR MGD: MGI:1101059; Tnfrsf9.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_C6; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; FALSE_NEG.
KW Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
FT SIGNAL 1 24
FT CHAIN 25 256
FT DOMAIN 25 187
FT TRANSMEM 188 208
FT DOMAIN 209 256
FT DOMAIN 17 159
FT REPEAT 17 45
FT REPEAT 46 85
FT REPEAT 86 117
FT REPEAT 118 159
FT CARBOHYD 128 128
FT CARBOHYD 138 138
FT SEQUENCE 256 AA; 27598 MW; 93A10D03C60813C4 CRC64;

Query Match 19.8%; Score 149; DB 1; Length 256;
Best Local Similarity 31.2%; Pred. No. 5.6e-07;
Matches 39; Conservative 17; Mismatches 51; Indels 18; Gaps 7;

QY 2 CGPGRLL-LLGTGTDARCCRVHTTRCCRDYPGECCSEW----DCMCVOPEFHCGDPCCTTC 57
DB 47 CPSTFSSIGGQPCNCICRV----CAGYFRFKFCSSTHNAECIEB-GFHCIGPQCTRC 101
QY 58 RHHPCCPPGQGVQSGKFSFGFCIDCASGTFSGGH-EGHCKPWTDCQFGFLTVFPGNK 116
DB 102 -EKDCRPGQELTKQG-----CKTCSLGTGTFNDONGTVGCRPWTNCSLDGRSVLKTGTE 153
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QY 117 HNAVC 121
Db 154 KDVC 158

RESULT 5
OX40_HUMAN STANDARD; PRT; 277 AA.
ID OX40_HUMAN OX40_HUMAN
AC P43489; Q13663;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ACTIVATED GLYCOPROTEIN 1 RECEPTOR (CD134 ANTIGEN).
GN TNFRSF4 OR TNFRP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94170844; PubMed=7510240;
RA Latza U., Duerkop H., Schnitger S., Ringeling J., Eitelbach F.,
Hummel M., Fonatsch C., Stein H.;
RT "The human OX40 homolog: cDNA structure, expression and chromosomal
assignment of the ACT35 antigen."
RL Eur. J. Immunol. 24:677-683(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9521981; PubMed=7704935;
RA Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A.,
Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.;
RT "Identification of OX40 ligand and preliminary characterization of
its activities on OX40 receptor."
RL Circ. Shock 44:30-34(1994).
CC - FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC - DATABASE: NAME=PROW; NOTE=CD guide CD134 entry;
WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd134.htm"
-----
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-----
DR EMBL; X75962; CAAS3576.1; -
DR EMBL; S76792; AAB33944.1; ALT_INIT.
DR HSSP; P25942; ICDF.
DR MIM; 600315; -
DR InterPro; IPR001368; -
DR Pfam; PF00020; TNFR_c6; 3.
DR PROSITE; PS00652; TNFR_NGFR.1; 3.
DR PROSITE; PS50050; TNFR_NGFR.2; 2.
KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
Signal.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 277 OX40L RECEPTOR.
FT DOMAIN 29 214 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 215 235 POTENTIAL.
FT DOMAIN 236 277 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 30 169 4 X TNFR-CYS.
FT REPEAT 30 65 TNFR-CYS 1.
FT REPEAT 66 107 TNFR-CYS 2.
FT REPEAT 108 126 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 127 167 TNFR-CYS 4.
FT CARBOHYD 146 146 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 277 AA; 49F15525941550BF CRC64;
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Query Match 19.3%; Score 145.5; DB 1; Length 277;
Best Local Similarity 31.0%; Pred. No. 1.2e-06;
Matches 39; Conservative 10; Mismatches 66; Indels 11; Gaps 4;

QY 2 CGPRLLLTGCTDARCCRVHTTRCRDYPG--EECCSEWDCM-CVQPEFHGCD---PQCT 55
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 46 CRP-----GNGMVSRCRSQNTVCRPCGPGFYNDVSSKPKCPCTWCNLRSGSRKQLCT 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 56 TCRHHPPPGGQVQSGKFSFGFCIDCASGTFSGGHEGCKPWTDCQTFQGLTVFPNGK 115
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 101 ATQTVTCRCRAGTQPLDSYKPGVDCAPCPGPHFSPGDNQACKPWTNCTLAGKHTLQPASN 160
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 116 THNAVC 121
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 161 SSDAIC 166

RESULT 6
CD40_MOUSE STANDARD; PRT; 289 AA.
ID CD40_MOUSE CD40_MOUSE
AC P27512;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
GN TNFRSF5 OR CD40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92105763; PubMed=1370315;
RA Torres R.M., Clark E.A.;
RT "Differential increase of an alternatively polyadenylated mRNA
species of murine CD40 upon B lymphocyte activation."
RL J. Immunol. 148:620-626(1992).
RN [2]
RP REVISIONS.
RC STRAIN=BALB/C;
RA Torres R.M.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE=93094586; PubMed=1281194;
RA Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
Howard M., Cockayne D.A.;
RT "Genomic structure and chromosomal mapping of the murine CD40 gene."
RL J. Immunol. 149:3921-3926(1992).
CC - FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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DR EMBL; M83312; AAB08705.1; -
DR EMBL; M94126; AAA37404.1; -
DR EMBL; M94129; AAA37404.1; JOINED.
DR EMBL; M94128; AAA37404.1; JOINED.
DR EMBL; M94127; AAA37404.1; JOINED.
DR PIR; A46476; A46476.
DR HSSP; P25942; ICDF.
DR MGI; MGI:88336; Tnfrsf5.
DR InterPro; IPR001368; -
```

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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:15:24 ; Search time 43.78 Seconds  
(without alignments)  
95,458 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_33\_154

Perfect score: 753

Sequence: 1 GCGPRLTGTGDARCRV.....TQFGFLTVFPGKTHNAVCV 122

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	162	21.5	272	1	OX40_MOUSE
2	152.5	20.3	255	1	41BB_HUMAN
3	149.5	19.9	271	1	OX40_RAT
4	149	19.8	256	1	41BB_MOUSE
5	145.5	19.3	277	1	OX40_HUMAN
6	127.5	16.9	289	1	CD40_MOUSE
7	122.5	16.3	269	1	CD40_BOVIN
8	117.5	15.6	1801	1	LMB2_RAT
9	114.5	15.2	277	1	CD40_HUMAN
10	113	15.0	461	1	TNR2_HUMAN
11	112.5	14.9	435	1	TNR2_MOUSE
12	112.5	14.9	1799	1	LMB2_MOUSE
13	105.5	14.0	2907	1	FN2_MOUSE
14	103.5	13.7	1798	1	LMB2_HUMAN
15	103.5	13.7	2911	1	FN2_HUMAN
16	103	13.7	474	1	TNR2_MOUSE
17	102	13.5	1370	1	IG1R_RAT
18	99.5	13.2	2569	1	LMA3_MOUSE
19	96.5	12.8	581	1	IRR_RAT
20	96.5	12.8	1713	1	LMA3_HUMAN
21	96	12.7	416	1	NGFR_CHICK
22	95	12.6	1297	1	IRR_HUMAN
23	95	12.6	1373	1	IG1R_MOUSE
24	93	12.4	212	1	AG1_HORVU
25	93	12.4	3635	1	LMA5_MOUSE
26	92	12.2	956	1	TSP3_MOUSE
27	92	12.2	1367	1	IG1R_HUMAN
28	92	12.2	2871	1	FN1_BOVIN
29	92	12.2	2871	1	FN1_HUMAN
30	92	12.2	4289	1	TENX_HUMAN
31	91.5	12.2	213	1	AG12_WHEAT
32	91.5	12.2	1106	1	STC_DROME
33	91	12.1	186	1	AG13_WHEAT
					P10741 mus musculus
					Q07011 homo sapien
					P15725 rattus norv
					P20334 mus musculus
					P43489 homo sapien
					P27512 mus musculus
					Q28203 bos taurus
					P15800 rattus norv
					P25942 homo sapien
					P20333 homo sapien
					P36941 homo sapien
					Q61292 mus musculus
					Q61555 mus musculus
					P5268 homo sapien
					P35556 homo sapien
					P25119 mus musculus
					TNR2_MOUSE
					P24062 rattus norv
					Q61789 mus musculus
					Q64716 rattus norv
					Q16787 homo sapien
					P18519 gallus gall
					P14616 homo sapien
					Q07051 mus musculus
					P15312 hordeum vul
					Q61001 mus musculus
					Q05895 mus musculus
					P08069 homo sapien
					P98133 bos taurus
					P35555 homo sapien
					P22105 homo sapien
					P02876 triticum ae
					P40798 drosophila
					P10969 triticum ae

## RESULT 1

OX40\_MOUSE STANDARD; PRT: 272 AA.

AC P47741;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).

GN TNFRSF4 OR TXGP1 OR OX40.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RP [1]

RN SEQUENCE FROM N.A.

RC STRAIN=BALB/C;

EX MEDLINE=94044750; PubMed=8228223;

RA Calderhead D.M., Buhlmann J.E., van den Bortwegh A.J.,

RT Claassen E., Noelle R.J., Fell H.;

RT "Cloning of mouse OX40; a T cell activation marker that may mediate

RT T-B cell interactions.";

RL J. Immunol. 151:5261-5271(1993).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=95255413; PubMed=7737295;

RA Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,

RA Barclay A.N.;

RT "Gene structure and chromosomal localization of the mouse homologue

RT of rat OX40 protein.";

RL Eur. J. Immunol. 25:926-930(1995).

CC -!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

EMBL; Z21674; CAA79772.1; -.

DR EMBL; X85214; CAA59476.1; -.

DR HSP; P25942; ICDP.

MGD; MGI:104512; Tnfrsf4.

DR InterPro; IPR001368; -.

DR Pfam; PF00020; TNFR\_c6; 3.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.

DR PROSITE; PS00050; TNFR\_NGFR\_2; 2.

KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;

KW Signal.

FT SIGNAL 1 19

FT CHAIN 20 272

FT DOMAIN 20 211

FT TRANSMEM 212 236

FT POTENTIAL. OX40L RECEPTOR.

FT EXTRACELLULAR (POTENTIAL).

FT POTENTIAL.

```
FT DOMAIN 237 272 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 165 4 X TNFR-CYS.
FT REPEAT 26 61 TNFR-CYS 1.
FT REPEAT 62 103 TNFR-CYS 2.
FT REPEAT 104 124 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 125 165 TNFR-CYS 4.
FT CARBOHYD 144 144 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 15 15 A -> G (IN REF. 2).
SQ SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;

Query Match 21.5%; Score 162; DB 1; Length 272;
Best Local Similarity 28.3%; Pred. No. 3.9e-08;
Matches 45; Conservative 11; Mismatches 51; Indels 52; Gaps 7;

QY 7 LLATGTDAR--CCRVHT-----TRCCRD-YPG-----EECCSEWDCMVQPEFHGCDPC-- 53
DB 14 LALTGLVTARLNCVKHTYPSGHKCCRECPQGHGMVSRCDHTRTLC-----HFCET 65

QY 54 -----CTTCRHPH-----CPPGGVQSQKFSFGFCID 82
DB 66 GFYNEAVNYDTCKQCTNHRSGSELKQNCPTQDTVCRCRPGTQPRQDSYKLGVDVCP 125

QY 83 CASGTFSGGHEGCKPWTCTQFGFLTVFGNKTHNVC 121
DB 126 CPPGHFSPGNQACKPWTNCTLSGKQTRHPASDSDAVC 164

RESULT 2
41BB_HUMAN STANDARD; PRT; 255 AA.
AC Q07011;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE 4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB HOMOLOG)
DE (T-CELL ANTIGEN ILA) (CD137 ANTIGEN).
GN TNFRSF9 OR ILA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=94374434; PubMed=8088337;
RA Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J.,
RA Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;
RT "Molecular and biological characterization of human 4-1BB and its
RT ligand.";
RL Eur. J. Immunol. 24:2219-2227(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=94085794; PubMed=8262389;
RA Schwarz H., Tuckwell J., Lotz M.;
RT "A receptor induced by lymphocyte activation (ILA): a new member of
RT the human nerve-growth-factor/tumor-necrosis-factor receptor
RT family.";
RL Gene 134:295-298(1993).
RN [3]
RP REVISION TO 107.
RA Schwarz H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95347766; PubMed=7622190;
RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,
RA Kwon B.S.;
RT "Characterization of human homologue of 4-1BB and its ligand.";
RL Immunol. Lett. 45:67-73(1995).
CC -I- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY
```

```
CC ACTIVE DURING T CELL ACTIVATION.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T
CC CELLS.
CC -I- SIMILARITY: CONTAINS A LA-NGRP/TNFR-TYPE CYSTEINE-RICH REGION.
CC -I- DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw137.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U03397; AAA53133.1; -.
CC EMBL: L12964; AAA62478.2; -.
CC HSP; P19438; TEXT.
CC MIM; 602250; -.
CC InterPro; IPR001368; -.
CC Pfam; PF00020; TNFR_C6; 2.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 255 4-1BB LIGAND RECEPTOR.
FT DOMAIN 18 186 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 187 213 POTENTIAL.
FT DOMAIN 214 255 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 47 159 3 X TNFR-CYS.
FT REPEAT 47 86 TNFR-CYS 1.
FT REPEAT 87 118 TNFR-CYS 2.
FT REPEAT 119 159 TNFR-CYS 3.
FT CARBOHYD 138 138 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 255 AA; 27899 MW; F3A563F85EF00460 CRC64;

Query Match 20.3%; Score 152.5; DB 1; Length 255;
Best Local Similarity 31.8%; Pred. No. 2.7e-07;
Matches 41; Conservative 11; Mismatches 50; Indels 27; Gaps 7;

QY 2 CGPGRLLGTGDARCCRVHTTRCCRDYPG-----EECCS-----EWDCCMVQPEFHGCDP 52
DB 48 CPPNFSFSSAGG--QRTCDI-----CROCKGVFTRKCSSTSNABCDG---TPGFHCLGA 97

QY 53 CCTTCRHHPCPPGGVQSQKFSFGFCIDCASGTFSGGHEGCKPWTCTQFGFLTVFP 112
DB 98 GCSMC-BODCKQGOELTKKG-----CKCCCFGTNDQKRGICRPWTNCSLDGKSVLNV 149

QY 113 GNKTHNVC 121
DB 150 GTERDVVC 158

RESULT 3
OX40_RAT STANDARD; PRT; 271 AA.
ID OX40_RAT
AC P15725;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).
GN TNFRSF4 OR TXGPIL OR OX40.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=90214614; PubMed=2157591;
```

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Query Match	23.7%	Score 60.5;	DB 2;	Length 177;
Best Local Similarity	38.7%	Pred. No. 7.9;		
Matches	12;	Conservative	3;	Mismatches 13;
				Indels 3;
				Gaps 2;

Search completed: September 4, 2001, 16:12:14  
Job time: 1111 sec

Db 29 CGPG-----GHGTPVDELDRCKFIHDD--CYGEAGKGCFFPKLTLYSWKC 71

||||| ||| |||||:| |::| | | |

RESULT 10

JC6547

high sulfur protein B2E - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jul-2000

C:Accession: JC6547

R:Mitsul, S.; Ohuchi, A.; Adachi-Yamada, T.; Hotta, M.; Tsuboi, R.; Ogawa, H.

Gene 208, 123-129, 1998

A:Title: Structure and hair follicle-specific expression of genes encoding the rat h

A:Reference number: JC6547; MUID:98201605

A:Accession: JC6547

A:Molecule type: DNA

A:Residues: 1-188 <MIT>

A:Cross-references: DBJ:AB003753; NID:g3046870; PIDN:BAA25573.1; PID:g3046871

C:Comment: This protein is a cysteine-rich, keratin associated protein.

C:Genetics:

A:Gene: b2E

C:Superfamily: keratin high-sulfur matrix protein IIIA

C:Keywords: hair

Query Match 24.1%; Score 61.5; DB 2; Length 188;

Best Local Similarity 38.7%; Pred. No. 6.4;

Matches 12; Conservative 4; Mismatches 12; Indels 3; Gaps 2;

QY 13 TDARCCRVHTTR--CCR-DYPGECCSEWDC 40

| |||:| : ||| | | | |

Db 140 TPPTCCQLHHAQSCRPSCYCGSCCRPACC 170

RESULT 11

A57474

extracellular matrix protein 1 precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 08-Dec-1995 #sequence\_revision 08-Dec-1995 #text\_change 08-Dec-1995

C:Accession: A57474

R:Bhalerao, J.; Tylzanowski, P.; Filie, J.D.; Kozak, C.A.; Merregaert, J.

J. Biol. Chem. 270, 16385-16394, 1995

A:Title: Molecular cloning, characterization, and genetic mapping of the cDNA coding

A:Reference number: A57474; MUID:95332952

A:Accession: A57474

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-559 <BHA>

A:Cross-references: GB:L33416

A:Experimental source: stromal osteogenic cell line MN7

C:Genetics:

A:Gene: Ecml

A:Map position: 3

C:Keywords: alternative splicing; extracellular matrix

Query Match 24.1%; Score 61.5; DB 2; Length 559;

Best Local Similarity 37.8%; Pred. No. 14;

Matches 14; Conservative 3; Mismatches 19; Indels 1; Gaps 1;

QY 2 CGPRLLLGTGTDAKCCRVHTTRCCR-DYPGECCSE 37

|| |||:| : ||| | | | |

Db 445 CGSGLVSKHKIPIGLIQNVTRCCCLPYEQACCGE 481

RESULT 12

C34860

phospholipase A2 (EC 3.1.1.4), Pa 5 - mulga snake

C:Species: Pseudochis australis (mulga snake)

C>Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 24-Jul-1997

C:Accession: C34860

R:Takasaki, C.; Yutani, F.; Kajiyashiki, T.

Toxicon 28, 329-339, 1990

Db 667 CGPCQRTTRGCLGPNQGQEATTCQGPSIETTLCTLC---EGQSCCNWSEW 710

RESOL  
T24272

C; Accession: 124272  
R; Sims, M.

Best local similarity 50.56; Recd. NO. 3.3;  
Matches 14; Conservative 1; Mismatches 12; Indels

D<sub>b</sub> 74 GGGG---GGGGCCCCRPRCCCCCR-----RCCT 100

C:Species: *Pseudechis australis* (mulga snake)  
C:Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change

A;Title: Amino acid sequences of eight phospholipases A-2 from

A;Molecule type: protein  
A;Residues: 1-118 <TAK>

Query Match	24.7%	Score 63	DB 2	Length 118
Query Match	24.7%	Score 63	DB 2	Length 118

C;Accession: T18975  
R:McMurray, A.

submitted to the EMBL Data Library, June 1995  
A-Reference number: Z10054

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2001, 16:12:13 ; Search time 80.15 Seconds  
(without alignments)  
38.966 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_33\_73

Perfect score: 255

Sequence: 1 GCGPGRLLLTGTGTARCCRV.....TTRCCRDYPGEECCSEWDCM 41

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_68.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	27.5	118	2 E34860	phospholipase A2 (
2	69	27.1	118	1 PSSNK3	phospholipase A2 (
3	66	25.9	416	2 G86232	hypothetical prote
4	64.5	25.3	788	2 T25061	hypothetical prote
5	63.5	24.9	164	2 T24272	hypothetical prote
6	63	24.7	118	2 H34860	phospholipase A2 (
7	63	24.7	152	2 T18975	hypothetical prote
8	63	24.7	295	2 JC5559	lectin-B - Virgini
9	62	24.3	117	2 B32416	phospholipase A2 (
10	61.5	24.1	188	2 JC6547	high sulfur protei
11	61.5	24.1	559	2 A57474	extracellular matr
12	61	23.9	118	2 C34860	phospholipase A2 (
13	61	23.9	188	2 T15651	hypothetical prote
14	60.5	23.7	177	2 S37650	high-sulfur kerati
15	60	23.5	119	1 PSNOAT	phospholipase A2 (
16	60	23.5	119	1 PSNOAS	phospholipase A2 (
17	59.5	23.3	122	2 JC6548	high sulfur protei
18	59.5	23.3	227	1 LNRZ	lectin precursor -
19	59	23.1	117	2 A32416	phospholipase A2 (
20	59	23.1	118	1 PSAXB	phospholipase A2 h
21	59	23.1	118	1 PSSNK1	phospholipase A2 (
22	59	23.1	118	2 F34860	phospholipase A2 (
23	59	23.1	152	1 KRSHHC	keratin high-sulfu
24	59	23.1	152	2 I47111	high-sulfur wool m
25	59	23.1	152	2 I47108	keratin high-sulfu
26	59	23.1	156	1 KRSHOB	keratin high-sulfu
27	59	23.1	172	2 I47106	keratin high-sulfu
28	59	23.1	182	1 KRSHHD	keratin high-sulfu
29	59	23.1	212	2 T05936	agglutinin isolect

30 58.5 22.9 175 2 S37649 high-sulfur kerati  
31 58.5 22.9 4135 2 T42629 tenascin-X - bovin  
32 58 22.7 133 1 PSOXG phospholipase A2 (

#### ALIGNMENTS

##### RESULT 1

E34860  
phospholipase A2 (EC 3.1.1.4), Pa 10A - mulga snake  
C:Species: Pseudechis australis (mulga snake)  
C:Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 24-Jul-1997  
C:Accession: E34860  
R:Takasaki, C.; Yutani, F.; Kajiyashiki, T.  
Toxicon 28, 329-339, 1990  
A:Title: Amino acid sequences of eight phospholipases A-2 from the venom of Australia  
A:Reference number: A34860; MUID:90360881  
A:Accession: E34860  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-118 <TRAK>  
C:Superfamily: phospholipase A2  
C:Keywords: carboxylic ester hydrolase  
F:48,92/Active site: His, Asp #status predicted

Query Match 27.5%; Score 70; DB 2; Length 118;  
Best Local Similarity 36.7%; Pred. No. 0.55;  
Matches 18; Conservative 4; Mismatches 11; Indels 16; Gaps 4;

QY 2 CGPGRLLLTGTDA----RCCRVHTTRCCRDYPGEECC-----SEWDC 40  
DB 29 CGWG-----GSGTPVDELDRCKVHDD--CYDQAGKKGCFPKLTLYSWDC 71

##### RESULT 2

PSSNK3  
phospholipase A2 (EC 3.1.1.4) Pa 13 - mulga snake  
N:Alternate names: phosphatidylcholine 2-acylhydrolase  
C:Species: Pseudechis australis (mulga snake)  
C:Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 28-Feb-1997  
C:Accession: A00748  
R:Nishida, S.; Terashima, M.; Taniya, N.  
Toxicon 23, 87-104, 1985  
A:Title: Amino acid sequences of phospholipases A-2 from the venom of an Australian e  
A:Reference number: A94319; MUID:85193286  
A:Accession: A00748  
A:Molecule type: protein  
A:Residues: 1-118 <NHS>  
C:Comment: There are many protein components with phospholipase A2 activity in the mu  
C:Function:  
A:Note: the reaction is strongly enhanced when the phospholipid is condensed into a m  
C:Superfamily: phospholipase A2  
A:Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; p  
F:4,67/Binding site: micellar substrate (Gln, Tyr) #status predicted  
F:11-71,27-117,29-45,44-98,51-91,60-84,78-89/disulfide bonds: #status predicted  
F:28,30,32,49/Binding site: calcium (Tyr, Gly, Asp) #status predicted  
F:48,92/Active site: His, Asp #status predicted



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CC	PHOSPHOCHOLINE + A FATTY ACID ANION.	
CC	-1- MISCELLANEOUS: LD(50) IS 0.24 MG/KG BY INTRAVENOUS INJECTION.	
CC	-1- MISCELLANEOUS: (THERE ARE MANY PROTEIN COMPONENTS WITH	
CC	PHOSPHOLIPASE A2 ACTIVITY IN THE MULGA SNAKE VENOM AND SOME OF	
CC	THEM ARE MYOTOXIC.	
CC	-1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.	
CC	P1R; A00747; PSSNK1.	
DR	HSSP; P00608; 1AE7.	
DR	InterPro; IPR001211; .	
DR	Pfam; PF00068; phoslip; 1.	
DR	PRINTS; PR00389; PHPHLIPASEA2.	
DR	PROSITE; PS00118; PA2_HIS; 1.	
DR	PROSITE; PS00119; PA2_ASP; 1.	
KW	Hydrolase; Lipid degradation;	
FT	ACT_SITE 48 48	Calcium; Multigene family; Venom.
FT	ACT_SITE 92 92	BY SIMILARITY.
FT	ACT_SITE 11 71	BY SIMILARITY.
FT	DISULFID 27 117	BY SIMILARITY.
FT	DISULFID 29 45	BY SIMILARITY.
FT	DISULFID 44 98	BY SIMILARITY.
FT	DISULFID 51 91	BY SIMILARITY.
FT	DISULFID 60 84	BY SIMILARITY.
FT	DISULFID 78 89	BY SIMILARITY.
FT	CA_BIND 49 49	BY SIMILARITY.
CC	SEQUENCE 118 AA; 12966 MW; F7C90529BB12D5A1 CRC64.	

Query Match	23.1%	Score 59;	DB 1;	Length 118;
Best Local Similarity	32.7%	Pred. No. 1.7;		
Matches 16;	Conservative	5;	Mismatches 12;	Indels 16;
Gaps 4;				

**QY.**    2 CGPGRLLGTGTD-----RCCRVHTTRCCRDYPGECC-----SEWDC 40  
       || | | :||| |||:|| | : ||| | | : ||| | |  
**D6**    29 CGWG----GGTGPVDELDRCCOVHDN--CYEOAGKKGCFPKLTLYSWKC 71

RESULT	11
PA22_OXYS	
ID	PA22_OXYS
AC	P00615; STANDARD; PRT; 118 AA.
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DE	15-DEC-1998 (Rel. 37, Last annotation update)
DE	PHOSPHOLIPASE A2 HOMOLOG, TAPOXIN BETA CHAIN.
OS	Oxyuranus scutellatus scutellatus (Australian taipan).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC	Elaeidae; Acanthophilineae; Oxyuranus.
OX	NCBI_TaxID=8667;
RN	[1]
RP	SEQUENCE.
RC	TISSUE-Venom;
RX	MEDLINE=83079319; PubMed=6756920;
RA	Link P.;
RT	"Amino-acid sequence of the beta 1 isosubunit of taipoxin, an
RT	extremely potent presynaptic neurotoxin from the Australian snake
RL	taipan (Oxyuranus s. scutellatus).";
RL	Eur. J. Biochem 128:71-75(1982).
CC	-I- FUNCTION: TAPOXIN IS THE MOST POTENT ANIMAL TOXIN KNOWN.
CC	THE BETA CHAIN IS NEITHER TOXIC NOR ENZYMATICALLY ACTIVE BY
CC	ITSELF. IT DOES NOT BIND CALCIUM.
CC	-I- SUBUNIT: CONTAINS THREE NONCOVALENTLY BOUND CHAINS (ALPHA, BETA,
CC	AND GAMMA), EACH RELATED TO PHOSPHOLIPASE A2
CC	-I- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
DR	PIR; A00753; PS0AB.
DR	HSP; P00593; 4BP2.
DR	InterPro: IPR001211; .-
DR	Pfam: PF00068; phoslip; 1.
DR	PRINTS: PR00389; PHPLIPASEA2.
DR	PROSITE: PS00118; PA2_HIS; 1.
DR	PROSITE: PS00119; PA2_ASP; 1.
KW	Presynaptic neurotoxic; Multigene family; Venom.
FT	DISULFID 11 71 BY SIMILARITY.

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FT    DISULFID    27    117    BY SIMILARITY.
FT    DISULFID    29    45     BY SIMILARITY.
FT    DISULFID    44    98     BY SIMILARITY.
FT    DISULFID    51    91     BY SIMILARITY.
FT    DISULFID    60    84     BY SIMILARITY.
FT    DISULFID    78    89     BY SIMILARITY.
SQ    SEQUENCE    118 AA; 13236 MW; 94392A8EA5A28273 CRC64;

Query Match          23.1%; Score 59; DB 1; Length 118;
Best Local Similarity 28.1%; Pred. No. 1.7;
Matches 16; Conservative 5; Mismatches 4; Indels 32; Gaps

QY    2    CGPGRLLLGTTGDA-----RCRVRHTRCCRDYPGEECCSE-----WDC 40
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB    29    CGKG----GSCTPDDLDRCQVH-----DECVAEAKHGKCPSLTYTWE 71

RESULT 12
PA2A_PSEAU
ID    PA2A_PSEAU    STANDARD;    PRT;    118 AA.
AC    P20255;
DT    01-FEB-1991 (Rel. 17, Created)
DT    01-FEB-1991 (Rel. 17, Last sequence update)
DT    15-DEC-1998 (Rel. 37, Last annotation update)
DE    PHOSPHOLIPASE A2 ISOZYME PA-12A (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-
DE    ACYLHYDROLASE).
OS    Pseudechis australis (Mulga snake) (King brown snake).
OC    Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;
OC    Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC    Elapidae; Acanthophinae; Pseudechis.
OX    NCBI_TaxID=8670;
RN    [1]
RP    SEQUENCE.
RC    TISSUE=Venom;
RX    MEDLINE=90260881; PubMed=2343466;
RA    Takasaki C., Yutani F., Kajiyashiki T.;
RT    "Amino acid sequences of eight phospholipases A2 from the venom of
RL    Australian king brown snake, Pseudechis australis.";
RL    Toxicon 28:329-339(1990).
CC    -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
CC    2-ACYL GROUPS IN 3'-SN-PHOSPHOGLYCERIDES.
CC    -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-ACYLGLYCERYL
CC    PHOSPHOCHOLINE + A FATTY ACID ANION.
CC    -1- MISCELLANEOUS: LD(50) IS 0.23 MG/KG BY INTRAVENOUS INJECTION.
CC    -1- MISCELLANEOUS: THERE ARE MANY PROTEIN COMPONENTS WITH
CC    PHOSPHOLIPASE A2 ACTIVITY IN THE MULGA SNAKE VENOM AND SOME OF
CC    THEM ARE MYOTOMIC.
CC    -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
PR    PR; F34860; F34860.
DR    HSPP; P00608; 1AE7.
DR    InterPro: IPR001211;
DR    Pfam: PF00068; phoslip; 1.
DR    PRINTS; PR00389; PHPLIPASEA2.
DR    PROSITE; PS00118; PA2_HIS; 1.
DR    PROSITE; PS00119; PA2_ASP; 1.
KW    Hydrolase; Lipid degradation; Calcium; Multigene family; Venom.
FT    ACT_SITE    48    48     BY SIMILARITY.
FT    ACT_SITE    92    92     BY SIMILARITY.
FT    DISULFID    11    71     BY SIMILARITY.
FT    DISULFID    27    117    BY SIMILARITY.
FT    DISULFID    29    45     BY SIMILARITY.
FT    DISULFID    44    98     BY SIMILARITY.
FT    DISULFID    51    91     BY SIMILARITY.
FT    DISULFID    60    84     BY SIMILARITY.
FT    DISULFID    78    89     BY SIMILARITY.
FT    DISULFID    92    92     BY SIMILARITY.
FT    CA_BIND     118 AA; 12969 MW; 75C705C7B33E5161 CRC64;
SQ    SEQUENCE

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Query Match 23.1%; Score 59; DB 1; Length 118;  
Best Local Similarity 32.7%; Pred. No. 1.7;  
Matches 16: Conservative 5; Mismatches 12; Indels 16; Gaps . 4;

CC -1- FUNCTION: N-ACETYL-D-GLUCOSAMINE BINDING LECTIN.  
 CC -1- SIMILARITY: CONTAINS FOUR COPIES OF A CHITIN-BINDING DOMAIN.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: M24504; AAA20873.1; -  
 CC PIR: J01102; LNR2.  
 CC PIR: A23616; A23616.  
 CC HSSP: P10968; IWGC.  
 CC InterPro: IPR001002; -  
 CC Pfam: PF00187; chitin\_binding; 4.  
 CC PRINTS: PR00451; CHITINBINDING.  
 CC PROSITE: PS00026; CHITIN\_BINDING; 4.  
 CC LECTIN; Duplication; Chitin-binding; Glycoprotein; Signal.  
 KW SIGNAL 1 28  
 FT CHAIN 29 201 LECTIN.  
 FT PROPEP 202 227  
 FT CHAIN 29 122  
 FT CHAIN 123 201  
 FT DOMAIN 29 72  
 FT DOMAIN 73 115  
 FT DOMAIN 116 158  
 FT DOMAIN 159 201  
 FT MOD\_RES 29 29  
 FT DISULFID 31 46  
 FT DISULFID 40 52  
 FT DISULFID 45 59  
 FT DISULFID 63 68  
 FT DISULFID 74 89  
 FT DISULFID 88 102  
 FT DISULFID 106 111  
 FT DISULFID 117 132  
 FT DISULFID 126 138  
 FT DISULFID 131 145  
 FT DISULFID 149 154  
 FT DISULFID 160 175  
 FT DISULFID 169 181  
 FT DISULFID 174 188  
 FT DISULFID 192 197  
 FT CARBOHYD 211 211  
 FT SEQUENCE 227 AA; 22795 MW; 691EB39F6690BAF1 CRC64;  
 SQ  
 Query Match 23.3%; Score 59.5; DB 1; Length 227;  
 Best Local Similarity 20.2%; Pred. No. 2.4;  
 Matches 17; Conservative 3; Mismatches 17; Indels 47; Gaps 3;  
 QY 2 CGPGRLLGLGTGDA-RCC-----RVHTTRCCRDY----- 29  
 DB 52 CGLGRDYCTGCGGACCSQRCSGGGATCSNNQCCSQYGYCGFGSEYCGSGCGNGPC 111  
 QY 30 -----PGEECCSEW 38  
 DB 112 RADIKGRNANGELCPNNMCCSQW 135  
 RESULT 9  
 ID PA2A\_PSEPO STANDARD; PRT; 117 AA.  
 AC P20258;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE PHOSPHOLIPASE A2 (EC 3.1.1.4) (PSEUDEKIN A CHAIN) (PHOSPHATIDYLCHOLINE  
 DE 2-ACYLHYDROLASE).  
 OS Pseudechis porphyriacus (Red-bellied black snake).  
 CC

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Elapidae; Acanthophiinae; Pseudechis.  
 OX NCBI\_TaxID=8671;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=89388835; PubMed=2675391;  
 RA Schmidt J.J., Middlebrook J.L.;  
 RT "Purification, sequencing and characterization of pseudexin  
 RT phospholipases A2 from Pseudechis porphyriacus (Australian  
 RT red-bellied black snake).";  
 RL Toxicon 27:805-818(1989).  
 CC -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE  
 CC 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.  
 CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O -> 1-ACYLGLYCERYL-  
 CC -1- PHOSPHOCHOLINE + A FATTY ACID ANION.  
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.  
 CC PIR: A32416; A32416.  
 CC HSSP: P00608; LAE7.  
 CC InterPro: IPR001211; -  
 CC Pfam: PF00068; phoslip; 1.  
 CC PRINTS: PR00389; PHPLIPASEA2.  
 CC PROSITE: PS00118; PA2\_HIS; 1.  
 CC PROSITE: PS00119; PA2\_ASP; 1.  
 KW Hydrolase; Lipid degradation; Calcium; Multigene family; Venom.  
 FT ACT\_SITE 48 48  
 FT ACT\_SITE 92 92 BY SIMILARITY.  
 FT DISULFID 11 71 BY SIMILARITY.  
 FT DISULFID 27 117 BY SIMILARITY.  
 FT DISULFID 29 45 BY SIMILARITY.  
 FT DISULFID 44 98 BY SIMILARITY.  
 FT DISULFID 51 91 BY SIMILARITY.  
 FT DISULFID 60 84 BY SIMILARITY.  
 FT DISULFID 78 89 BY SIMILARITY.  
 FT CA\_BIND 49 49 BY SIMILARITY.  
 FT SEQUENCE 117 AA; 43804BC379277D9D CRC64;  
 SQ  
 Query Match 23.1%; Score 59; DB 1; Length 117;  
 Best Local Similarity 32.7%; Pred. No. 1.7;  
 Matches 16; Conservative 4; Mismatches 13; Indels 16; Gaps 4;  
 QY 2 CGPGRLLGLGTGDA----RCCRVHTTRCCRDYPCECC-----SEWDC 40  
 DB 29 CGWG----GSGTPVDELDRCCQTHDN--CYDQAGKGCFFKLTLYSWRC 71  
 RESULT 10  
 ID PA2L\_PSEAU STANDARD; PRT; 118 AA.  
 AC P04056;  
 DT 01-NOV-1986 (Rel. 03, Created)  
 DT 01-NOV-1986 (Rel. 03, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE PHOSPHOLIPASE A2 ISOZYME PA-11 (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-  
 DE ACYLHYDROLASE).  
 OS Pseudechis australis (Mulga snake) (King brown snake).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Elapidae; Acanthophiinae; Pseudechis.  
 OX NCBI\_TaxID=8670;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=85193286; PubMed=3887651;  
 RA Nishida S., Terashima M., Tamiya N.;  
 RT "Amino acid sequences of phospholipases A2 from the venom of an  
 RT Australian elapid snake (king brown snake, Pseudechis australis).";  
 RL Toxicon 23:87-104(1985).  
 CC -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE  
 CC 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.  
 CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O -> 1-ACYLGLYCERYL-



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CC entitles requires a license agreement (See http://www.lsb-slb.ch/announcement/
CC or send an email to license@lsb-slb.ch).
CC -----
CC EMBL; L33416; AAA37535.1; -.
CC DR MGD; MGI:103060; Ecml.
CC KW Signal; Alternative splicing; Extracellular matrix; Glycoprotein;
CC Repeat.
CC FT SIGNAL 1 19
CC FT CHAIN 20 559
CC FT DOMAIN 170 424
CC FT REPEAT 170 298
CC FT REPEAT 302 424
CC FT CARBOHYD 373 373
CC FT CARBOHYD 463 463
CC FT CARBOHYD 535 535
CC FT VARSPLIC 256 380
CC FT SEQUENCE 559 AA; 62775 MW; BBF37FAB7D67E2E8 CRC64;
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CC Query Match 24.1%; Score 61.5; DB 1; Length 559;
CC Best Local Similarity 37.8%; Pred. No.2.9;
CC Matches 14; Conservative 3; Mismatches 19; Indels 1; Gaps 1;
CC
CC QY 2 CGGCRLLLTGTGTCRCRVHTTCCR-DYPGECCSE 37
CC ||||| : ||||| ||: |||
CC DB 445 CGSGRVLSKHKQIPGLTQNNTVRCCELPYEQACCGE 481
CC
CC RESULT 6
CC PA25_PSEAU
CC ID PA25_PSEAU STANDARD; PRT; 118 AA.
CC AC P20252;
CC DT 01-FEB-1991 (Rel. 17, Created)
CC DT 01-FEB-1991 (Rel. 17, Last sequence update)
CC DT 15-DEC-1998 (Rel. 37, Last annotation update)
CC DE PHOSPHOLIPASE A2 ISOZYME PA-5 (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-
CC DE ACYLHYDROLASE).
CC OS Pseudechis australis (Mulga snake) (King brown snake).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
CC OC Elapidae; Acanthophinae; Pseudechis.
CC OX NCBI_Taxid=8670;
CC [1]
CC RN
CC RP SEQUENCE.
CC RC TISSUE=Venom;
CC RX MEDLINE=90260881; PubMed=2343456;
CC RA Takasaki C., Iutani F., Kajiyashiki T.:
CC RT "Amino acid sequences of eight phospholipases A2 from the venom of
CC RT Australian king brown snake, Pseudechis australis.";
CC RL Toxicon 28:329-339(1990).
CC CC -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
CC CC 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
CC CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O - 1-ACYLGLYCERYL-
CC CC PHOSPHOCHOLINE + A FATTY ACID ANION.
CC CC -1- MISCELLANEOUS: LD(50) IS 0.09 MG/KG BY INTRAVENOUS INJECTION.
CC CC -1- MISCELLANEOUS: THERE ARE MANY PROTEIN COMPONENTS WITH
CC CC PHOSPHOLIPASE A2 ACTIVITY IN THE MULGA SNAKE VENOM AND SOME OF
CC CC THEM ARE MYOTOXIC.
CC CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
CC CC PIR; C34860; C34860.
CC DR HSSP; P00608; 1AE7.
CC DR InterPro; IPR001211; -.
CC DR Pfam; PF00068; phoslip; 1.
CC DR PRINTS; PR00389; PHPLIPASEA2.
CC DR PROSITE; PS00118; PA2_HIS; 1.
CC DR PROSITE; PS00119; PA2_ASP; FALSE_NEG.
CC KW Hydrolyase; Lipid degradation; Calcium; Multigene family; Venom.
CC FT ACT_SITE 48 48
CC FT ACT_SITE 92 92
CC FT DISULFID 11 71
CC FT DISULFID 27 117
CC FT DISULFID 29 45
CC FT DISULFID 44 98
CC FT ACT_SITE 48 48
CC FT BY SIMILARITY.
CC FT ACT_SITE 92 92
CC FT BY SIMILARITY.
CC FT DISULFID 11 71
CC FT BY SIMILARITY.
CC FT DISULFID 27 117
CC FT BY SIMILARITY.
CC FT DISULFID 29 45
CC FT BY SIMILARITY.
CC FT DISULFID 44 98
CC FT BY SIMILARITY.

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Db 29 CGWG---GSGTPVDELDRCKVHDD--CYDQAGKGCFCFKLTLYSWDC 71
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RESULT 2
PA2D_PSEAU STANDARD; PRT; 118 AA.
AC P04057;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PHOSPHOLIPASE A2 ISOZYME PA-13 (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-
DE ACYLHYDROLASE).
OS Pseudechis australis (Mulga snake) (King brown snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophilineae; Pseudechis.
OX NCBI_TaxID=8670;
RN [1]
RP SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE=90260881; PubMed=2343466;
RA Takasaki C., Yutani F., Kajiyashiki T.;
RT "Amino acid sequences of eight phospholipases A2 from the venom of
RT Australian king brown snake, Pseudechis australis.";
RL Toxicon 28:329-339(1990).
CC -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
CC 2-ACYL GROUPS IN 3-SN-PHOSPHOGlycerides.
CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-ACYLGLYCERYL-
CC PHOSPHOCHOLINE + A FATTY ACID ANION.
CC -1- MISCELLANEOUS: LD(50) IS 3.4 MG/KG BY INTRAVENOUS INJECTION.
CC -1- MISCELLANEOUS: THERE ARE MANY PROTEIN COMPONENTS WITH
CC PHOSPHOLIPASE A2 ACTIVITY IN THE MULGA SNAKE VENOM AND SOME OF
CC THEM ARE MYOTOXIC.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
DR PIR: H34860; H34860.
DR HSSP: P00608; 1AE7.
DR InterPro: IPR001211; -.
DR Pfam: PF00068; phoslip; 1.
DR PRINTS: PR00389; PHPLIPASEA2.
DR PROSITE: PS00118; PA2_HIS; 1.
DR PROSITE: PS00119; PA2_ASP; 1.
KW Hydrolase; Lipid degradation; Calcium; Multigene family; Venom.
FT ACT_SITE 48 48
FT ACT_SITE 92 92 BY SIMILARITY.
FT DISULFID 11 71 BY SIMILARITY.
FT DISULFID 27 117 BY SIMILARITY.
FT DISULFID 29 45 BY SIMILARITY.
FT DISULFID 44 98 BY SIMILARITY.
FT DISULFID 51 91 BY SIMILARITY.
FT DISULFID 60 84 BY SIMILARITY.
FT DISULFID 78 89 BY SIMILARITY.
FT CA_BIND 49 49 BY SIMILARITY.
SQ SEQUENCE 118 AA; 13213 MW; ECCFDB8D91AC8F CRC64;

Query Match 27.1%; Score 69; DB 1; Length 118;
Best Local Similarity 34.7%; Pred. No. 0.11;
Matches 17; Conservative 4; Mismatches 12; Indels 16; Gaps 4;

QY 2 CGGRLLLGTGTD-----RCRVHTTRCCRDYPGEECC-----SEWDC 40
||||| ||||| ||||| ||||| |||||
Db 29 CGPG---GRGTPVDELDRCKIHDD--CYIEAGKDCGCPKLTWYSWDC 71
||||| ||||| ||||| ||||| |||||
RESULT 3
PA2E_PSEAU STANDARD; PRT; 118 AA.
AC P20257;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PHOSPHOLIPASE A2 ISOZYME PA-15 (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-
DE ACYLHYDROLASE).
OS Pseudechis porphyriacus (Red-bellied black snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophilineae; Pseudechis.
OX NCBI_TaxID=8671;
RN [1]
RP SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE=89388835; PubMed=2675391;
RA Schmidt J.J., Middlebrook J.L.;
RT "Purification, sequencing and characterization of pseudexin

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DE ACYLHYDROLASE).
OS Pseudechis australis (Mulga snake) (King brown snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophilineae; Pseudechis.
OX NCBI_TaxID=8670;
RN [1]
RP SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE=90260881; PubMed=2343466;
RA Takasaki C., Yutani F., Kajiyashiki T.;
RT "Amino acid sequences of eight phospholipases A2 from the venom of
RT Australian king brown snake, Pseudechis australis.";
RL Toxicon 28:329-339(1990).
CC -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
CC 2-ACYL GROUPS IN 3-SN-PHOSPHOGlycerides.
CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-ACYLGLYCERYL-
CC PHOSPHOCHOLINE + A FATTY ACID ANION.
CC -1- MISCELLANEOUS: LD(50) IS 3.4 MG/KG BY INTRAVENOUS INJECTION.
CC -1- MISCELLANEOUS: THERE ARE MANY PROTEIN COMPONENTS WITH
CC PHOSPHOLIPASE A2 ACTIVITY IN THE MULGA SNAKE VENOM AND SOME OF
CC THEM ARE MYOTOXIC.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
DR PIR: H34860; H34860.
DR HSSP: P00608; 1AE7.
DR InterPro: IPR001211; -.
DR Pfam: PF00068; phoslip; 1.
DR PRINTS: PR00389; PHPLIPASEA2.
DR PROSITE: PS00118; PA2_HIS; 1.
DR PROSITE: PS00119; PA2_ASP; 1.
KW Hydrolase; Lipid degradation; Calcium; Multigene family; Venom.
FT ACT_SITE 48 48
FT ACT_SITE 92 92 BY SIMILARITY.
FT DISULFID 11 71 BY SIMILARITY.
FT DISULFID 27 117 BY SIMILARITY.
FT DISULFID 29 45 BY SIMILARITY.
FT DISULFID 44 98 BY SIMILARITY.
FT DISULFID 51 91 BY SIMILARITY.
FT DISULFID 60 84 BY SIMILARITY.
FT DISULFID 78 89 BY SIMILARITY.
FT CA_BIND 49 49 BY SIMILARITY.
SQ SEQUENCE 118 AA; 13200 MW; EA0FDFC13D91AC9A CRC64;

Query Match 24.7%; Score 63; DB 1; Length 118;
Best Local Similarity 32.7%; Pred. No. 0.57;
Matches 16; Conservative 4; Mismatches 13; Indels 16; Gaps 4;

QY 2 CGGRLLLGTGTD-----RCRVHTTRCCRDYPGEECC-----SEWDC 40
||||| ||||| ||||| ||||| |||||
Db 29 CGPG---GRGTPVDELDRCKIHDD--CYIEAGKDCGCPKLTWYSWDC 71
||||| ||||| ||||| ||||| |||||
RESULT 4
PA2B_PSEPO STANDARD; PRT; 117 AA.
AC P20259;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PHOSPHOLIPASE A2 (EC 3.1.1.4) (PSEUDEXIN B CHAIN) (PHOSPHATIDYLCHOLINE
DE 2-ACYLHYDROLASE).
OS Pseudechis porphyriacus (Red-bellied black snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophilineae; Pseudechis.
OX NCBI_TaxID=8671;
RN [1]
RP SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE=89388835; PubMed=2675391;
RA Schmidt J.J., Middlebrook J.L.;
RT "Purification, sequencing and characterization of pseudexin

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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:15:24 ; Search time 43.78 Seconds  
(without alignments)  
32.080 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_33\_73

Perfect score: 255

Sequence: 1 GCGPGRLLLTGTGDARCRV.....TTRCCRDYPGECCSEWDCM 41

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	70	27.5	118	1	PA20_PSEAU
2	69	27.1	118	1	PA2D_PSEAU
3	63	24.7	118	1	PA2E_PSEAU
4	62	24.3	117	1	PA2B_PSEPO
5	61.5	24.1	559	1	ECM1_MOUSE
6	61	23.9	118	1	PA25_PSEAU
7	60	23.5	119	1	PA22_NOTSC
8	59.5	23.3	227	1	AG1_ORYSA
9	59	23.1	117	1	PA2A_PSEPO
10	59	23.1	118	1	PA21_PSEAU
11	59	23.1	118	1	PA22_OXYSC
12	59	23.1	118	1	PA2A_PSEAU
13	59	23.1	151	1	KR2C_SHEEP
14	59	23.1	156	1	KR2B_SHEEP
15	59	23.1	181	1	KR2D_SHEEP
16	59	23.1	212	1	AG1_HORVU
17	58.5	22.9	2482	1	VWF_PIG
18	58	22.7	133	1	PA23_OXYSC
19	58	22.7	171	1	KR2A_SHEEP
20	57.5	22.5	99	1	NIC1_HUMAN
21	57.5	22.5	145	1	PA2_LATLA
22	57.5	22.5	4289	1	TENX_HUMAN
23	57	22.4	118	1	PA23_PSEAU
24	57	22.4	2907	1	FBN2_MOUSE
25	57	22.4	3083	1	POLG_ZYMYR
26	56.5	22.2	60	1	TXW3_NAJHA
27	56.5	22.2	61	1	TXW4_NAJHA
28	56.5	22.2	1063	1	POLS_RUBVH
29	56.5	22.2	1063	1	POLS_RUBVT
30	56	22.0	118	1	PA21_LATSE
31	56	22.0	118	1	PA26_BUNFA
32	56	22.0	118	1	PA2A_BUNFA
33	56	22.0	118	1	PA2B_BUNFA

34 56 22.0 121 1 PA22\_BOTAS  
35 56 22.0 145 1 PA20\_NOTSC  
36 56 22.0 374 1 MTB1\_BACBR  
37 56 22.0 1799 1 LMB2\_MOUSE  
38 56 22.0 1801 1 LMB2\_RAT  
39 55.5 21.8 677 1 SP87\_DICDI  
40 55.5 21.8 3106 1 LMA2\_MOUSE  
41 55.5 21.8 4544 1 LRP1\_HUMAN  
42 55 21.6 118 1 PA2C\_PSEAU  
43 55 21.6 138 1 PA25\_TRIGA  
44 55 21.6 275 1 VA16\_VACCV  
45 55 21.6 377 1 VA16\_VARV

#### ALIGNMENTS

RESULT 1  
ID PA20\_PSEAU STANDARD; PRT; 118 AA.  
AC P20254:  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE PHOSPHOLIPASE A2 ISOZYME PA-10A (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-DE ACYLHYDROLASE).  
OS Pseudechis australis (Mulga snake) (King brown snake).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Elapidae; Acanthophiinae; Pseudechis.  
OX NCBI\_TaxID=8670;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=90260881; PubMed=2343466;  
RA Takasaki C., Yutani F., Kajiyashiki T.;  
RT "Amino acid sequences of eight phospholipases A2 from the venom of Australian king brown snake, Pseudechis australis.";  
RL Toxicon 28:329-339(1990).  
CC -!- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.  
CC -!- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-ACYLGLYCERYL-PHOSPHOCHOLINE + A FATTY ACID ANION.  
CC -!- MISCELLANEOUS: THERE ARE MANY PROTEIN COMPONENTS WITH PHOSPHOLIPASE A2 ACTIVITY IN THE MULGA SNAKE VENOM AND SOME OF THEM ARE MYOTOXIC.  
CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.  
DR PIR: E34860; E34860.  
DR HSP: P00608; LAE7.  
DR InterPro: IPR001211; .  
DR Pfam: PF00068; phoslip; 1.  
DR PRINTS: PR00389; PHPLIPASEA2.  
DR PROSITE: PS00118; PA2\_HIS; 1.  
DR PROSITE: PS00119; PA2\_ASP; 1.  
KW Hydrolase; Lipid degradation; Calcium; Multigene family; Venom.  
FT ACT\_SITE 48 48 BY SIMILARITY.  
FT ACT\_SITE 92 92 BY SIMILARITY.  
FT DISULFID 11 71 BY SIMILARITY.  
FT DISULFID 27 117 BY SIMILARITY.  
FT DISULFID 29 45 BY SIMILARITY.  
FT DISULFID 44 98 BY SIMILARITY.  
FT DISULFID 51 91 BY SIMILARITY.  
FT DISULFID 60 84 BY SIMILARITY.  
FT DISULFID 78 89 BY SIMILARITY.  
FT CA\_BIND 49 49 BY SIMILARITY.  
SQ SEQUENCE 118 AA; 13027 MW; 884D1D3A6E2B5FCB CRC64;

Query Match 27.5%; Score 70; DB 1; Length 118;  
Best Local Similarity 36.7%; Pred. No. 0.087;  
Matches 18; Conservative 4; Mismatches 11; Indels 16; Gaps 4;

OY 2 CGPGRLLLTGTGTD-----RCRVHTTRCCRDYPGECC-----SEWDC 40





von Willebrand factor precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 04-Dec-1986 #sec\_revision 30-Jun-1993 #Text\_change 22-Jun-1999  
 C:Accession: A34480; S02377; S23676; A25298; A25469; A25366; S23618; S23645; A940060  
 R:Mancuso, D.J.; Tuley, E.A.; Westfield, L.A.; Worrall, N.K.; Shelton-Inloes, B.B.; Sorace, J. Biol. Chem. 264, 19514-19527, 1989  
 A:Title: Structure of the gene for human von Willebrand factor.  
 A:Reference number: A34480; MUID:90062044  
 A:Accession: A34480  
 A:Molecule type: DNA  
 A:Residues: 1-2813 <MAN>  
 A:Cross-references: EMBL:M25864  
 R:Bonthron, D.; Orkin, S.H.  
 Eur. J. Biochem. 171, 51-57, 1988  
 A:Title: The human von Willebrand factor gene. Structure of the 5' region.  
 A:Reference number: S02377; MUID:88111704  
 A:Accession: S02377  
 A:Molecule type: DNA  
 A:Residues: 1-177 <BO2>  
 A:Cross-references: EMBL:X06828  
 R:Mancuso, D.J.; Tuley, E.A.; Westfield, L.A.; Lester-Mancuso, T.L.; Le Beau, M.M.; Sorace, J. Biochemistry 30, 253-269, 1991  
 A:Title: Human von Willebrand factor gene and pseudogene: structural analysis and difference.  
 A:Reference number: A37139; MUID:91105089  
 A:Accession: A37139  
 A:Molecule type: DNA  
 A:Residues: 990-1947 <MAD>  
 A:Cross-references: GB:M06075; NID:g340357; PIDN:AAA61295.1; PID:g553810  
 A:Note: The authors translated the codon GCG for residue 156 as Gln  
 R:Collins, C.J.; Underdahl, J.P.; Levene, R.B.; Ravera, C.P.; Morin, M.J.; Dombalagian, Proc. Natl. Acad. Sci. U.S.A. 84, 4393-4397, 1987  
 A:Title: Molecular cloning of the human gene for von Willebrand factor and identification.  
 A:Reference number: S23676; MUID:87260814  
 A:Accession: S23676  
 A:Molecule type: DNA  
 A:Residues: 2731-2813 <COL>  
 A:Cross-references: EMBL:M16945  
 R:Bonthron, D.; Orr, E.C.; Mitsosk, L.M.; Ginsburg, D.; Handin, R.I.; Orkin, S.H.  
 Nucleic Acids Res. 14, 7125-7127, 1986  
 A:Title: Nucleotide sequence of pre-pro-von Willebrand factor cDNA.  
 A:Reference number: A25298; MUID:87016349  
 A:Accession: A25298  
 A:Molecule type: mRNA  
 A:Residues: 1-470, 'V', 472-2813 <BON>  
 A:Cross-references: EMBL:X04385  
 R:Verweij, C.L.; Diergaarde, P.J.; Hart, M.; Pannekoek, H.  
 EMBO J. 5, 1839-1847, 1986  
 A:Title: Full-length von Willebrand factor (vWF) cDNA encodes a highly repetitive protein.  
 A:Reference number: A91044; MUID:87004550  
 A:Accession: A25469  
 A:Molecule type: mRNA  
 A:Residues: 1-470, 'V', 472-483, 'R', 485-1022, 'K', 1024-1025, 'E', 1027-1400 <VER>  
 A:Cross-references: EMBL:X04146  
 A:Note: This sequence has been revised in reference A91056  
 R:Verweij, C.L.; Diergaarde, P.J.; Hart, M.; Pannekoek, H.  
 EMBO J. 5, 3074, 1986  
 A:Reference number: A91056  
 A:Accession: A25366  
 A:Molecule type: mRNA  
 A:Residues: 1021-1030 <VE2>  
 A:Note: This is a revision to the sequence from reference A91044  
 R:Shelton-Inloes, B.B.; Broze Jr., G.J.; Miletich, J.P.; Sadler, J.E.  
 Biochem. Biophys. Res. Commun. 144, 657-665, 1987  
 A:Title: Evolution of human von Willebrand factor: cDNA sequence polymorphisms, repeated.  
 A:Reference number: S23618; MUID:87213253  
 A:Accession: S23618  
 A:Molecule type: mRNA  
 A:Residues: 1-120 <SH2>  
 A:Cross-references: EMBL:M17588; NID:g799330; PIDN:AAA65940.1; PID:g340316  
 A:Accession: S23645  
 A:Molecule type: protein  
 A:Residues: 23-56 <SH3>  
 R:Sadler, J.E.; Shelton-Inloes, B.B.; Sorace, J.M.; Harlan, J.M.; Titani, K.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 82, 6394-6398, 1985  
 A:Title: Cloning and characterization of two cDNAs coding for human von Willebrand factor.  
 A:Reference number: A94060; MUID:86016708  
 A:Accession: A94060  
 A:Molecule type: mRNA  
 A:Residues: 'WA', 739, 'C', 744-769, 'H', 771-788, 'A', 790-803, 'S', 805-873, 1289-1471, 'D', 14  
 A:Note: The authors translated the codon TCG for residue 2168 as Cys  
 R:Shelton-Inloes, B.B.; Titani, K.; Sadler, J.E.  
 Biochemistry 25, 3164-3171, 1986  
 A:Title: cDNA sequences for human von Willebrand factor reveal five types of repeated.  
 A:Reference number: A90504; MUID:86269894  
 A:Accession: A90504  
 A:Molecule type: mRNA  
 A:Residues: 781-788, 'A', 790-1424 <SHE>  
 A:Note: 852-Gln, 857-Asp, and 1381-Thr were also found  
 R:Ginsburg, D.; Handin, R.I.; Bonthron, D.T.; Donlon, T.A.; Bruns, G.A.P.; Latt, S.A.  
 Science 228, 1401-1406, 1985  
 A:Title: Human von Willebrand factor (vWF): isolation of complementary DNA (cDNA) clo  
 A:Reference number: A44178; MUID:85244588  
 A:Accession: A44178  
 A:Molecule type: mRNA  
 A:Residues: 2621-2813 <GIN>  
 A:Cross-references: EMBL:X03028; NID:g340308; PIDN:AAA61293.1; PID:g340309  
 R:Verweij, C.L.; de Vries, C.J.M.; Distel, B.; van Zonneveld, A.J.; van Kessel, A.G.;  
 Nucleic Acids Res. 13, 4699-4717, 1985  
 A:Title: Construction of cDNA coding for human von Willebrand factor using antibody p  
 A:Reference number: S07363; MUID:85269603  
 A:Accession: S07363  
 A:Molecule type: mRNA  
 A:Residues: 2731-2813 <VE3>  
 A:Cross-references: EMBL:X02672; NID:g37939; PIDN:CAA26503.1; PID:g37940  
 R:Lynch, D.C.; Zimmerman, T.S.; Collins, C.J.; Brown, M.; Morin, M.J.; Ling, E.H.; Li  
 Cell 41, 49-56, 1985  
 A:Title: Molecular cloning of cDNA for human von Willebrand factor: authentication by  
 A:Reference number: S23678; MUID:85201687  
 A:Accession: S23678  
 A:Molecule type: mRNA  
 A:Residues: 2731-2813 <LYN>  
 A:Cross-references: EMBL:X03028  
 R:Titani, K.; Kumar, S.; Takio, K.; Ericsson, L.H.; Wade, R.D.; Ashida, K.; Walsh, K.  
 Biochemistry 25, 3171-3184, 1986  
 A:Title: Amino acid sequences of human von Willebrand factor.  
 A:Reference number: A90505; MUID:86269895  
 A:Accession: A90505  
 A:Molecule type: protein  
 A:Residues: 764-788, 'A', 790-1471, 'D', 1473-2813 <TTT>  
 A:Note: 789-Thr was also found  
 R:Chopek, M.W.; Girma, J.P.; Fujikawa, K.; Davie, E.W.; Titani, K.  
 Biochemistry 25, 3146-3155, 1986  
 A:Title: Human von Willebrand factor: a multivalent protein composed of identical sub  
 A:Reference number: A23464; MUID:86269892  
 A:Accession: A23464  
 A:Molecule type: protein  
 A:Residues: 764-773; 2803-2813 <CHO>  
 R:Deft, J.A.; Berkowitz, S.D.; Ware, J.; Kasper, C.K.; Ruggeri, Z.M.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 6306-6310, 1990  
 A:Title: Identification of a cleavage site directing the immunochemical detection of  
 A:Reference number: A36013; MUID:90349604  
 A:Accession: A36013  
 A:Molecule type: protein  
 A:Residues: 1506-1617 <DEN>  
 R:Pay, P.J.; Kawai, Y.; Wagner, D.D.; Ginsburg, D.; Bonthron, D.; Ohlsson-Wilhelm, B.  
 Science 232, 995-998, 1986  
 A:Title: Protopolypeptide of von Willebrand factor circulates in blood and is identical  
 A:Reference number: A60913; MUID:86208144  
 A:Accession: A60913  
 A:Molecule type: protein  
 A:Residues: 576-590 <FAY>  
 C:Genetics:  
 A:Gene: GDB:VWF  
 A:Cross-references: GDB:119125; OMIM:193400  
 A:Map position: 12p13.3-12p13.2  
 A:Introns: 19/1; 74/1; 108/2; 178/1; 219/3; 292/1; 333/1; 370/2; 386/1; 431/3; 478/1;

A;Molecule type: protein  
A;Residues: 740-744,'X',746-747 <RUS>



```
Query Match      24.0%; Score 60.5; DB 2; Length 216;
Best Local Similarity 43.6%; Pred. No. 7.1;
Matches 17; Conservative 4; Mismatches 11; Indels 7; Gaps 4;

QY 7 HCGDPC--TTCRHH---PCPPGGVQSGQKF-SFGFQC 39
      :| ||| |||:| | | | | | | | | | | | | | | |
Db 29 NCRDPCDDATCKLHSWESGE-CCGCKFTSAGNEC 66

RESULT 6
S56015
gastric mucin MUC5AC - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Apr-2000
C:Accession: S56015; S53361
R:Klomp, L.W.J.; van Rens, L.; Strous, G.J.
Biochem. J. 308, 831-838, 1995
A:Title: Cloning and analysis of human gastric mucin cDNA reveals two types of conserved
A:Reference number: S56015; MUID:97104281
A:Accession: S56015
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-850 <KLO>
A:Cross-references: EMBL:X81649; NID:g547516; PIDN:CAA57309.1; PID:g547517
R:Guyonnet-Duperat, V.; Audie, J.P.; Debailleul, V.; Laine, A.; Buisine, M.P.; Galliege-
Biochem. J. 305, 211-219, 1995
A:Title: Characterization of the human mucin gene MUC5AC: a consensus cysteine-rich doma
A:Reference number: S53361; MUID:95126907
A:Accession: S53361
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 648-678, 'L', 680-733, 'L', 735-760 <GUY>
A:Cross-references: EMBL:X34280; NID:g563380; PIDN:CAA84034.1; PID:g563381
A:Experimental source: clone JUI32
A:Note: this publication is not cited in GenBank entry HSMUCIN5, release 113.0

Query Match      24.0%; Score 60.5; DB 2; Length 850;
Best Local Similarity 29.8%; Pred. No. 19;
Matches 17; Conservative 6; Mismatches 11; Indels 23; Gaps 4;

QY 3 QPEFH---CGDPCCTTCRH-----HP-CPPGGVQSGQKFSFGFQCI 40
      | | | | | | | | | | | | | | | | | | | | | |
Db 169 QCEWHYQCGVPCLCRPNRGDCLRDVRGLGECYKCPPEAFIFDEDK----MQCV 221

RESULT 7
JE0095
gastric mucin MUC5AC precursor - human
C:Species: Homo sapiens (man)
C>Date: 22-May-1998 #sequence_revision 29-May-1998 #text_change 07-May-1999
C:Accession: JE0095
R:vian de Bovenkamp, J.H.B.; Hau, C.M.; Strous, G.J.A.M.; Bueller, H.A.; Dekker, J.; Eine
Biochem. Biophys. Res. Commun. 245, 853-859, 1998
A:Title: Molecular cloning of human gastric mucin MUC5AC reveals conserved cysteine-rich
A:Reference number: JE0095; MUID:98249803
A:Accession: JE0095
A:Molecule type: mRNA
A:Residues: 1-1373 <BOV>
A:Cross-references: GB:AF043909
A:Experimental source: stomach
F:1-19/Domain: signal sequence #status predicted <SIG>
F:273-300/Domain: leucine zipper #status predicted <LZP>

Query Match      24.0%; Score 60.5; DB 2; Length 1373;
Best Local Similarity 29.8%; Pred. No. 27;
Matches 17; Conservative 6; Mismatches 11; Indels 23; Gaps 4;

QY 3 QPEFH---CGDPCCTTCRH-----HP-CPPGGVQSGQKFSFGFQCI 40
      | | | | | | | | | | | | | | | | | | | | | |
Db 1176 QCEWHYQCGVPCLCRPNRGDCLRDVRGLGECYKCPPEAFIFDEDK----MQCV 1228
```

```
RESULT 8
B59037
cytochrome c, tetraheme, precursor - Nitrosomonas europaea
C:Species: Nitrosomonas europaea
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 04-Mar-2000
C:Accession: B59037
R:Bergmann, D.J.; Arciero, D.M.; Hooper, A.B.
J. Bacteriol. 176, 3148-3153, 1994
A:Title: Organization of the hao gene cluster of Nitrosomonas europaea: genes for two
A:Reference number: A59037; MUID:94252980
A:Accession: B59037
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-233 <BER>
A:Cross-references: GB:U08288; NID:g476339; PIDN:AAA19968.1; PID:g476341
A:Note: submitted to GenBank, April 1994
C:Keywords: chromoprotein; heme; iron; metalloprotein
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-233/Product: cytochrome c, tetraheme #status predicted <MAT>
F:39,42/Binding site: heme (Cys) (covalent) #status predicted
F:43/Binding site: heme iron (His) (axial ligand) #status predicted
F:67,70/Binding site: heme (Cys) (covalent) #status predicted
F:71/Binding site: heme iron (His) (axial ligand) #status predicted
F:131,134/Binding site: heme (Cys) (covalent) #status predicted
F:135/Binding site: heme iron (His) (axial ligand) #status predicted
F:159,162/Binding site: heme (Cys) (covalent) #status predicted
F:163/Binding site: heme iron (His) (axial ligand) #status predicted

Query Match      23.8%; Score 60; DB 2; Length 233;
Best Local Similarity 45.0%; Pred. No. 8.5;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 13 CTTCTRRHPCPPGGVQSGQK 32
      | | | | | | | | | | | | | |
Db 131 CRTCHKKPPAPGESAQAEHK 150

RESULT 9
A36325
epidermal growth factor receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 25-Jan-1991 #sequence_revision 25-Jan-1991 #text_change 10-Oct-1997
C:Accession: A36325
R:Fetch, L.A.; Harris, J.; Raymond, V.W.; Blasband, A.; Lee, D.C.; Earp, H.S.
Mol. Cell. Biol. 10, 2973-2982, 1990
A:Title: A truncated, secreted form of the epidermal growth factor receptor is encode
A:Reference number: A36325; MUID:90258888
A:Accession: A36325
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-644 <PET>
A:Cross-references: GB:M37394
C:Superfamily: epidermal growth factor receptor; protein kinase homology
C:Keywords: alternative splicing; ATP; growth factor receptor

Query Match      23.8%; Score 60; DB 2; Length 644;
Best Local Similarity 33.3%; Pred. No. 18;
Matches 12; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 5 EFHCGDPCCTTCRHHPCPPGGVQSGQKFSFGFQCI 40
      | | | | | | | | | | | | | | | | | |
Db 257 EATCKDTCPLMLYNTPTQMDVNPGEKYSFGATCV 292

RESULT 10
GQHUE
epidermal growth factor receptor precursor - human
N:Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C:Species: Homo sapiens (man)
C>Date: 15-Nov-1984 #sequence_revision 27-Nov-1985 #text_change 11-Jun-1999
```

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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:12:14 ; Search time 80.15 seconds  
(without alignments)  
38.016 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_74\_113

Perfect score: 232

Sequence: 1 CVQPEFHCGDPCCTCRHHPCPPGQGVQSQGKFSFGQCI 40

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_68:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72	28.6	1574	2 T13954	MEGF6 protein - rat
2	67	25.6	256	2 B32393	T-cell antigen 4-1
3	64	23.4	1210	2 A53183	epidermal growth f
4	62.5	24.8	1077	2 T41146	probable cysteine-
5	60.5	24.0	216	2 JX0265	platelet aggregati
6	60.5	24.0	850	2 S56015	gastric mucin MUC5
7	60.5	24.0	1373	2 JE0095	gastric mucin MUC5
8	60	23.8	233	2 B59037	cytochrome c, tetr
9	60	23.8	644	2 A36325	epidermal growth f
10	60	23.8	1210	1 GQHUE	epidermal growth f
11	59.5	23.6	1104	2 I38869	transcription fact
12	59.5	23.6	2813	1 VWHU	von Willebrand fac
13	59	23.4	58	1 SKMD1S	metallothionein 1
14	59	23.4	266	2 S65778	chitinase class IV
15	59	23.4	527	2 A42032	epidermal growth f
16	59	23.4	1223	1 TVCHLV	epidermal growth f
17	58.5	23.2	437	2 C35147	integrase homolog
18	58.5	23.2	1321	2 JE0352	mucin MUC5B, trach
19	58	23.0	271	2 S12783	OX40 antigen, precu
20	58	23.0	295	2 JC5559	lectin-B - Virgini
21	58	23.0	2907	2 A57278	fibrillin-2 precu
22	58	23.0	2918	2 A54105	fibrillin-2 precu
23	57.5	22.8	305	2 A46476	B cell-associated
24	57.5	22.8	540	2 B47417	insulin receptor-r
25	57.5	22.8	961	1 TSHUP4	thrombospondin 4 p
26	57.5	22.8	1268	2 B36502	insulin receptor-r
27	57	22.6	329	2 A48805	insulin-like growt
28	57	22.6	488	2 T29562	hypothetical prote
29	57	22.6	1371	2 A33837	insulin-like growt

30 57 22.6 2318 2 S45306 notch 3 protein 2  
31 56.5 22.4 277 2 A60771 B-cell activation  
32 56.5 22.4 1297 2 T30274 proteolisin - se  
33 56 22.2 63 2 S07127 chymotrypsin/elast  
34 56 22.2 419 2 S41607 atrolysin A (EC 3.  
35 55.5 22.0 62 2 A53640 metallothionein 4  
36 55.5 22.0 277 2 I37552 OX40 homolog - hum  
37 55.5 22.0 502 2 A48679 differentiated ker  
38 55 21.8 921 2 S40495 collagen alpha 1(I  
39 55 21.8 921 2 S42617 collagen alpha 1(I  
40 55 21.8 931 2 S13580 collagen alpha 1(I  
41 55 21.8 1106 2 T13938 gene shuttle craft  
42 55 21.8 1106 2 T44598 hypothetical prote  
43 55 21.8 1466 1 CGHU7L collagen alpha 1(I  
44 54.5 21.6 62 2 B53640 metallothionein IV  
45 54.5 21.6 258 2 C86541 CRI05 hypothetical

RESULT 1  
T13954  
MEGF6 protein - rat  
C:Species: Rattus norvegicus. (Norway rat)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000  
C:Accession: T13954  
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.  
Genomics 51, 27-34, 1998  
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like moti  
A:Reference number: Z14126; MUID:98360089  
A:Accession: T13954  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1574 <NAK>  
A:Cross-references: EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g3449294  
A:Experimental source: strain Sprague-Dawley; brain  
C:Genetics:  
A:Gene: MEGF6

Query Match 28.6%; Score 72; DB 2; Length 1574;  
Best Local Similarity 40.5%; Pred. No. 1.6;  
Matches 15; Conservative 1; Mismatches 13; Indels 8; Gaps 2;

QY 1 CVQPEFHCGDPCCT-----CRHHPCPPGQGVQSQGK 32  
DB 127 CASANGCEGCPCCNTGVGFYCR---CPPGQLQGDGK 160

RESULT 2  
B32393  
T-cell antigen 4-1BB precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 21-Jul-2000  
C:Accession: B32393; I48879  
R:Kwon, B.S.; Weissman, S.M.  
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989  
A:Title: cDNA sequence of two inducible T-cell genes.  
A:Reference number: A32393; MUID:89184547  
A:Accession: B32393  
A:Molecule type: mRNA  
A:Residues: 1-256 <KWO>  
A:Cross-references: GB:J04492; NID:g201121; PIDN:AAAM0167.1; PID:g201122  
R:Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.  
J. Immunol. 152, 2256-2262, 1994  
A:Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1B  
A:Reference number: I48879; MUID:94179805  
A:Accession: I48879  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-256 <RES>  
A:Cross-references: EMBL:U02567; NID:gl117783; PIDN:AAA93113.1; PID:g409178

ALIGNMENTS

C;Genetics:  
C;Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1  
C;Superfamily: CD27 antigen; NGF receptor repeat homology  
C;Keywords: transmembrane protein  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-256/Product: 4-1BB protein #status predicted <MAT>

Query Match 26.6%; Score 67; DB 2; Length 256;  
Best Local Similarity 45.2%; Pred. No. 1.5;  
Matches 14; Conservative 3; Mismatches 12; Indels 2; Gaps 2;

Qy 1 CVQPEFHCGDPCCTCRHHPCPPGQGVQSQ 31  
Db 87 CIE-GFHLGPGQCTRC-EKDCRPGQELTKG 115

RESULT 3  
A53183  
epidermal growth factor receptor precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 18-Jun-1999  
C;Accession: A53183; A43818; S24942; A28941; S45325; I49643  
R;Luetteke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jenkins, N.A.;  
Genes Dev. 8, 399-413, 1994  
A;Title: The mouse waved-2 phenotype results from a point mutation in the EGF receptor  
A;Reference number: A53183; MUID:94170986  
A;Accession: A53183  
A;Molecule type: mRNA  
A;Residues: 1-1210 <LUE>  
A;Cross-references: GB:003425  
R;Avivi, A.; Lax, I.; Ullrich, A.; Schlessinger, J.; Givol, D.; Morse, B.  
Oncogene 6, 673-676, 1991  
A;Title: Comparison of EGF receptor sequences as a guide to study the ligand binding site  
A;Reference number: A43818; MUID:91232866  
A;Accession: A43818  
A;Molecule type: mRNA  
A;Residues: 1-714 <AVI>  
A;Cross-references: GB:X59698  
R;Eisinger, D.P.; Serrero, G.  
Submitted to the EMBL Data Library, June 1992  
A;Reference number: S24942  
A;Accession: S24942  
A;Molecule type: mRNA  
A;Residues: 969-971, 'K', 973-1115, 'D' <EIS>  
A;Cross-references: EMBL:Z12608  
R;Heisermann, G.J.; Gill, G.N.  
J. Biol. Chem. 263, 13152-13156, 1988  
A;Title: Epidermal growth factor receptor threonine and serine residues phosphorylated in  
A;Reference number: A28941; MUID:88330814  
A;Accession: A28941  
A;Molecule type: protein  
A;Residues: 689-694, 'X', 696-704, 'L', 706-707; 989-992, 'XX', 995-996, 'X', 998-1000; 1002-1009,  
R;Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.  
Submitted to the EMBL Data Library, April 1994  
A;Description: The complete cDNA sequence of the Mouse Epidermal Growth Factor Receptor  
A;Reference number: S45325  
A;Accession: S45325  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-971, 'K', 973-1210 <VER>  
A;Cross-references: EMBL:X78987; NID:g488830; PIDN:CAA55367.1; PID:g488831  
R;Paria, B.C.; Das, S.K.; Andrews, G.K.; Dev, S.K.  
Proc. Natl. Acad. Sci. U.S.A. 90, 55-59, 1993  
A;Title: Expression of the epidermal growth factor receptor gene is regulated in mouse b  
A;Reference number: I49643; MUID:93126380  
A;Accession: I49643  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 12-20, 22-132 <RES>  
A;Cross-references: GB:L06864; NID:g193001; PIDN:AAA53029.1; PID:g567201  
C;Genetics:  
A;Gene: EGFR

C;Superfamily: epidermal growth factor receptor; protein kinase homology  
C;Keywords: ATP; growth factor receptor; kinase-related transforming protein; phospho  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;648-670/Domain: transmembrane #status predicted <TMM>  
F;712-977/Domain: protein kinase homology <KIN>  
F;720-728/Region: protein kinase ATP-binding motif  
F;680,695/Binding site: phosphate (Thr) (covalent) #status experimental  
F;697,1070,1071/Binding site: phosphate (Ser) (covalent) #status experimental  
F;993/Binding site: (or 997) phosphate (Ser) (covalent) #status experimental  
F;1028/Binding site: (or 1030 or 1032) phosphate (Ser) (covalent) #status experimental  
F;1197/Binding site: phosphate (Tyr) (covalent) #status experimental

Query Match 25.4%; Score 64; DB 2; Length 1210;  
Best Local Similarity 34.2%; Pred. No. 10;  
Matches 13; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 3 QPEFHCGDPCCTCRHHPCPPGQGVQSQKFSFGQCI 40  
Db 255 QDEATCKDTCPLMLNPTTYQMDVNPGEKYSFGATCV 292

RESULT 4  
T41146  
probable cysteine-rich transcription regulator - fission yeast (Schizosaccharomyces p  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 02-Sep-2000  
C;Accession: T41146  
R;Hilbert, H.; Duesterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, October 1998  
A;Reference number: Z21973  
A;Accession: T41146  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1077 <HIL>  
A;Cross-references: EMBL:AL031907; PIDN:CAA21417.1; GSPDB:GN00068; SPDB:SPCC18.03  
A;Experimental source: strain 972h-; cosmid c18  
C;Genetics:  
A;Gene: SPDB:SPCC18.03  
A;Map position: 3  
C;Superfamily: RING finger homology  
F;193-252/Domain: RING finger homology <RRN>

Query Match 24.8%; Score 62.5; DB 2; Length 1077;  
Best Local Similarity 30.0%; Pred. No. 14;  
Matches 18; Conservative 3; Mismatches 16; Indels 23; Gaps 3;

Qy 3 QPEF-----HCGDPCCTT-----CRHHPCPPGQGVQSQ-----GKFSFGQFC 39  
Db 266 KPEFVKNLVPHSGDPCGCKTRGQDCHEPCPLCHPGCPCTATVEKFLCGKESIARC 325

RESULT 5  
JX0265  
platelet aggregation inhibitor - red diamond rattlesnake (fragment)  
N;Alternate names: disintegrin  
C;Species: Crocalus ruber ruber (red diamond rattlesnake)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 03-Nov-2000  
C;Accession: JX0265  
R;Takeya, H.; Nishida, S.; Nishino, N.; Makino, Y.; Omori-Sato, T.; Nikai, T.; Sug  
J. Biochem. 113, 473-483, 1993  
A;Title: Primary structures of platelet aggregation inhibitors (disintegrins) autopro  
hese enzymes.  
A;Reference number: JX0265; MUID:93293798  
A;Accession: JX0265  
A;Molecule type: protein  
A;Residues: 1-216 <TAK>  
A;Experimental source: venom  
C;Superfamily: mouse meltrin alpha; disintegrin homology  
F;7-89/Domain: disintegrin homology <DIS>

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FT DISULFID 527 542 BY SIMILARITY.
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FT DISULFID 684 699 BY SIMILARITY.
FT DISULFID 725 737 BY SIMILARITY.
FT DISULFID 732 750 BY SIMILARITY.
FT DISULFID 744 759 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 409 409 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 867 867
SQ SEQUENCE 867 AA; 91817 MW; 9538F2108E787B49 CRC64;

Query Match 23.0%; Score 58; DB 1; Length 867;
Best Local Similarity 36.1%; Pred. No. 13;
Matches 13; Conservative 5; Mismatches 12; Indels 6; Gaps 1;

QY 4 PEHCGDPCCCTTCRHHPPGQGVQSQGKFSFGFC 39
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Db 118 PDRPCGGPGCW-----CPAGQVLGAGRCVWPQC 147

Search completed: September 4, 2001, 16:15:26
Job time: 1138 sec

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DR Pfam; PF00093; vwc; 3.  
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DR Pfam; PF01826; TIL; 3.  
DR PRINTS; PR00365; ENDOTHELIN.  
DR PRINTS; PR00453; VWFADOMAIN.  
DR PROSITE; PS02324; VWF; 3.  
DR PROSITE; PS01208; VWF; 3.  
DR PROSITE; PS01185; CTCK\_1; 1.  
DR PROSITE; PS01225; CTCK\_2; 1.  
KW Blood coagulation; Platelet; Glycoprotein; Extracellular matrix;  
KW Plasma; Endothelial cell; Repeat; Cell adhesion.  
FT NON\_TER 1  
FT PROPEP <1 437 BY SIMILARITY.  
FT CHAIN 438 2482 VON WILLEBRAND FACTOR.  
FT DOMAIN 62 215 VWF2.  
FT DOMAIN 438 461 AMINO-TERMINAL.  
FT DOMAIN 462 507 EL.  
FT DOMAIN 500 527 CX.  
FT DOMAIN 541 687 VWF3.  
FT DOMAIN 947 1127 VWF4 1.  
FT DOMAIN 1167 1334 VWF4 2.  
FT DOMAIN 1360 1540 VWF4 3.  
FT DOMAIN 1619 1771 VWF4 4.  
FT DOMAIN 1885 1930 E2.  
FT DOMAIN 1924 1997 VWF5 1.  
FT DOMAIN 2098 2164 VWF5 2.  
FT DOMAIN 2249 2319 VWF5 3.  
FT DOMAIN 2393 2481 CTCK.  
FT SITE 2176 2178 CELL ATTACHMENT SITE (POTENTIAL).  
FT DISULFID 441 482 BY SIMILARITY.  
FT DISULFID 450 478 BY SIMILARITY.  
FT DISULFID 484 495 BY SIMILARITY.  
FT DISULFID 541 670 BY SIMILARITY.  
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FT DISULFID 745 785 BY SIMILARITY.  
FT DISULFID 763 765 BY SIMILARITY.  
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FT DISULFID 833 843 BY SIMILARITY.  
FT DISULFID 800 804 BY SIMILARITY.  
FT DISULFID 870 873 BY SIMILARITY.  
FT DISULFID 908 911 BY SIMILARITY.  
FT DISULFID 942 1128 BY SIMILARITY.  
FT DISULFID 1338 1339 BY SIMILARITY.  
FT DISULFID 1355 1541 BY SIMILARITY.  
FT DISULFID 1548 1573 BY SIMILARITY.  
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FT DISULFID 2419 2473 BY SIMILARITY.  
FT DISULFID 2423 2475 BY SIMILARITY.  
FT DISULFID ? 2480 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 340 340 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 905 905 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 1184 1184 N-LINKED (GLCNAC. .) (POTENTIAL).  
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FT CARBOHYD 1892 1892 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 1959 1959 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 2026 2026 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 2069 2069 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 2215 2215 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 2254 2254 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 2459 2459 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 2482 AA; 272394 MW; D499E7DDFBCAEDD CRC64;

Query Match 23.2%; Score 58.5; DB 1; Length 2482;  
Best Local Similarity 30.8%; Pred. No. 26;  
Matches 16; Conservative 2; Mismatches 19; Indels 15; Gaps 2;  
QY 3 QPEFHCGDPCCTTCR--HHP-----CPPGGGVSGQKFSFGFC 39  
DB 330 QVYLQCGTPCNLTCRSLSPDECAEDLCGFCPPGLYLDGSGDCVPKAC 381  
RESULT 14  
OX40\_RAT ID OX40\_RAT STANDARD; PRT; 271 AA.  
AC PL5725;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).  
GN TNFRSF4 OR TXGPIL OR OX40.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=T-cell;  
RX MEDLINE=90214614; PubMed=2157591;  
RA Mallett S., Fossum S., Barclay A.N.;  
RT 'Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes -- a molecule related to nerve growth factor receptor.';  
RL EMBO J. 9:1063-1068(1990).  
CC -!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -!- TISSUE SPECIFICITY: ACTIVATED T-CELLS.  
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
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CC -----  
CC EMBL: X17037; CAA34897.1; -  
DR PIR; S08036; S08036.  
DR PIR; S12783; S12783.  
DR HSSP; P25942; ICDF.  
DR InterPro; IPR001368; -  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
DR PROSITE; PS00500; TNFR\_NGFR\_2; 2.  
DR Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
KW Signal.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 271 OX40L RECEPTOR.  
FT DOMAIN 20 210 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 211 235 POTENTIAL.  
FT DOMAIN 236 271 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 25 164 4 X TNFR-CYS.  
FT REPEAT 25 60 TNFR-CYS 1.  
FT REPEAT 61 102 TNFR-CYS 2.  
FT REPEAT 103 123 TNFR-CYS 3 (INCOMPLETE).  
FT REPEAT 124 164 TNFR-CYS 4.  
FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;  
Query Match 23.0%; Score 58; DB 1; Length 271;  
Best Local Similarity 30.0%; Pred. No. 5;  
Matches 12; Conservative 3; Mismatches 9; Indels 16; Gaps 2;  
QY 1 CVOPERHCGDPCCTTCR-----H-----HPCPPG 24  
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Query Match 23.4%; Score 59; DB 1; Length 58;
Best Local Similarity 37.5%; Pred. No. 1.1;
Matches 15; Conservative 3; Mismatches 12; Indels 10; Gaps 2;

QY 1 CVOPEHCGDPC-CITCRHHPCPPGGVQSQKFSFGFC 39
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DB 9 CVCKEGGCKGCOCTSCRCSPCE-----KCSSGCKC 39

RESULT 10
EGFR_CHICK STANDARD; PRT; 703 AA.
ID EGFR_CHICK
AC P13387;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (CER)
DE (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88261272; PubMed=3260329;
RA Lax I., Johnson A., Howk R., Sap J., Bellot F., Winkler M.,
RA Ullrich A., Vennstrom B., Schlessinger J., Givol D.;
RT "Chicken epidermal growth factor (EGF) receptor: cDNA cloning,
RT expression in mouse cells, and differential binding of EGF and
RT transforming growth factor alpha.";
RL Mol. Cell. Biol. 8:1970-1978(1988).
CC -!- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF,
CC AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AND
CC VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- MISCELLANEOUS: BINDING OF EGF TO THE RECEPTOR LEADS TO
CC INTERNALIZATION OF THE EGF-RECEPTOR COMPLEX, INDUCTION OF THE
CC TYROSINE KINASE ACTIVITY, STIMULATION OF CELL DNA SYNTHESIS, AND
CC CELL PROLIFERATION.
CC -!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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CC EMBL; M20386; AAA48760.1; -.
CC InterPro; IPR000494; -.
CC InterPro; IPR000719; -.
CC InterPro; IPR001245; -.
CC InterPro; IPR002174; -.
CC Pfam; PF00757; Furin-like; 1.
CC PROSITE; PS01030; Recep_L_domain; 2.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; PARTIAL.
CC PROSITE; PS00109; PROTEIN_KINASE_TYR; PARTIAL.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; PARTIAL.
CC Transmembrane; Glycoprotein; Duplication; Receptor; Signal;
CC Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation.
CC SIGNAL
CC 1 30
FT CHAIN 31 >703 EPIDERMAL GROWTH FACTOR RECEPTOR.
FT DOMAIN 31 654 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 655 667 POTENTIAL.
FT DOMAIN 668 >703 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 23.4%; Score 59; DB 1; Length 437;
Best Local Similarity 33.3%; Pred. No. 8.3;
Matches 11; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 8 CGDPCCTCRHHPCPPGGVQSQKFSFGFC 40
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DB 267 CKDTCPLVLYNPTTYQMDVNPGEKYSFGATCV 299

RESULT 11
INTR_SACER STANDARD; PRT; 437 AA.
ID INTR_SACER
AC P22877;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTEGRASE (RECOMBINASE).
GN INT.
OS Saccharopolyspora erythraea (Streptomyces erythraeus).
OG Plasmid PSE211.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Pseudonocardineae; Pseudonocardaceae;
OC Saccharopolyspora.
OX NCBI_TaxID=1836;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90202705; PubMed=2180909;
RA Brown D.P., Idler K.B., Katz L.;
RT "Characterization of the genetic elements required for site-specific
RT integration of plasmid pSE211 in Saccharopolyspora erythraea.";
RL J. Bacteriol. 172:1877-1888(1990).
CC -!- FUNCTION: IS A RECOMBINASE (OR INTEGRASE). CATALYZING THE CUTTING
CC AND REJOINING OF THE RECOMBINATING DNA MOLECULES.
CC -!- SIMILARITY: BELONGS TO THE "PHAGE" INTEGRASE FAMILY.
CC -----
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CC -----
CC EMBL; M35138; AAA98345.1; -.
CC PIR; C35147; C35147.
CC InterPro; IPR002104; -.
CC Pfam; PF00589; Phage_integrase; 1.
CC DNA recombination; DNA integration; plasmid.
CC ACT_SITE 414 414 STRAND CLEAVAGE AND REJOINING (BY
CC ACT_SITE 414 414 SIMILARITY).
CC SEQUENCE 437 AA; 50323 MW; 29EED7108CC5AFBD CRC64;

Query Match 23.2%; Score 58.5; DB 1; Length 437;
Best Local Similarity 32.4%; Pred. No. 6.4;
Matches 11; Conservative 3; Mismatches 9; Indels 11; Gaps 2;

QY 1 CVOPE-----FHCGDPCCTTCRHH-----PCPP 23
      | | | | | | | | | | | | | | | | | |
DB 248 CSDPHRCGATYHTEPCCKACKRHRTRACPPCPP 281
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FT DISULFID 406 421 BY SIMILARITY.
FT DISULFID 424 436 BY SIMILARITY.
FT DISULFID 442 456 BY SIMILARITY.
FT DISULFID 450 466 BY SIMILARITY.
FT DISULFID 468 480 BY SIMILARITY.
FT CARBOHYD 631 631 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 960 960 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 980 AA; 108213 MW; 056D41EB6E206FCF CRC64;

Query Match 23.2%; Score 58.5; DB 1; Length 980;
Best Local Similarity 31.9%; Pred. No. 12;
Matches 15; Conservative 6; Mismatches 9; Indels 17; Gaps 4;

QY 6 FHCDGPC-----CT---TCRRHPCPPGGVQSQGKFSFGFC 39
   ||||| : :||| : :|||
Db 326 FQCG-PCPDGTYNGITCSVDDECKYHPCYPGVRCNTN---LAGFRC 368
   ||||| : :||| : :|||

RESULT 13
VWF_PIG ID VWF_PIG STANDARD; PRT; 2482 AA.
AC Q28833;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE DE VON WILLEBRAND FACTOR PRECURSOR (VWF) (FRAGMENT).
GN F8VWF OR VWF.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Seaman W.T., Read M.S., Bellinger D.A., Nichols T.C.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE OF 397-553 FROM N.A.
RX MEDLINE=93356762; PubMed=8352759;
RA Lavigne J.M., Piao Y.C., Ferreira V., Kerbirou-Nabias D.,
RA Bahnk B.R., Meyer D.;
RT "Primary structure of the factor VIII binding domain of human, porcine
RT and rabbit von Willebrand factor.";
RL Biochem. Biophys. Res. Commun. 194:1019-1024(1993).
CC -1- FUNCTION: IMPORTANT IN THE MAINTENANCE OF HOMEOSTASIS, IT
CC PARTICIPATES IN PLATELET-VESSEL WALL INTERACTIONS BY FORMING A
CC NONCOVALENT COMPLEX WITH COAGULATION FACTOR VIII AT THE SITE OF
CC VASCULAR INJURY (BY SIMILARITY).
CC -1- SUBUNIT: MULTIMERIC (BY SIMILARITY).
CC -1- PTM: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR
CC INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 3 VWFc DOMAINS.
CC -1- SIMILARITY: CONTAINS A C-TERMINAL CYSTEINE KNOT-LIKE DOMAIN (CTCK).
CC -1- SIMILARITY: SOME, TO SILKWORM HEMOCYTIN.
-----
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-----
DR EMBL; AF052036; AAC06229.1; -
DR EMBL; S64541; AAB27829.2; -.
DR HSSP; P04275; 1ATZ.
DR InterPro; IPR000359; -
DR InterPro; IPR001007; -
DR InterPro; IPR001846; -
DR InterPro; IPR002035; -
DR InterPro; IPR002919; -
DR Pfam; PF00007; Cys_knot; 1.
DR Pfam; PF00092; vwa; 3.

```

RESULT	12
TSP4_RAT	
ID	TSP4_RAT            STANDARD;         PRT;      980 AA.
AC	P49744;
DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DE	01-OCT-2000 (Rel. 40, Last annotation update)
DE	THROMBOSPONDIN 4 PRECURSOR.
OS	THBS4 OR TSP4 OR Tsp-4.
GN	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
[1]	
RN	SEQUENCE FROM N.A.
RP	STRAIN=LEWIS; TISSUE=Skeletal muscle;
RC	MEDLINE=96074771; PubMed=7490284;
RA	Arber S., Caroni P.;
RT	"Thrombospondin-4, an extracellular matrix protein expressed in the
RT	developing and adult nervous system promotes neurite outgrowth.";
RL	J. Cell Biol. 131:1083-1094(1995).
CC	-1- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND
CC	CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINOGEN, FIBRONECTIN,
CC	LAMININ AND TYPE V COLLAGEN.
CC	-1- SUBUNIT: HOMOTRIMER, CROSS-LINKED BY DISULFIDE BONDS (BY
CC	SIMILARITY).
CC	-1- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
CC	-1- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.
CC	-1- SIMILARITY: CONTAINS 7 TSP TYPE-3 DOMAINS.
-----	
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-----	
EMBL:	X89963; CAA62002.1; --
DR	HSSP; P35444; LVDF.
DR	InterPro: IPR000561; --
DR	InterPro: IPR001881; --
DR	PROSITE; PS00022; EGF_1; FALSE_NEG.
DR	PROSITE; PS01186; EGF_2; 1.
DR	PROSITE; PS01187; EGF_CA; 2.
KW	Glycoprotein; Cell adhesion; Calcium-binding; Repeat; EGF-like domain;
KW	Signal.
FT	1          39
FT	CHAIN       SIGNAL
FT	40         980
FT	DOMAIN     THROMBOSPONDIN 4.
FT	303         N-TERMINAL.
FT	304         343
FT	DOMAIN     EGF-LIKE 1.
FT	344         396
FT	DOMAIN     EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT	397         437
FT	DOMAIN     EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT	438         481
FT	DOMAIN     EGF-LIKE 4.
FT	511         546
FT	DOMAIN     TSP TYPE-3 1.
FT	547         569
FT	DOMAIN     TSP TYPE-3 2.
FT	570         605
FT	DOMAIN     TSP TYPE-3 3.
FT	606         628
FT	DOMAIN     TSP TYPE-3 4.
FT	629         666
FT	DOMAIN     TSP TYPE-3 5.
FT	667         706
FT	DOMAIN     TSP TYPE-3 6.
FT	707         742
FT	DOMAIN     TSP TYPE-3 7.
FT	743         980
FT	DOMAIN     C-TERMINAL.
FT	DISULFID   INTERCHAIN (PROBABLE).
FT	276         276
FT	DISULFID   INTERCHAIN (PROBABLE).
FT	279         279
FT	DISULFID   BY SIMILARITY.
FT	308         319
FT	DISULFID   BY SIMILARITY.
FT	313         328
FT	DISULFID   BY SIMILARITY.
FT	331         342
FT	DISULFID   BY SIMILARITY.
FT	348         359
FT	DISULFID   BY SIMILARITY.
FT	353         368
FT	DISULFID   BY SIMILARITY.
FT	371         395
FT	DISULFID   BY SIMILARITY.
FT	401         412
FT	DISULFID   BY SIMILARITY.



[16] DISULFIDE BONDS.  
RP  
RX MEDLINE=88163465; PubMed=3502076;  
RX Marti T., Rosselet S.J., Titani K., Walsh K.A.;  
RT "Identification of disulfide-bridged substructures within human von  
RT Willebrand factor.";  
RT Biochemistry 26:8099-8109(1987).  
RN [17]  
RN  
RN STRUCTURE OF CARBOHYDRATES.  
RP  
RX MEDLINE=86274702; PubMed=3089784;  
RX Samor B., Michalski J.C., Debray H., Mazurier C., Goudemand M.,  
RA van Halbeek H., Vliegencourt J.F.G., Montreuil J.;  
RA "Primary structure of a new tetraantennary glycan of the N-  
RT acetylactosaminic type isolated from human factor VIII/von  
RT Willebrand factor.";  
RT Eur. J. Biochem. 158:295-298(1986).  
RN [18]  
RN  
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1261-1458.  
RP  
RX MEDLINE=98221174; PubMed=9553097;  
RX Emsley J., Cruz M., Handin R., Liddington R.;  
RA "Crystal structure of the von Willebrand factor A1 domain and  
RT implications for the binding of platelet glycoprotein Ib.";  
RL J. Biol. Chem. 273:10396-10401(1998).  
RN [19]  
RN  
RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 1685-1873.  
RP  
RX MEDLINE=97472999; PubMed=9331419;  
RX Huizenga E.G., Martijn van der Plas R., Kroon J., Sixma J.J., Gros P.;  
RA "Crystal structure of the A3 domain of human von Willebrand factor:  
RT implications for collagen binding.";  
RL Structure 5:1147-1156(1997).  
RN [20]  
RN  
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1686-1872.  
RP  
RX MEDLINE=97460108; PubMed=9312128;  
RX Bienkowska J., Cruz M., Atlemo A., Handin R., Liddington R.;  
RA "The von Willebrand factor A3 domain does not contain a metal ion-  
RT dependent adhesion site motif.";  
RL J. Biol. Chem. 272:25162-25167(1997).  
RN [21]  
RN  
RN VARIANTS TRP-1597 AND ASP-1607.  
RP  
RX MEDLINE=89264495; PubMed=2786201;  
RX Ginsburg D., Konkle B.A., Gill J.C., Montgomery R.R.,  
RA Bockenstedt P.L., Johnson T.A., Tang A.Y.;  
RT "Molecular basis of human von Willebrand disease: analysis of  
RT platelet von Willebrand factor mRNA.";  
RN Proc. Natl. Acad. Sci. U.S.A. 86:3723-3727(1989).  
RN [22]  
RN  
RN VARIANT THR-1628.  
RP  
RX MEDLINE=91196734; PubMed=1673047;  
RX Iannuzzi M.C., Hidak N., Boehnke M., Bruck M.E., Hanna W.T.,  
RA Collins F.S., Ginsburg D.;  
RA "Analysis of the relationship of von Willebrand disease (vWD) and  
RT hereditary hemorrhagic telangiectasia and identification of a  
RT potential type IIA vWD mutation (I18865 to Thr).";  
RL Am. J. Hum. Genet. 48:757-763(1991).  
RN [23]  
RN  
RN VARIANTS NORMANDY-2 AND NORMANDY-3.  
RP  
RX MEDLINE=92001464; PubMed=1832934;  
RX Gaucher C., Mercier B., Jorileux S., Oufkir D., Mazurier C.;  
RT "Identification of two point mutations in the von Willebrand factor  
RT gene of three families with the 'Normandy' variant of von Willebrand  
RT disease.";  
RL Br. J. Haematol. 78:506-514(1991).  
RN [24]  
RN  
RN VARIANT CYS-1308.  
RP  
RX MEDLINE=92104315; PubMed=1761120;  
RX Donner M., Andersson A.-M., Kristoffersson A.-C., Nilsson I.M.,  
RA Dahlback B., Holmberg L.;  
RA "An Arg545-->Cys545 substitution mutation of the von Willebrand  
RT factor in type IIB von Willebrand's disease.";  
RL Eur. J. Haematol. 47:342-345(1991).  
RN [25]  
RN  
RN VARIANTS TRP-1306; CYS-1308 AND PRO-1613.  
RP  
RX MEDLINE=91185601; PubMed=2010538;  
RX

RA	Randi A.M., Rabinowitz I., Mancuso D.J., Mannucci P.M., Sadler J.E.;
RT	"Molecular basis of von Willebrand disease type IIB. Candidate
RT	mutations cluster in one disulfide loop between proposed platelet
RL	glycoprotein Ib binding sequences.";
RL	J. Clin. Invest. 87:1220-1226(1991).
RN	[26]
RP	VARIANTS TRP-1306; CYS-1308; MET-1316; GLN-1341 AND HTS-1399.
RX	MEDLINE=91185602; PubMed=1672694;
Query Match	23 6%; Score 59.5; DB 1; Length 2813;
Best Local Similarity	30.8%; Pred. No. 22;
Matches 16; Conservative 3; Mismatches 18; Indels 15; Gaps:	
Qy	3 QPEFHGDCPCCTCR--HHP-----CPPGGVQSOGKSGFSGFC 39           :             :
Dd	656 QVVLCQTTCNLTRSLSPDEECNEACLEGCFPPGLYMDRGDCVPKAQC 707           :             :
RESULT 9	
MTL_SCYSE	STANDARD; PRT; 58 AA.
ID	P02805;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	01-NOV-1997 (Rel. 35, Last annotation update)
DE	METALLOTHIONEIN-I (MT-I).
OS	Scylla serrata (Mud crab).
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC	Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC	Brachyura; Portunoidae; Scylla.
OX	NCBI_TaxID=6761;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=82142340; PubMed=7061431;
RA	Lerch K., Ammer D., Olafson R.W.;
RT	"Crab metallothionein. Primary structures of metallothioneins 1 and
RT	2.";
RL	J. Biol. Chem. 257:2420-2426(1982).
CC	-I- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC	RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I WTS IN MARINE
CC	CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS
CC	OF HEAVY-METAL IONS.
CC	-I- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR	PIR; A03283; SWKDL.
DR	HSSP; P55949; LDMP.
DR	InterPro; IPRO02045; -.
DR	InterPro; IPRO03019; -.
DR	Pfam; PF00131; metaalthio; 1.
DR	PRINTS; PR00858; MTRCRUSTACEAN.
KW	Metal-binding; Metal-thiolate cluster; Chelation.
FT	DOMAIN 1 28 BETA.
FT	DOMAIN 29 58 ALPHA.
FT	METAL 4 4 CLUSTER B.
FT	METAL 5 5 CLUSTER B.
FT	METAL 9 9 CLUSTER B.
FT	METAL 11 11 CLUSTER B.
FT	METAL 16 16 CLUSTER B.
FT	METAL 20 20 CLUSTER B.
FT	METAL 22 22 CLUSTER B.
FT	METAL 25 25 CLUSTER B.
FT	METAL 27 27 CLUSTER B.
FT	METAL 30 30 CLUSTER A.
FT	METAL 33 33 CLUSTER A.
FT	METAL 37 37 CLUSTER A.
FT	METAL 39 39 CLUSTER A.
FT	METAL 45 45 CLUSTER A.
FT	METAL 49 49 CLUSTER A.
FT	METAL 53 53 CLUSTER A.
FT	METAL 55 55 CLUSTER A.
FT	METAL 56 56 CLUSTER A.
SQ	SEQUENCE 58 AA; 6001 MW; CEBA24C590B0278B CRC64;

FI	METAL	30	30	CLUSTER A.
SQ	SEQUENCE	58 AA;	6001 MW;	CE8A24C590B027B8 CRC64;



\*ATP-stimulated interaction between epidermal growth factor receptor and supercoiled DNA.;  
 Nature 309:270-273(1984).  
 [10]  
 RN PHOSPHORYLATION.  
 RX MEDLINE=89278137; PubMed=2543678;  
 RA Margolis B.U., Lax J., Kris R., Dombalagian M., Honegger A.M.,  
 RA Hawk R., Givol D., Ullrich A., Schlessinger J.;  
 RA "All autophosphorylation sites of epidermal growth factor (EGF)  
 RT receptor and HGR2/neu are located in their carboxyl-terminal tails.  
 RT Identification of a novel site in EGF receptor.;"  
 RL J. Biol. Chem. 264:10667-10671(1989).  
 [11]  
 RN REVIEW.  
 RP MEDLINE=87297456; PubMed=3039909;  
 RX Carpenter G.;  
 RA Receptors for epidermal growth factor and other polypeptide  
 RT mitogens.;"  
 CC Annu. Rev. Biochem. 56:881-914(1987).  
 CC -1- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF,  
 CC AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AND  
 CC VACCINIA VIRUS GROWTH FACTOR.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +  
 CC PROTEIN TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- MISCELLANEOUS: BINDING OF EGF TO THE RECEPTOR LEADS TO  
 CC INTERNALIZATION OF THE EGF-RECEPTOR COMPLEX, INDUCTION OF THE  
 CC TYROSINE KINASE ACTIVITY, STIMULATION OF CELL DNA SYNTHESIS, AND  
 CC CELL PROLIFERATION.  
 CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.  
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 -----  
 DR EMBL; X00588; CAA25240.1; -  
 DR EMBL; X06370; CAA29668.1; -  
 DR EMBL; X00663; CAA25282.1; -  
 DR EMBL; M38425; AAA63171.1; -  
 DR EMBL; M11234; AAA52370.1; -  
 DR PIR; A00641; GQHUE.  
 DR PIR; A00642; GQHUE2.  
 DR PIR; A23062; A23062.  
 DR HSSP; P11362; IFGI.  
 DR SWISS-2DPAGE; P00533; HUMAN.  
 DR MIM; I31550; -  
 DR InterPro; IPR000494; -  
 DR InterPro; IPR000719; -  
 DR InterPro; IPR001245; -  
 DR InterPro; IPR002174; -  
 DR Pfam; PF00757; Furin-like; 1.  
 DR Pfam; PF01030; Recep\_Ldomain; 2.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR Transmembrane; Glycoprotein; Duplication; Receptor; Signal;  
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation.  
 DR SIGNAL 1 24  
 FT CHAIN 25 1210; EPIDERMAL GROWTH FACTOR RECEPTOR.  
 FT DOMAIN 25 645 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 646 668 POTENTIAL.  
 FT DOMAIN 669 1210 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 75 300 APPROXIMATE.  
 FT REPEAT 390 600 APPROXIMATE.  
 FT DOMAIN 1025 1071 SER-RICH.  
 FT DOMAIN 712 979 PROTEIN KINASE.  
 FT NP\_BIND 718 726 ATP (BY SIMILARITY).  
 FT BINDING 745 745 ATP (BY SIMILARITY).  
 -----

FT	ACT_SITE	837	837	BY SIMILARITY.			
FT	MOD_RES	678	678	PHOSPHORYLATION (BY PKC).			
FT	MOD_RES	1092	1092	PHOSPHORYLATION (AUTO-).			
FT	MOD_RES	1110	1110	PHOSPHORYLATION (AUTO-).			
FT	MOD_RES	1172	1172	PHOSPHORYLATION (AUTO-).			
FT	MOD_RES	1197	1197	PHOSPHORYLATION (AUTO-).			
FT	CARBOHYD	128	128	N-LINKED (GLCNAC. .) (POTENTIAL).			
FT	CARBOHYD	175	175	N-LINKED (GLCNAC. .) (POTENTIAL).			
FT	CARBOHYD	196	196	N-LINKED (GLCNAC. .) (POTENTIAL).			
FT	CARBOHYD	352	352	N-LINKED (GLCNAC. .) (POTENTIAL).			
FT	CARBOHYD	361	361	N-LINKED (GLCNAC. .) (POTENTIAL).			
FT	CARBOHYD	413	413	N-LINKED (GLCNAC. .) (POTENTIAL).			
FT	CARBOHYD	444	444	N-LINKED (GLCNAC. .) (POTENTIAL).			
FT	CARBOHYD	528	528	N-LINKED (GLCNAC. .) (POTENTIAL).			
FT	CARBOHYD	568	568	N-LINKED (GLCNAC. .) (POTENTIAL).			
FT	CARBOHYD	603	603	N-LINKED (GLCNAC. .) (POTENTIAL).			
FT	CARBOHYD	623	623	N-LINKED (GLCNAC. .) (POTENTIAL).			
FT	CONFLICT	540	540	N-> K (IN REF. 1).			
SEQ	SEQUENCE	1210 AA;	134277 MW;	D8A2A50B4EFB6ED2 CRC64;			
Query Match							
Best Local Similarity		23.88;	Score 60;	DB 1; Length 1210;			
Matches 12;		Conservative 5;	Mismatches 19;	Indels 0; Gaps 0;			
QY	5 EFHCGDPCCTCRHPCPPGQGVQSGQKFSFGFCI 40						
DB	257 EATCKDCTCPMLNLNPTYQNDVNPGEKYSFGATCV 292						
RESULT 7							
NFX1_HUMAN							
ID	NFX1_HUMAN	STANDARD;	PRT;	1104 AA.			
AC	Q12986;						
DT	01-NOV-1997 (Rel. 35, Created)						
DT	01-NOV-1997 (Rel. 35, Last sequence update)						
DT	01-NOV-1997 (Rel. 35, Last annotation update)						
DE	TRANSCRIPTIONAL REPRESSOR NF-X1.						
GN	NFX1.						
OS	Homo sapiens (Human).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
NCBI	TaxID=9606;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RX	MEDLINE 95053707; PubMed=7964459;						
RA	Song Z., Krishna S., Thanos D., Strominger J.L., Ono S.J.;						
RT	"A novel cysteine-rich sequence-specific DNA-binding protein						
RT	interacts with the conserved X-box motif of the human major						
RT	histocompatibility complex class II genes via a repeated Cys-His						
RT	domain and functions as a transcriptional repressor.";						
RL	J. Exp. Med. 180:1763-1774(1994).						
CC	-1- FUNCTION: REPRESSOR OF HUA-DNA TRANSCRIPTION. BINDS TO THE X-BOX						
CC	MOTIF OF CLASS II MHC GENES. MAY PLAY AN IMPORTANT ROLE IN						
CC	REGULATING THE DURATION OF AN INFLAMMATORY RESPONSE BY LIMITING						
CC	THE PERIOD IN WHICH CLASS II MHC MOLECULES ARE INDUCED BY						
CC	INTERFERON-GAMMA.						
CC	-1- SUBCELLULAR LOCATION: NUCLEAR.						
CC	-1- INDUCTION: BY INTERFERON-GAMMA.						
CC	-1- SIMILARITY: TO D.MELANOGASTER SHUTTLE CRAFT PROTEIN (STC) AND						
CC	YEAST YNL023C.						
-----							
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).						
-----							
CC	EMBL; U15306; AAA69517.1; .						
DR	HSSP; P02876; 2WGC.						
DR	InterPro; IPR000967; .						



[1] SEQUENCE FROM N.A.  
 RA Stoy S.J., Shibuya H., Nonneman D.J., Holzhauer J., Mohammed I.H.,  
 RA Johnson G.S.;  
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RA SEQUENCE FROM N.A.  
 RA Montgomery R.R., Fahs S., Montgomery M.W.;  
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RA SEQUENCE FROM N.A.  
 RA Venta P.J., Li J., Yuzbasiyan-Gurkan V., Brewer G.J., Schall W.D.;  
 RT "Complete sequence of the structural gene for canine von Willebrand  
 RT factor and identification of a mutation causing Scottish terrier von  
 RT Willebrand's disease.";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RA SEQUENCE OF 1234-1669 FROM N.A.  
 RC TISSUE=Blood;  
 RA Mancuso D.J., Christopherson P.A., Kroner P.A., Montgomery R.R.;  
 RT "the canine von Willebrand factor gene: sequence and expression of  
 RT a region encoding the glycoprotein Ib/IX binding domain.";  
 RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: IMPORTANT IN THE MAINTENANCE OF HOMEOSTASIS. IT  
 CC PARTICIPATES IN PLATELET-VESSEL WALL INTERACTIONS BY FORMING A  
 CC NONCOVALENT COMPLEX WITH COAGULATION FACTOR VIII AT THE SITE OF  
 CC VASCULAR INJURY (BY SIMILARITY).  
 CC -1- SUBUNIT: MULTIMERIC (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: BLOOD.  
 CC -1- PPM: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR  
 CC INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).  
 CC -1- SIMILARITY: CONTAINS 3 VNFA DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 4 VNFC DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 4 VNFD DOMAINS.  
 CC -1- SIMILARITY: CONTAINS A C-TERMINAL CYSTEINE KNOT-LIKE DOMAIN (CTCK).  
 CC -1- SIMILARITY: SOME, TO SILKWORM HEMOCYTIN.  
 CC -----  
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 CC -----  
 DR EMBL; L76227; AAB05549.1; -;  
 DR EMBL; L16903; AAA30903.1; -;  
 DR EMBL; AF099154; AAD04919.1; -;  
 DR EMBL; U66246; AAB93766.1; -;  
 DR HSSP; P04275; IATZ.  
 DR InterPro; IPR000359; -;  
 DR InterPro; IPR001007; -;  
 DR InterPro; IPR001846; -;  
 DR InterPro; IPR002035; -;  
 DR InterPro; IPR002919; -;  
 DR Pfam; PF00007; Cys\_knot; 1.  
 DR Pfam; PF01826; TIL; 4.  
 DR Pfam; PF00092; vwa; 3.  
 DR Pfam; PF00093; vwc; 3.  
 DR Pfam; PF00094; vwd; 4.  
 DR PRINTS; PR00453; VWFADOMAIN.  
 DR PROSITE; PS01185; CTCK\_1; 1.  
 DR PROSITE; PS01225; CTCK\_2; 1.  
 DR PROSITE; PS50234; VVFA; 3.  
 DR PROSITE; PS01208; VVFC; 3.  
 KW Blood coagulation; Platelet; Glycoprotein; Extracellular matrix;  
 KW Plasma; Endothelial cell; Repeat; Cell adhesion; Signal.  
 FT SIGNAL 1 22  
 FT PROPEP 23 763  
 FT CHAIN 764 2813  
 FT DOMAIN 35 179  
 FT DOMAIN 388 541  
 FT DOMAIN 764 787  
 FT AMINO-TERMINAL.

FT	DOMAIN	788	833	EL
FT	DOMAIN	826	853	CA.
FT	DOMAIN	867	1013	VNFD 3.
FT	DOMAIN	1277	1453	VVFA 1.
FT	DOMAIN	1498	1665	VVFA 2.
FT	DOMAIN	1691	1871	VVFA 3.
FT	DOMAIN	1950	2102	VVFA 4.
FT	DOMAIN	2216	2261	E2.
FT	DOMAIN	2255	2326	VNFC 1.
FT	DOMAIN	2429	2495	VNFC 2.
FT	DOMAIN	2580	2650	VNFC 3.
FT	DOMAIN	2724	2812	CTCK.
FT	SITE	531	533	CELL ATTACHMENT SITE (POTENTIAL).
FT	SITE	698	700	CELL ATTACHMENT SITE (POTENTIAL).
FT	SITE	2507	2509	CELL ATTACHMENT SITE (POTENTIAL).
FT	DISULFID	767	808	BY SIMILARITY.
FT	DISULFID	776	804	BY SIMILARITY.
FT	DISULFID	810	821	BY SIMILARITY.
FT	DISULFID	867	996	BY SIMILARITY.
FT	DISULFID	889	1031	BY SIMILARITY.
FT	DISULFID	998	993	BY SIMILARITY.
FT	DISULFID	914	921	BY SIMILARITY.
FT	DISULFID	1060	1084	BY SIMILARITY.
FT	DISULFID	1071	1111	BY SIMILARITY.
FT	DISULFID	1089	1091	BY SIMILARITY.
FT	DISULFID	1153	1165	BY SIMILARITY.
FT	DISULFID	1149	1169	BY SIMILARITY.
FT	DISULFID	1126	1130	BY SIMILARITY.
FT	DISULFID	1196	1199	BY SIMILARITY.
FT	DISULFID	1234	1237	BY SIMILARITY.
FT	DISULFID	1272	1458	BY SIMILARITY.
FT	DISULFID	1669	1670	BY SIMILARITY.
FT	DISULFID	1686	1872	BY SIMILARITY.
FT	DISULFID	1879	1904	BY SIMILARITY.
FT	DISULFID	1899	1940	OR 1942 (BY SIMILARITY).
FT	DISULFID	1972	2123	BY SIMILARITY.
FT	DISULFID	1950	2085	BY SIMILARITY.
FT	DISULFID	1927	2088	BY SIMILARITY.
FT	DISULFID	1993	2001	BY SIMILARITY.
FT	DISULFID	2724	2774	BY SIMILARITY.
FT	DISULFID	2739	2788	BY SIMILARITY.
FT	DISULFID	2750	2804	BY SIMILARITY.
FT	DISULFID	2754	2806	BY SIMILARITY.
FT	DISULFID	?	2811	BY SIMILARITY.
FT	CARBOHYD	99	99	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	156	156	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	211	211	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	666	666	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	857	857	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1231	1231	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1515	1515	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1574	1574	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2223	2223	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2290	2290	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2357	2357	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2400	2400	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2546	2546	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2585	2585	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2790	2790	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CONFLICT	55	55	G -> E (IN REF. 2).
FT	CONFLICT	70	70	V -> I (IN REF. 3).
FT	CONFLICT	266	266	A -> G (IN REF. 2).
FT	CONFLICT	280	280	I -> V (IN REF. 2).
FT	CONFLICT	409	411	VCH -> ICQ (IN REF. 2).
FT	CONFLICT	994	994	G -> A (IN REF. 1).
FT	CONFLICT	1021	1021	F -> L (IN REF. 2).
FT	CONFLICT	2381	2381	L -> P (IN REF. 2).
FT	CONFLICT	2406	2406	P -> L (IN REF. 2).
SQ	SEQUENCE	2813 AA;	309716 MW;	5DF931E1E5E72F80C CRC64;

Query Match 24.0%; Score 60.5; DB 1; Length 2813;  
 Best Local Similarity 30.4%; Pred. No. 17;

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FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 528 528 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 568 568 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 603 603 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 19- 19 C -> S (IN REF. 2).
FT CONFLICT 539 539 C -> W (IN REF. 5).
FT CONFLICT 991 991 L -> F (IN REF. 4).
FT CONFLICT 1116 1117 HP -> DR (IN REF. 6).
SQ SEQUENCE 1210 AA; 134853 MW; 690E20D46DF2D2F5 CRC64;

Query Match 25.4%; Score 64; DB 1; Length 1210;
Best Local Similarity 34.2%; Pred. No. 3.4; Indels 0; Gaps 0;
Matches 13; Conservative 5; Mismatches 20;

QY 3 QPEFHGCDPCTTCRHHPCPPGQGVQSGKFSFGFCI 40
D 255 QDEATCKDTCPLMLNPTTYQMDVNPCKYSGATCV 292

RESULT 3
VWF_BOVIN STANDARD; PRT; 937 AA.
AC P80012; Q28011;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE VON WILLEBRAND FACTOR PRECURSOR (VWF) (FRAGMENT).
GN F8VWF OR VWF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97307751; PubMed=9165093;
RA Janel N., Ribba A.S., Cherel G., Kerbiriou-Nabias D., Meyer D.;
RT "Primary structure of the propeptide and factor VIII-binding domain of
RT bovine von Willebrand factor."
RL Biochim. Biophys. Acta 1339:4-8(1997).
RN [2]
RP SEQUENCE OF 1-177 FROM N.A.
RX MEDLINE=96144290; PubMed=8566794;
RA Janel N., Schwachtgen J.L., Bakhshi M.R., Barek L., Meyer D.,
RA Kerbiriou-Nabias D.;
RT "Comparison of the 5'-flanking sequences of the human and bovine von
RT Willebrand factor-encoding genes reveals alternation of highly
RT homologous domains with species-specific Alu-type repeats."
RL Gene 167:291-295(1995).
RN [3]
RP PARTIAL SEQUENCE.
RX MEDLINE=91192039; PubMed=1707363;
RA Fujisawa T., Takagi J., Sekiya F., Goto A., Miake F., Saito Y.;
RT "Monoclonal antibodies that inhibit binding of propeptide of von
RT Willebrand factor to collagen. Localization of epitopes."
RL Eur. J. Biochem. 196:673-677(1991).
RN [4]
RP PARTIAL SEQUENCE.
RX MEDLINE=96028118; PubMed=7588715;
RA Takagi J., Aoyama T., Ueki S., Ohba H., Saito Y., Lorand L.;
RT "Identification of bovine-xiii-reactive glutamyl residues in the
RT propeptide of factor von Willebrand factor."
RL Eur. J. Biochem. 232:773-777(1995).
CC -!- FUNCTION: IMPORTANT IN THE MAINTENANCE OF HOMEOSTASIS, IT
CC PARTICIPATES IN PLATELET-VESSEL WALL INTERACTIONS BY FORMING A
CC NONCOVALENT COMPLEX WITH COAGULATION FACTOR VIII AT THE SITE OF
CC VASCULAR INJURY.
CC -!- SUBUNIT: MULTIMERIC (BY SIMILARITY).
CC -!- PTM: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR
```

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CC INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS AT LEAST 3 VWF DOMAINS.
CC -----
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CC -----
CC EMBL; Y09353; CAA70525.1; -.
CC EMBL; U28147; AAA96953.1; -.
CC InterPro; IPR000359; -.
CC InterPro; IPR001007; -.
CC InterPro; IPR001846; -.
CC InterPro; IPR002919; -.
CC Pfam; PF01826; TIL; 3.
CC Pfam; PF00094; vwd; 3.
CC PROSITE; PS01185; CTCK_1; PARTIAL.
CC PROSITE; PS01235; CTCK_2; PARTIAL.
CC PROSITE; PS01208; WVFC; PARTIAL.
CC Blood coagulation; Platelet; Glycoprotein; Extracellular matrix;
KW Plasma; Endothelial cell; Cell adhesion; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT PROPEP 23 762 BY SIMILARITY.
FT CHAIN 763 >937 VON WILLEBRAND FACTOR.
FT DOMAIN 35 179 VWF 1.
FT DOMAIN 387 540 VWF 2.
FT DOMAIN 763 786 AMINO-TERMINAL.
FT DOMAIN 787 832 E1.
FT DOMAIN 825 852 CX.
FT DOMAIN 841 >937 VWF 3.
FT SITE 410 410 FACTOR XIII-BINDING.
FT SITE 414 414 FACTOR XIII-BINDING.
FT SITE 605 605 FACTOR XIII-BINDING.
FT DISULFID 766 807 BY SIMILARITY.
FT DISULFID 775 803 BY SIMILARITY.
FT DISULFID 913 920 BY SIMILARITY.
FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 665 665 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 856 856 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 330 330 MISSING (IN REF. 3).
FT CONFLICT 523 523 MISSING (IN REF. 4).
FT CONFLICT 528 528 G -> Q (IN REF. 4).
FT NON_TER 937 937
SQ SEQUENCE 937 AA; 102599 MW; 9BF4C94A254A5629 CRC64;

Query Match 25.2%; Score 63.5; DB 1; Length 937;
Best Local Similarity 34.0%; Pred. No. 3.2;
Matches 16; Conservative 1; Mismatches 15; Indels 15; Gaps 2;

QY 8 CGDPCCTTCR--HHP-----CPPGQGVQSGKFSFGFCQ 39
D 660 CGTPCNLTCSRSLSHPBDECTVCLGCGFCPPGLFDETGSCVPKRAQC 706

RESULT 4
VWF_CANFA STANDARD; PRT; 2813 AA.
AC Q28295; Q28311; Q9TSI4;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE VON WILLEBRAND FACTOR PRECURSOR (VWF).
GN F8VWF OR VWF.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
```

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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:15:25 ; Search time 43.78 Seconds  
(without alignments)  
31.298 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_74\_113

Perfect score: 232

Sequence: 1 CVQPEFHGDPCCCTCRHHPCPGQGVQSQKFSFGQCI 40

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 segs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	26.6	256	1 41BB_MOUSE	P20334 mus musculus
2	64	25.4	1210	1 EGFR_MOUSE	Q01279 mus musculus
3	63.5	25.2	937	1 VWF_BOVIN	P80012 bos taurus
4	60.5	24.0	2813	1 VWF_CANFA	Q28295 canis familiar
5	60	23.8	233	1 CYCX_NITEU	O50926 nitrosomona
6	60	23.8	1210	1 EGFR_HUMAN	P00533 homo sapien
7	59.5	23.6	1104	1 NF1_HUMAN	Q12986 homo sapien
8	59.5	23.6	2813	1 VWF_HUMAN	P04275 homo sapien
9	59	23.4	58	1 MT1_SCVSE	P02805 scylla serr
10	59	23.4	703	1 EGFR_CHICK	P13387 gallus gall
11	58.5	23.2	437	1 INTR_SACER	P22877 saccharopol
12	58.5	23.2	980	1 TSP4_RAT	P49744 rattus norv
13	58.5	23.2	2482	1 VWF_PIG	Q28833 sus scrofa
14	58	23.0	271	1 OX40_RAT	P15725 rattus norv
15	58	23.0	867	1 SSPO_BOVIN	P98167 bos taurus
16	58	23.0	2907	1 FBN2_MOUSE	Q61555 mus musculus
17	58	23.0	2911	1 FBN2_HUMAN	P35356 homo sapien
18	57.5	22.8	289	1 CD40_MOUSE	P27512 mus musculus
19	57.5	22.8	581	1 IRR_RAT	Q64716 rattus norv
20	57.5	22.8	961	1 TSP4_HUMAN	P35443 homo sapien
21	57.5	22.8	1297	1 IRR_HUMAN	P14616 homo sapien
22	57	22.6	60	1 MTA_THCCR	P52721 thermarces
23	57	22.6	1370	1 IGR1_RAT	P24062 rattus norv
24	57	22.6	1373	1 IGR1_MOUSE	Q60751 mus musculus
25	57	22.6	2318	1 NTC3_MOUSE	Q61982 mus musculus
26	56.5	22.4	277	1 CD40_HUMAN	P25942 homo sapien
27	56	22.2	63	1 ICE1_ASCSU	P07851 ascaris suu
28	56	22.2	1687	1 Z142_HUMAN	P52746 homo sapien
29	55.5	22.0	62	1 MT4_HUMAN	P47944 homo sapien
30	55.5	22.0	277	1 OX40_HUMAN	P34389 homo sapien
31	55	21.8	269	1 CD40_BOVIN	Q28203 bos taurus
32	55	21.8	448	1 K1M2_HUMAN	Q14532 homo sapien
33	55	21.8	921	1 CA19_MOUSE	Q05722 mus musculus

34	55	21.8	931	1	CA19_HUMAN	P20849 homo sapien
35	55	21.8	1106	1	STC_DROME	P40798 drosophila
36	55	21.8	1466	1	CA13_HUMAN	P02461 homo sapien
37	54.5	21.6	62	1	MT4_MOUSE	P47945 mus musculus
38	54	21.4	230	1	SPIT_DROME	Q01083 drosophila
39	54	21.4	677	1	SP87_DICDI	P54643 dictyostell
40	54	21.4	798	1	HEPA_HCMVA	P16827 human cytom
41	54	21.4	837	1	LDLR_RABIT	P20063 oryctolagus
42	53.5	21.2	431	1	WMSA_WHV8	P06432 woodchuck h
43	53.5	21.2	1429	1	L112_CABEL	P14585 caenorhabd1
44	53	21.0	65	1	ICE2_ASCSU	P07852 ascaris suu
45	53	21.0	91	1	VE4_RHPV1	P24832 rhesus papi

## ALIGNMENTS

RESULT 1	
41BB_MOUSE	
ID	41BB_MOUSE STANDARD; PRT; 256 AA.
AC	P20334;
DT	01-FEB-1991 (Rel. 17, Created)
DT	01-FEB-1991 (Rel. 17, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB).
GN	TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=89184547; PubMed=2784565;
RA	Kwon B.S., Weissman S.M.;
RT	"CDNA sequences of two inducible T-cell genes.";
RL	Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BALB/C;
RX	MEDLINE=94179805; PubMed=8133039;
RA	Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;
RT	"Genomic organization and chromosomal localization of the T-cell antigen 4-1BB.";
RL	J. Immunol. 152:2256-2262(1994).
RN	[3]
RP	CHARACTERIZATION, AND SEQUENCE OF 25-29.
RX	MEDLINE=93139510; PubMed=7678621;
RA	Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kim K.K., Pickard R.T.,
RA	Kwon B.S.;
RT	"Inducible T cell antigen 4-1BB. Analysis of expression and function.";
RL	J. Immunol. 150:771-781(1993).
CC	-I- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY ACTIVE DURING T CELL ACTIVATION.
CC	-I- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.
CC	-I- ASSOCIATES WITH P56-LCK.
CC	-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC	-I- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.
CC	-I- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.
CC	-I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC	-----
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CC	-----
DR	EMBL; J04492; AAA40167.1; --
DR	EMBL; U02567; AAA93113.1; --
DR	PIR; B32393; B32393.
DR	HSSP; P25942; ICDF.

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DR MGD: MGI:1101059; Tnfrsf9.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_C6; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00505; TNFR_NGFR_2; FALSE_NEG.
KW Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
FT SIGNAL 1 24
FT CHAIN 25 256 4-1BB LIGAND RECEPTOR.
FT DOMAIN 25 187 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 188 208 POTENTIAL.
FT DOMAIN 209 256 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 17 159 4 X TNFR-CYS.
FT REPEAT 17 45 TNFR-CYS 1.
FT REPEAT 46 85 TNFR-CYS 2.
FT REPEAT 86 117 TNFR-CYS 3.
FT REPEAT 118 159 TNFR-CYS 4.
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 256 AA; 27598 MW; 93A10D03C60813C4 CRC64;

Query Match 26.6%; Score 67; DB 1; Length 256;
Best Local Similarity 45.2%; Pred. No. 0.45;
Matches 14; Conservative 3; Mismatches 12; Indels 2; Gaps 2;

QY 1 CVQPEFHGDCPCTTCRHHPCPPGQVSQ 31
D 1: ||| ||| | ||| |
Db 87 CIE-GFCHLGPQCTRC-EKDCRPGELTKQG 115

RESULT 2
EGFR_MOUSE
ID EGFR_MOUSE STANDARD; PRT; 1210 AA.
AC Q01279;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112).
GN EGFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=Liver;
RX MEDLINE=93026370; PubMed=1408137;
RA Avivi A., Skorecki K., Yayon A., Givol D.;
RT "Promoter region of the murine fibroblast growth factor receptor 2
RL (bek/KGFR) gene.";
RL Oncogene 7:1957-1962(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C, AND CD-1; TISSUE=Liver, and Decidua;
RX MEDLINE=93146380; PubMed=7678348;
RA Paria B.C., Das S.K., Andrews G.K., Dey S.K.;
RT "Expression of the epidermal growth factor receptor gene is regulated
RL in mouse blastocysts during delayed implantation.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=Liver;
RX Hibbs M.L.;
RA Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-B6/C3; TISSUE=Liver;
RX MEDLINE=94170986; PubMed=9125255;
RA Luetkeke N.C., Phillips H.K., Qiu T.H., Copeland N.G., Earp H.S.,
RA Jenkins N.A., Lee D.C.;
RT "The mouse waved-2 phenotype results from a point mutation in the EGF
RT receptor tyrosine kinase.";
RL Genes Dev. 8:399-413(1994).

[5]
RN SEQUENCE OF 1-714 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=91232866; PubMed=2030916;
RA Avivi A., Lax I., Ullrich A., Schlessinger J., Givol D., Morse B.;
RT "Comparison of EGF receptor sequences as a guide to study the ligand
RT binding site.";
RL Oncogene 6:673-676(1991).
RN [6]
RP SEQUENCE OF 969-1117 FROM N.A.
RC STRAIN=C3H;
RA Eisinger D.P., Serrero G.;
RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF,
CC AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AND
CC VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- MISCELLANEOUS: BINDING OF EGF TO THE RECEPTOR LEADS TO
CC INTERNALIZATION OF THE EGF-RECEPTOR COMPLEX, INDUCTION OF THE
CC TYROSINE KINASE ACTIVITY, STIMULATION OF CELL DNA SYNTHESIS, AND
CC CELL PROLIFERATION.
CC -!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X78987; CAA55587.1; -
CC EMBL; U03425; AAA17899.1; -
CC EMBL; X59698; CAA42219.1; -
CC EMBL; L06864; AAA53029.1; -
CC EMBL; Z12608; CAA78249.1; -
CC HSSP; P11362; 1FG1.
CC MGD; MGI:95294; Egfr.
CC InterPro; IPR000494; -
CC InterPro; IPR000719; -
CC InterPro; IPR001245; -
CC InterPro; IPR002174; -
CC Pfam; PF00757; Furin-like; 1.
CC Pfam; PF01030; Recep_L_domain; 2.
CC Pfam; PF00069; kinase_1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC Transmembrane; Glycoprotein; Receptor; Signal; Transferase;
KW Tyrosine-protein kinase; ATP-binding; Phosphorylation; Repeat.
FT SIGNAL 1 24
FT CHAIN 25 1210 EPIDERMAL GROWTH FACTOR RECEPTOR.
FT DOMAIN 25 647 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 648 670 POTENTIAL.
FT DOMAIN 671 1210 CYTOPLASMIC (POTENTIAL).
FT REPEAT 75 300 APPROXIMATE.
FT REPEAT 390 600 APPROXIMATE.
FT DOMAIN 1028 1071 SER-RICH.
FT DOMAIN 714 981 PROTEIN KINASE.
FT NP_BIND 720 728 ATP (BY SIMILARITY).
FT BINDING 747 747 ATP (BY SIMILARITY).
FT ACT_SITE 839 839 BY SIMILARITY.
FT MOD_RES 680 680 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
FT MOD_RES 1092 1092 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 1110 1110 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 1172 1172 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 1197 1197 PHOSPHORYLATION (AUTO-, MAJOR SITE) (BY SIMILARITY).
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).

```



A: Molecule type: mRNA

A: Residues: 1-152 <CHE>

A: Cross-references: GB:AF176420

A: Experimental source: venom gland

A: Accession: PC7037

A: Molecule type: protein

A: Residues: 24-53;84-86;87-94;125-136;137-152 <CH2>

C: Superfamily: tetranectin; C-type lectin homology

C: Keywords: disulfide bond; heterodimer; venom

F: 1-23/Domain: signal sequence #status predicted <SIG>

F: 24-152/Product: agkiscutacin alpha chain #status experimental <MAT>

Query Match 23.4%; Score 57.5; DB 2; Length 152;

Best Local Similarity 41.9%; Pred. No. 4.6;

Matches 13; Conservative 2; Mismatches 7; Indels 9; Gaps 2;

QY 1 DCASGTFSGGHEGHC-----KPWTDCTQF 24

Db 24 DCSSGWSS--YEGHCYKVFQSKTWADAESF 52

RESULT 13

S56828

finger protein YJL056c - yeast (Saccharomyces cerevisiae)

N: Alternate names: protein J1145

C: Species: Saccharomyces cerevisiae

C: Date: 05-May-1995 #sequence\_revision 08-Sep-1995 #text\_change 05-Nov-1999

C: Accession: S56828

R: Pohl, T.M.; Aljinovic, G.

submitted to the Protein Sequence Database, September 1995

A: Reference number: S56793

A: Accession: S56828

A: Molecule type: DNA

A: Residues: 1-880 <TOV>

A: Cross-references: EMBL:Z49331; NID:gl008196; PIDN:CAA89347.1; PID:gl008197; GSPDB:GN00

C: Genetics:

A: Gene: MIPS:YJL056c

A: Map position: 10L

C: Keywords: zinc finger

Query Match

Best Local Similarity 22.8%; Score 56; DB 2; Length 880;

Matches 16; Conservative 7; Mismatches 15; Indels 18; Gaps 3;

QY 1 DCASGTFSGG--HE-----GHCKPMTDCTQGF-----LTVFPGNKTTHA 38

Db 78 DAATSAFASGASHDMGGDCHVNEKKEYTDCQHFELNHNPNLSLTKNYNDTATYNS 133

RESULT 14

JC4329

coagulation factor IX-binding protein A chain - habu

C: Species: Trimeresurus flavoviridis (habu)

C: Date: 06-Dec-1995 #sequence\_revision 08-Feb-1996 #text\_change 13-Mar-1998

C: Accession: JC4329

R: Atoda, H.; Ishikawa, M.; Yoshihara, E.; Sekiya, F.; Morita, T.

J. Biochem. 118, 965-973, 1995

A: Title: Blood coagulation factor IX-binding protein from the venom of Trimeresurus flav

A: Reference number: JC4329; MUID:96318509

A: Accession: JC4329

A: Molecule type: protein

A: Residues: 1-129 <ATO>

C: Comment: This protein binds calcium.

C: Superfamily: tetranectin; C-type lectin homology

C: Keywords: anticoagulant; blood coagulation; calcium binding; venom

F: 2-127/Domain: C-type lectin homology <LCH>

F: 2-13,30-127,102-119/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 22.6%; Score 55.5; DB 2; Length 129;

Matches 13; Conservative 2; Mismatches 7; Indels 9; Gaps 2;

Matches 13; Conservative 2; Mismatches 7; Indels 9; Gaps 2;

QY 1 DCASGTFSGGHEGHC-----KPWTDCTQF 24

Db 1 DCPGSGWSS--YEGHCYKPFKLYKTWDAERF 29

RESULT 15

JC7105

aggreitin beta chain - Malayan pit viper

C: Species: Calloselasma rhodostoma (Malayan pit viper)

C: Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 11-May-2000

C: Accession: JC7105

R: Chung, C.H.; Au, L.C.; Huang, T.F.

Biochem. Biophys. Res. Commun. 263, 723-727, 1999

A: Title: Molecular cloning and sequence analysis of aggreitin, a collagen-like platele

A: Reference number: PC7027; MUID:99443731

A: Accession: JC7105

A: Molecule type: mRNA

A: Residues: 1-146 <CHU>

A: Experimental source: venom gland

C: Superfamily: tetranectin; C-type lectin homology

C: Keywords: disulfide bond; platelet aggregation; venom

Query Match

Best Local Similarity 22.6%; Score 55.5; DB 2; Length 146;

Matches 13; Conservative 2; Mismatches 7; Indels 9; Gaps 2;

QY 1 DCASGTFSGGHEGHC-----KPWTDCTQF 24

Db 24 DCPGSGWSS--YEGHCYKPFNEPKNWADAERF 52

Search completed: September 4, 2001, 16:12:15

Job time: 1112 sec

---

Query Match 24.8%; Score 61; DB 2; Length 459;  
 Best Local Similarity 36.6%; Pred. No. 4.6;  
 Matches 15; Conservative 5; Mismatches 15; Indels 6; Gaps 2;

Qy 2 CASGTFSG--GHEGCKPWTCTQGFGLTVFPGNTHNAVC 40  
 ||||| : : : ||| : |||  
 Db 151 CAPGTFSDTSTDCRPHRCS-----ILAIPGNASTDAVC 187

RESULT 7  
 A35356  
 tumor necrosis factor receptor 2 precursor [validated] - human  
 A:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2  
 C:Species: Homo sapiens (man)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 08-Dec-2000  
 C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094  
 R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K.  
 Science 248, 1019-1023, 1990  
 A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular and  
 A:Reference number: A35356; MUID:90260639  
 A:Accession: A35356  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-461 <SMI>  
 A:Cross-references: GB:M32315; NID:q189185; PIDN:AAA59929.1; PID:q189186  
 R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires,  
 Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990  
 A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occur  
 A:Reference number: A36475; MUID:91045991  
 A:Accession: A36475  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-195; 'R', 197-461 <KOH>  
 A:Cross-references: GB:M55994; GB:M38549; NID:q339757; PIDN:AAA36755.1; PID:q339758  
 R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gents, R.; Brockhaus, M.  
 Cytokine 2, 231-237, 1990  
 A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular,  
 A:Reference number: A48416; MUID:91370690  
 A:Accession: A48416  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 23-461 <DEM>  
 A:Cross-references: GB:S63368; NID:q235648; PIDN:AAB19824.1; PID:q235649  
 R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990  
 A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra  
 A:Reference number: A36007; MUID:90349572  
 A:Accession: A36007  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>  
 A:Cross-references: GB:M35857; NID:q339751; PIDN:AAA63262.1; PID:q339752  
 R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.  
 J. Biol. Chem. 265, 20131-20138, 1990  
 A:Title: Purification and partial amino acid sequence analysis of two distinct tumor nec  
 A:Reference number: A23666; MUID:91056048  
 A:Accession: A23666  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 23-40; 65-69; 136-141; 300-306 <LOE>  
 R:Engelmann, H.; Novick, D.; Wallach, D.  
 J. Biol. Chem. 265, 1531-1536, 1990  
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence;  
 A:Reference number: A35010; MUID:90110215  
 A:Accession: B35010  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 27-31 <ENG>  
 R:Kuhnert, P.; Kemper, O.; Wallach, D.  
 Gene 150, 381-386, 1994

A:Title: Cloning, sequencing and partial functional characterization of the 5' region  
 A:Reference number: I38094; MUID:95121934  
 A:Accession: I38094  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-37 <RES>  
 A:Cross-references: EMBL:X80021; NID:q666044; PIDN:CAA56324.1; PID:q825701  
 C:Genetics:  
 A:Gene: GDB:TNFR2  
 A:Cross-references: GDB:125914; OMIM:191191  
 A:Map position: lp36.2-lp36.2  
 A:Introns: 26/3  
 A>Note: the list of introns is incomplete  
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
 C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>  
 F:40-76/Domain: NGF receptor repeat homology <NG1>  
 F:78-119/Domain: NGF receptor repeat homology <NG2>  
 F:120-162/Domain: NGF receptor repeat homology <NG3>  
 F:164-201/Domain: NGF receptor repeat homology <NG4>  
 F:262-279/Domain: transmembrane #status predicted <TMN>  
 F:280-461/Domain: intracellular #status predicted <INT>  
 F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 24.8%; Score 61; DB 1; Length 461;  
 Best Local Similarity 36.6%; Pred. No. 4.6;  
 Matches 15; Conservative 4; Mismatches 16; Indels 6; Gaps 2;

Qy 2 CASGTFSG--GHEGCKPWTCTQGFGLTVFPGNTHNAVC 40  
 ||||| : : : ||| : |||  
 Db 164 CAPGTFSTSTSDICRPHQICN----VVAIPGNASMDAVC 200

RESULT 8  
 B38634  
 tumor necrosis factor receptor type 2 precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Jul-1999  
 C:Accession: B38634; A40254; S54816  
 R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,  
 Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
 A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto  
 A:Reference number: A38634; MUID:91187885  
 A:Accession: B38634  
 A:Molecule type: mRNA  
 A:Residues: 1-474 <LEW>  
 A:Cross-references: GB:M60469; NID:q199827; PIDN:AAA39752.1; PID:q199828  
 R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J  
 Mol. Cell. Biol. 11, 3020-3026, 1991  
 A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f  
 A:Reference number: A40254; MUID:91246168  
 A:Accession: A40254  
 A:Molecule type: mRNA  
 A:Residues: 1-474 <GOO>  
 A:Cross-references: GB:M60469; NID:q199827; PIDN:AAA39752.1; PID:q199828  
 R:Kisssnerghis, M.; Fellows, R.; Feldmann, M.; Chernaiovsky, Y.  
 submitted to the EMBL Data Library, May 1995  
 A:Description: Characterization of the promoter region of the murine p75-TNF receptor  
 A:Reference number: S54816  
 A:Accession: S54816  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-22 <KIS>  
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
 C:Keywords: cytokine receptor; transmembrane protein  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>  
 F:40-77/Domain: NGF receptor repeat homology <NG1>  
 F:79-120/Domain: NGF receptor repeat homology <NG2>  
 F:166-203/Domain: NGF receptor repeat homology <NG4>



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:12:14 ; Search time 80.15 Seconds  
(without alignments)  
38.966 Million cell updates/sec

Title: US-09-512-363-2\_COPY\_114\_154  
Perfect score: 246  
Sequence: 1 DCASGTFSGHGCHKPWT.....TQPGFLTPFGNKHNAVCV 41

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	39.0	272	2 137552	Ox40 homolog - hum
2	95	38.6	272	2 148700	gene ox40 protein
3	93	37.8	255	2 138426	lymphocyte activat
4	84	34.1	271	2 S12783	Ox40 antigen precu
5	70.5	28.7	256	2 B32393	T-cell antigen 4-1
6	61	24.8	459	2 148854	gene murine tumour
7	61	24.8	461	1 A35356	tumor necrosis fac
8	61	24.8	474	2 B38634	tumor necrosis fac
9	60.5	24.6	416	1 JN0006	nerve growth facto
10	59	24.0	998	1 Q0BB81	BI protein - black
11	59	24.0	998	2 S41397	protein A - flock
12	57.5	23.4	152	2 JC7134	agkisacutacin alph
13	56	22.8	880	2 S56828	finger protein VIL
14	55.5	22.6	129	2 JC4329	coagulation factor
15	55.5	22.6	146	2 JC7105	aggreitin beta chai
16	54.5	22.2	123	2 B42972	coagulation factor
17	54.5	22.2	231	2 S55078	hypothetical prote
18	54.5	22.2	350	2 JQ1656	ethylene-forming e
19	54.5	22.2	425	1 A26431	nerve growth facto
20	54	22.0	435	2 134182	tumor necrosis fac
21	54	22.0	612	2 T39666	WD-repeat protein
22	54	22.0	616	2 C86239	protein t10024.21
23	53.5	21.7	152	2 JC4690	coagulation factor
24	53.5	21.7	327	2 D75263	hypothetical prote
25	53	21.5	305	2 A46476	B cell-associated
26	53	21.5	420	2 T01172	GI/S transition co
27	53	21.5	504	2 T50983	probable pleiotrop
28	53	21.5	524	2 S38539	disintegrin-like m
29	53	21.5	584	2 T01173	GI/S transition co

30	53	21.5	670	2 I65967	disintegrin-like m
31	53	21.5	898	2 T14764	hypothetical prote
32	53	21.5	1786	1 MMMSB1	laminin beta-1 cha
33	52.5	21.3	469	2 G69267	conserved hypothet
34	52.5	21.3	1208	2 T09049	competence factor
35	52	21.1	264	2 B82619	exodeoxyribonuclea
36	52	21.1	1321	2 JE0352	mucin MUC5B, trach
37	52	21.1	1786	1 MMHUB1	laminin beta-1 cha
38	51.5	20.9	278	2 A84169	molybdenum cofacto
39	51.5	20.9	579	2 S35237	cytochrome c-type
40	51	20.7	84	2 T03787	metallothionein-11
41	50.5	20.5	327	2 S48839	guanine nucleotide
42	50.5	20.5	538	2 S76085	hypothetical prote
43	50.5	20.5	700	2 A96690	hypothetical prote
44	50	20.3	277	2 A60771	B-cell activation
45	50	20.3	415	2 T24307	hypothetical prote

## ALIGNMENTS

## RESULT 1

I37552  
OX40 homolog - human  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000  
C:Accession: I37552  
R:Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fo  
Eur. J. Immunol. 24, 677-683, 1994  
A:Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignmen  
A:Reference number: I37552; MUID:94170844  
A:Accession: I37552  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-277 <RES>  
A:Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958  
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 39.0%; Score 96; DB 2: Length 277;  
Best Local Similarity 43.6%; Pred. No. 0.00014;  
Matches 17; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

OY 2 CASGTFSGHGCHKPWTCTQPGFLTPFGNKHNAVC 40  
DB 128 CPPGHPGDNQACKPWTNCTLAGKHTLQPASNSDAIC 166

## RESULT 2

I48700  
gene ox40 protein - mouse  
N:Alternate names: OX40 antigen  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 11-Jan-2000  
C:Accession: I48700; I48334; S34377  
R:Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J  
J. Immunol. 151, 5261-5271, 1993  
A:Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell  
A:Reference number: I48700; MUID:94044750  
A:Accession: I48700  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-272 <RES>  
A:Cross-references: EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g312828  
R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.  
Eur. J. Immunol. 25, 926-930, 1995  
A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX  
A:Reference number: I48334; MUID:95255413  
A:Accession: I48334  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-14, 'G', 16-272 <RES2>  
A:Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819

## C:Genetics:

A:Gene: OX40  
A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1  
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 38.6%; Score 95; DB 2; Length 272;

Best Local Similarity 46.2%; Pred. No. 0.00018;

Matches 18; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 2 CASGTFSGGHEGCHKPWTDCQFGFLTVFPNGKTHNAVC 40

Db 126 CPPGHFSPGNQACKPWTNCTLSGKQIRHPASDLDAVC 164

## RESULT 3

I38426

lymphocyte activation-induced receptor ILA precursor - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 01-Dec-2000

C:Accession: I38426; JT0752

R:Allderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; R

Eur. J. Immunol. 24, 2219-2227, 1994

A:Title: Molecular and biological characterization of human 4-1BB and its ligand.

A:Reference number: I38426; MUID:94374434

A:Accession: I38426

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-255 <RES>

A:Cross-references: EMBL:U03397; NID:g571320; PIDN:AAA53133.1; PID:g571321

R:Schwarz, H.; Tuckwell, J.; Lotz, M.

Gene 134, 295-298, 1993

A:Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne

A:Reference number: JT0752; MUID:94085794

A:Accession: JT0752

A:Molecule type: mRNA

A:Residues: 1-106, 'R', 108-255 <SCH>

C:Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-neuro

C:Comment: This receptor recognizes soluble, cell-surface bound or extracellular matrix

C:Superfamily: CD27 antigen; NGF receptor repeat homology

C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT>

F:138-213/Domain: transmembrane #status predicted <TMM>

F:138-149/Binding site: carboxylate (Asn) (covalent) #status predicted

F:234-235/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predict

F:242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 37.8%; Score 93; DB 2; Length 255;

Best Local Similarity 40.0%; Pred. No. 0.00031;

Matches 16; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 1 DCASGTFSGGHEGCHKPWTDCQFGFLTVFPNGKTHNAVC 40

Db 119 DCCGFTNDQKRGICRPWTNCTLSGKSLDGRSVLVNGTKERDVVC 158

## RESULT 4

SI2783

OX40 antigen precursor - rat

N:Alternate names: nerve growth factor receptor homolog

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 05-Nov-1999

C:Accession: SI2783; S08036

R:Mallett, S.; Fossum, S.; Barclay, A.N.

EMBO J. 9, 1063-1068, 1990

A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte

A:Reference number: SI2783; MUID:90214614

A:Accession: SI2783

A:Molecule type: mRNA

A:Residues: 1-271 <MAL>

A:Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831

C:Superfamily: CD27 antigen; NGF receptor repeat homology

C:Keywords: growth factor receptor; transmembrane protein

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-271/Product: OX40 antigen #status predicted <MAT>

F:211-235/Domain: transmembrane #status predicted <TMM>

Query Match 34.1%; Score 84; DB 2; Length 271;

Best Local Similarity 41.0%; Pred. No. 0.0042;

Matches 16; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 2 CASGTFSGGHEGCHKPWTDCQFGFLTVFPNGKTHNAVC 40

Db 125 CPPGHFSPGSNACKPWTNCTLSGKQIRHPASNSLDTVVC 163

## RESULT 5

B32393

T-cell antigen 4-1BB precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 21-Jul-2000

C:Accession: B32393; I48879

R:Kwon, B.S.; Weissman, S.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989

A:Title: cDNA sequence of two inducible T-cell genes.

A:Reference number: A32393; MUID:89184547

A:Accession: B32393

A:Molecule type: mRNA

A:Residues: 1-256 <KWO>

A:Cross-references: GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122

R:Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.

J. Immunol. 152, 2256-2262, 1994

A:Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1B

A:Reference number: I48879; MUID:94179805

A:Accession: I48879

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-256 <RES>

A:Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178

C:Genetics:

A:Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1

C:Superfamily: CD27 antigen; NGF receptor repeat homology

C:Keywords: transmembrane protein

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-256/Product: 4-1BB protein #status predicted <MAT>

Query Match 28.7%; Score 70.5; DB 2; Length 256;

Best Local Similarity 35.0%; Pred. No. 0.16;

Matches 14; Conservative 8; Mismatches 17; Indels 1; Gaps 1;

QY 2 CASGTFSGGH-EGHCKPWTDCQFGFLTVFPNGKTHNAVC 40

Db 119 CSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVC 158

## RESULT 6

I48854

gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 23-Jul-1999

C:Accession: I48854

R:Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.

Mamm. Genome 5, 726-727, 1994

A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.

A:Reference number: I48854; MUID:95178848

A:Accession: I48854

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-459 <RES>

A:Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831

C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology

F:151-188/Domain: NGF receptor repeat homology <NGF>

```

DR EMBL; L04270; AAA36757.1; -.
DR HSSP; P25942; ICDF.
DR MIN; 600979; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_NGR_1; 2.
DR PROSITE; PS00652; TNFR_NGR_1; 2.
DR PROSITE; PS00652; TNFR_NGR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 435
FT DOMAIN 31 227
FT TRANSF 228 248
FT DOMAIN 249 435
FT DOMAIN 42 211
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 168
FT REPEAT 169 211
FT DISULFID 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 148
FT DISULFID 142 167
FT DISULFID 170 185
FT CARBOHYD 40 40
FT CARBOHYD 177 177
SQ SEQUENCE 435 AA; 46709 MW; 624626E6022F656F CRC64;

Query Match 22.0%; Score 54; DB 1; Length 435;
Best Local Similarity 26.8%; Pred. No. 9.6;
Matches 11; Conservative 5; Mismatches 23; Indels 2; Gaps 1;

Qy 2 CASGTF--SGGHEGHCWPTDCTQFGFLTVFPGNKTHNAV 40
| | | | | | | | | | | | | | | | | | | | |
Db 170 CKAGHFQNTSSPSARCQPHTRCENQGLVEAPGTAQSDTTC 210

RESULT 14
IXA_TRIPL
ID IXA_TRIPL STANDARD; PRT; 152 AA.
AC P23806; Q91246;
DT 01-NOV-1991 (Rel. 20, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE COAGULATION FACTOR IX/FACTOR X-BINDING PROTEIN A CHAIN PRECURSOR
(IX/X-BP).
OS Trimeresurus flavoviridis (Habu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=88087;
RN [1]
RP MEDLINE=96184662; PubMed=86453114;
RX Matsuzaki R., Yoshikawa E., Yamada M., Shima K., Atoda H., Morita T.;
"CDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant
protein from snake venom.";
RL Biochem. Biophys. Res. Commun. 220:382-387(1996).
RN [2]
RP SEQUENCE OF 24-152.
RC TISSUE=Venom;
RX MEDLINE=91332000; PubMed=1831197;
RA Atoda H., Hyuga M., Morita T.;
RT "The primary structure of coagulation factor IX/factor X-binding
protein isolated from the venom of Trimeresurus flavoviridis.
Homology with asialoglycoprotein receptors, proteoglycan core
protein, tetranectin, and lymphocyte Fc epsilon receptor for
immunoglobulin E.";

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RL J. Biol. Chem. 266:14903-14911(1991).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=97331317; PubMed=9187649;
RA Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.;
"Structure of coagulation factors IX/X-binding protein, a heterodimer
of C-type lectin domains.";
RL Nat. Struct. Biol. 4:438-441(1997).
CC -|- FUNCTION: ANTICOAGULANT PROTEIN WHICH BINDS WITH FACTOR IX AND
CC FACTOR X IN THE PRESENCE OF CALCIUM WITH A 1 TO 1 STOICHIOMETRY.
CC -|- SUBUNIT: HETERODIMER OF CHAINS A AND B LINKED BY A DISULFIDE BOND.
CC -|- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
CC -|- SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.
CC -----
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CC -----
DR EMBL; D83331; BAAL1887.1; -.
DR PIR; A39332; A39332.
DR PDB; 1LXX; 06-MAY-98.
DR InterPro; IPR001304; -.
DR Pfam; PF00059; lectin_c; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Lectin; Calcium; Signal; 3D-structure.
FT SIGNAL 1 23
FT CHAIN 24 152
FT DOMAIN 24 152
FT COAGULATION FACTOR IX/FACTOR X-BINDING
FT PROTEIN A CHAIN.
FT DISULFID 25 36
FT BY SIMILARITY.
FT DISULFID 53 150
FT BY SIMILARITY.
FT DISULFID 102 102
FT INTERCHAIN (WITH C-98 OF B CHAIN).
FT DISULFID 125 142
FT BY SIMILARITY.
FT SEQUENCE 152 AA; 17213 MW; FB3DD2369009263 CRC64;

Query Match 21.7%; Score 53.5; DB 1; Length 152;
Best Local Similarity 41.2%; Pred. No. 4.4;
Matches 14; Conservative 2; Mismatches 5; Indels 13; Gaps 3;

Qy 1 DCASGTFSGGHEGHC-----KPWTD-----CTQ 23
| | | | | | | | | | | | | | |
Db 24 DCLSGWSS--YEGHCYKAFKYEKWTWEDAEKVC 55

RESULT 15
CD40_MOUSE
ID CD40_MOUSE STANDARD; PRT; 289 AA.
AC P27512;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
GN TNFRSF5 OR CD40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92105763; PubMed=1370315;
RA Torres R.M., Clark E.A.;
RT "Differential increase of an alternatively polyadenylated mRNA
species of murine CD40 upon B lymphocyte activation.";
RL J. Immunol. 148:620-626(1992).
RN [2]
RP REVISIONS.
RC STRAIN=BALB/C;

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RA Torres R.M.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C; TISSUE=Liver;
RX MEDLINE=93094586; PubMed=1281194;
RA Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
RA Howard M., Cockayne D.A.;
RT "Genomic structure and chromosomal mapping of the murine CD40 gene.";
RL J. Immunol. 149:3921-3926(1992).
CC -|- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC -----
DR EMBL; M83312; AAB08705.1; .
DR EMBL; M94126; AAA37404.1; .
DR EMBL; M94128; AAA37404.1; JOINED.
DR EMBL; M94128; AAA37404.1; JOINED.
DR EMBL; M94127; AAA37404.1; JOINED.
DR PIR; A46476; A46476.
DR HSSP; P25942; 1CDF.
DR MGD; MGI:88336; Tnfrsf5.
DR InterPro; IPR001368; .
DR Pfam; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 4.
KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 289 CD40L RECEPTOR.
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194 215 POTENTIAL.
FT DOMAIN 216 289 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 187 4 X TNFR-CYS.
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
FT CARBOHYD 153 153 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 289 AA; 32111 MW; C791CB6D2FEA574E CRC64;

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Query Match 21.5%; Score 53; DB 1; Length 289;

Best Local Similarity 29.3%; Pred. No. 9;

Matches 12; Conservative 2; Mismatches 25; Indels 2; Gaps 1;

QY 2 CASGTFSGGHE--GHCKPWTDCIOFGFLTVPPGNKTHNAVC 40

Db 146 CPVGFFSNQSLFEKCYPTWSCDKNLEVLQKGTSTQTNVIC 186

Search completed: September 4, 2001, 16:15:26

Job time: 1136 sec



DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 1.  
KW DNA-binding; Nuclear protein; zinc-finger; Metal-binding; Repressor;  
KW Transcription regulation; Repeat.  
FT ZN\_FING 174 196 C2H2-TYPE.  
FT ZN\_FING 202 226 C2H2-TYPE.  
SQ SEQUENCE 231 AA; 26743 MW; 50F7E7ED4690D109 CRC64;

Query Match 22.2%; Score 54.5; DB 1; Length 231;  
Best Local Similarity 33.3%; Pred.No. 4.8;  
Matches 11; Conservative 3; Mismatches 8; Indels 11; Gaps 1;

QY 2 CASGTFSGGH-----EGHKCPWTDCTQ 23  
||| : || : || : |||  
Db 179 CARGFTTSGHLARHNRIHTGEKNHCPCYKGCQTQ 211

RESULT 11  
ACCO\_PSESH STANDARD; PRT; 350 AA.

ID AC P32021;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (EC 1.-.-.) (ACC OXIDASE)  
DS (ETHYLENE-FORMING ENZYME) (EFE).  
OS Pseudomonas syringae (pv. phaseolicola).  
OG Plasmid pPSPI.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
OC Pseudomonas.  
OX NCBI\_TaxID=319;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PK2;  
RX MEDLINE=93075170; Pubmed=1445325;  
RA Fukuda H., Ogawa T., Ishihara K., Fujii T., Nagahama K., Omata T.,  
RA Inoue Y., Tanase S., Morino Y.;  
RW "Molecular cloning in Escherichia coli, expression, and nucleotide  
sequence of the gene for the ethylene-forming enzyme of Pseudomonas  
syringae pv. phaseolicola PK2.";  
RL Biochem. Biophys. Res. Commun. 188:826-832(1992).  
CC -|- CATALYTIC ACTIVITY: 1-AMINOCYCLOPROPANE-1-CARBOXYLATE + O2 -  
CC ETHYLENE + HCN + CO(2) + 2 H(2)O.  
CC -|- COFACTOR: IRON AND ASCORBATE.  
CC -|- PATHWAY: LAST STEP IN THE BIOSYNTHESIS OF ETHYLENE..  
CC -|- SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF  
CC OXIDOREDUCTASES.

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DR EMBL; D13182; BAA02477.1; -.  
DR PIR; JQ1656; JQ1656.  
DR InterPro; IPR002419; -.  
DR Pfam; PF00671; Fe\_Asc\_Oxidored; 1.  
KW Ethylene biosynthesis; Oxidoreductase; Iron; Vitamin C; Plasmid.  
SQ SEQUENCE 350 AA; 39444 MW; 5FD86F07ECD392B CRC64;

Query Match 22.2%; Score 54.5; DB 1; Length 350;  
Best Local Similarity 46.7%; Pred.No. 6.9;  
Matches 14; Conservative 2; Mismatches 13; Indels 1; Gaps 1;

QY 5 GTSTGGHGHCKPWTDCTQF-GFLTVPFGN 33  
| | | | : | | | | | | | |  
Db 224 GESSAGMFEDHPWFVPTTPPGVTVPFGD 253

RESULT 12	NGFR_RAT	NGFR_RAT	STANDARD;	PRT;	425 AA.
ID	NGFR_RAT				
AC	P07174;				
DT	01-APR-1988	(Rel. 07, Created)			
DT	01-APR-1988	(Rel. 07, Last sequence update)			
DT	01-OCT-2000	(Rel. 40, Last annotation update)			
DE	LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)				
DE	(GP80-LNGFR) (P75 ICD).				
GN	NGFR.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=87115859; PubMed=3027580;				
RA	Radeke M.J., Misko T.P., Hsu C., Herzenberg L.A., Shooter E.M.;				
RT	"Gene transfer and molecular cloning of the rat nerve growth factor receptor.";				
RT	Nature 325:593-597(1987).				
RL	[2]				
RN	SEQUENCE OF 1-22 FROM N.A.				
RP	TISSUE=Liver;				
RC	MEDLINE=93077038; PubMed=1446821;				
RX	Metsis M., Timmusk T., Allikmets R., Saarma M., Persson H.;				
RA	"Regulatory elements and transcriptional regulation by testosterone				
RT	and retinoic acid of the rat nerve growth factor receptor promoter.";				
RT	Gene 121:247-254(1992).				
RL	[3]				
RN	STRUCTURE BY NMR OF 334-418.				
RP	MEDLINE=97449145; PubMed=9305641;				
RX	Liepinsh E., Ilag L.L., Otting G., Ibanez C.F.;				
RA	"NMR structure of the death domain of the p75 neurotrophin receptor.";				
RT	EMBO J. 16:4999-5005(1997).				
RL	[4]				
CC	-1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,				
CC	NT-3, AND NT-4.				
CC	-1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE				
CC	BOND FORMATION.				
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.				
CC	-1- FMW: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.				
CC	-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.				
CC	-1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.				
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CC	or send an email to <a href="mailto:license@lsb-sib.ch">license@lsb-sib.ch</a> ).				
CC	EMBL; X05137; CAA28783.1; -				
DR	EMBL; X61269; -; NOT_ANNOTATED_CDS.				
DR	PIR; A26431; A26431.				
DR	PDB; INGR; 29-JUL-97.				
DR	InterPro; IPR000488; -				
DR	InterPro; IPR001368; -				
DR	Pfam; PF00020; TNFR_cg; 4.				
DR	Pfam; PF00531; death; 1.				
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.				
DR	PROSITE; PS50050; TNFR_NGFR_2; 4.				
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.				
KW	Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;				
KW	Phosphorylation; Signal; 3D-structure.				
FT	SIGNAL	1	29		
FT	CHAIN	30	425		
FT					LOW-AFFINITY NERVE GROWTH FACTOR
FT					RECEPTOR.
FT	DOMAIN	30	251		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	252	273		POTENTIAL.
FT	DOMAIN	274	425		CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	32	190		4 X TNFR-CYS.
FT	REPEAT	32	166		TNFR-CYS 1.

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DR EMBL; M32315; AAA59929.1; -;  
 DR EMBL; M35857; AAA63262.1; -;  
 DR EMBL; U52165; AAC50622.1; -;  
 DR EMBL; U52156; AAC50622.1; JOINED.  
 DR EMBL; U52157; AAC50622.1; JOINED.  
 DR EMBL; U52158; AAC50622.1; JOINED.  
 DR EMBL; U52159; AAC50622.1; JOINED.  
 DR EMBL; U52160; AAC50622.1; JOINED.  
 DR EMBL; U52161; AAC50622.1; JOINED.  
 DR EMBL; U52162; AAC50622.1; JOINED.  
 DR EMBL; U52163; AAC50622.1; JOINED.  
 DR EMBL; U52164; AAC50622.1; JOINED.  
 DR EMBL; M55994; AAA36755.1; -;  
 DR PIR; A35356; A35356.  
 DR PIR; A36007; A36007.  
 DR PIR; A36475; A36475.  
 DR PIR; B35010; B35010.  
 DR PIR; A23666; A23666.  
 DR POB; ICA9; 12-APR-99.  
 DR MIM; 191191; -;  
 DR InterPro; IPR001368; -;  
 DR Pfam; PF00020; TNFR\_C6; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS00505; TNFR\_NGFR\_2; 4.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;  
 KW Phosphorylation; Pharmaceutical; 3D-structure.  
 FT SIGNAL 1 22  
 FT CHAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.  
 FT DOMAIN 23 257 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 258 287 POTENTIAL.  
 FT DOMAIN 288 461 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 39 201 4 X TNFR-CYS.  
 FT REPEAT 39 76 TNFR-CYS 1.  
 FT REPEAT 77 118 TNFR-CYS 2.  
 FT REPEAT 119 162 TNFR-CYS 3.  
 FT REPEAT 163 201 TNFR-CYS 4.  
 FT DISULFID 40 53 BY SIMILARITY.  
 FT DISULFID 54 67 BY SIMILARITY.  
 FT DISULFID 57 75 BY SIMILARITY.  
 FT DISULFID 78 93 BY SIMILARITY.  
 FT DISULFID 96 110 BY SIMILARITY.  
 FT DISULFID 100 118 BY SIMILARITY.  
 FT DISULFID 120 126 BY SIMILARITY.  
 FT DISULFID 134 143 BY SIMILARITY.  
 FT DISULFID 137 161 BY SIMILARITY.  
 FT DISULFID 164 179 BY SIMILARITY.  
 FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 141 141 R -> P (IN REF. 4).  
 FT CONFLICT 196 196 R -> M (IN REF. 1 AND 3).  
 FT CONFLICT 363 363 A -> T (IN REF. 4).  
 SQ SEQUENCE 461 AA; 48316 MW; 603B580ECD67636F CRC64;

Query Match 25.68; Score 53; DB 1; Length 461;  
 Best Local Similarity 36.6%; Pred. No. 0.74;  
 Matches 15; Conservative 4; Mismatches 16; Indels 6; Gaps 2;

QY 2 CASGTFSG--GHEGHCQKPTDCTQFGELTVRPGNKNHNAV 40  
 ||||| 1:1 | :||| :|||  
 Db 164 CAPGTFSTSTSDICRPHQICN-----VVAIPGNASRQAV 200

RESULT 7  
 TNR2\_MOUSE

ID AC P25119; P97893; STANDARD; PRT; 474 AA.  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).  
 GN TNFRSF1B OR TNFR2 OR TNFR-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91187885; PubMed=1849278;  
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,  
 RA Wong G.H., Chen E.Y., Goeddel D.V.;  
 RT "Cloning and expression of cDNAs for two distinct murine tumor  
 RT necrosis factor receptors demonstrate one receptor is species  
 RT specific.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91246168; PubMed=1645445;  
 RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,  
 RA Copeland N.G., Jenkins N.A., Smith C.A.;  
 RT "Molecular cloning and expression of the type 1 and type 2 murine  
 RT receptors for tumor necrosis factor.";  
 RL Mol. Cell. Biol. 11:3020-3026(1991).  
 RN [3]  
 RP SEQUENCE OF 1-26 FROM N.A.  
 RC STRAIN=NOD;  
 RA Jacob C.O., Liu J.;  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RC TISSUE=Liver;  
 RA Kissingerghis M., Fellows R., Feldmann M., Chernajovsky Y.;  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -----  
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DR EMBL; M60469; AAA39752.1; -;  
 DR EMBL; M59378; AAA40463.1; -;  
 DR EMBL; U39488; AAA85021.1; -;  
 DR EMBL; X87128; AAA60618.1; -;  
 DR PIR; B38634; B38634.  
 DR HSP; P19438; INCF.  
 DR MGD; MGI:1314883; Tnfrsf1b.  
 DR InterPro; IPR001368; -;  
 DR Pfam; PF00020; TNFR\_C6; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS00505; TNFR\_NGFR\_2; 3.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.  
 FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 259 288 POTENTIAL.  
 FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 39 203 4 X TNFR-CYS.  
 FT REPEAT 39 77 TNFR-CYS 1.  
 FT REPEAT 78 119 TNFR-CYS 2.  
 FT REPEAT 120 164 TNFR-CYS 3.  
 FT REPEAT 165 203 TNFR-CYS 4.  
 FT DISULFID 40 54 BY SIMILARITY.

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FT DISULFID      55    68          BY SIMILARITY.
FT DISULFID      58    76          BY SIMILARITY.
FT DISULFID      79    94          BY SIMILARITY.
FT DISULFID      97   111         BY SIMILARITY.
FT DISULFID     101   119         BY SIMILARITY.
FT DISULFID     121   127         BY SIMILARITY.
FT DISULFID     136   145         BY SIMILARITY.
FT DISULFID     139   163         BY SIMILARITY.
FT DISULFID     166   181         BY SIMILARITY.
FT CARBOHYD      69    69         N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD     195   195         N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE      474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Query Match           24.8%; Score 61; DB 1; Length 474;
Best Local Similarity 36.6%; Pred.No. 1-4;
Matches 15; Conservative 5; Mismatches 15; Indels 6; Gaps 2;

QY 2 CASGTFSG--GHGECHKPWDTQTGFGLTVFPGNKTNHNAV 40
||| ||| | | : ||| : |||
Db 166 CAPGTFSDDTTSSTDCVRPHRCS----ILAIPGNASTDAVC 202

RESULT 8
NGFR_CHKCK STANDARD; PRT; 416 AA.
ID NGFR_CHKCK AC PL8519;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE (GP80-LINGFR) (P75 ICD).
GN NGFR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RX NCBI_OX
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=90166579; PubMed=2560385;
RA Large T.H., Weskamp G.; Helder J.C., Radeke M.J., Misko T.P.,
RA Shooter E.M., Reichardt L.F.;
RT "Structure and developmental expression of the nerve growth factor receptor in the chicken central nervous system.";
RL Neuron 2:1123-1134(1989).
[2]
SEQUENCE OF 21-416 FROM N.A.
RX MEDLINE=90152140; PubMed=2154393;
RA Heuer J.G., Fatemie-Nainie S., Wheeler E.F., Bothwell M.;
RT "Structure and developmental expression of the chicken NGF receptor.";
Dev. Biol. 137:287-304(1990).
CC -1 FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF, NT-3, AND NT-4.
CC CC
CC -1 SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE BOND FORMATION.
CC CC
CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC CC
CC -1 PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC CC
CC -1 SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC CC
CC -1 SIMILARITY: CONTAINS 1 DEATH DOMAIN.
DR PIR; JN0006; JN0006.
DR FIC; A60504; A60504.
DR HSSP; P07174; INGR.
DR InterPro; IPRO00488; -.
DR InterPro; IPRO01368; -.
DR Pfam; PF00020; TNFR_c6; 4.
DR Pfam; PF00531; death_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat; Phosphorylation; Signal.
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J. Immunol. 150:771-781(1993).
-|- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-LBBL. POSSIBLY
-|- ACTIVE DURING T CELL ACTIVATION.
-|- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.
-|- ASSOCIATES WITH P56-LCK.
-|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-|- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.
-|- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN
-|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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DR EMBL: J04492; AAA40167.1; -
DR EMBL: U02567; AAA93113.1; -
DR PIR: B32393; B32393.
DR HSP: P25942; ICDF.
DR MGD; MGI:1101059; Tnfrsf9.
DR InterPro: IP0001368; -.
DR Pfam: PF00020; TNFR_C6; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; FALSE_NEG.
KW Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
FT SIGNAL 1 24
FT CHAIN 25 256 4-LBB LIGAND RECEPTOR.
FT DOMAIN 25 187 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 188 208 POTENTIAL.
FT DOMAIN 209 236 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 17 159 4 X TNFR-CYS.
FT REPEAT 17 45 TNFR-CYS 1.
FT REPEAT 46 85 TNFR-CYS 2.
FT REPEAT 86 117 TNFR-CYS 3.
FT REPEAT 118 159 TNFR-CYS 4.
FT CARBOHYD 128 138 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 256 AA; 27598 MW; 93A10D03C60813C4 CRC64;

Query Match 28.7%; Score 70.5; DB 1; Length 256;
Best Local Similarity 35.0%; Pred. No. 0.049;
Matches 14; Conservative 8; Mismatches 17; Indels 1; Gaps 1;

QY 2 CASGTFSGGH-EGHCKPWTDTQFGFLTVPPGNKTHNAV 40
I: |||: : ||: |||: | : | : ||
Db 119 CSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVC 158

RESULT 6
TNFR2_HUMAN
ID TNFR2_HUMAN STANDARD; PRT; 461 AA.
AC P20333;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR
DE BINDING PROTEIN 2) (TFPII) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).
GN TNFRSF1B OR TNFR2 OR TNFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RX MEDLINE-90260639; PubMed-2160731;
RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA Dower S.K., Cosman D., Goodwin R.G.;
RT "A receptor for tumor necrosis factor defines an unusual family of
cellular and viral proteins."

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RL Science 248:1019-1023(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-91045991; PubMed-2172983;
RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
RT "A second tumor necrosis factor receptor gene product can shed a
naturally occurring tumor necrosis factor inhibitor."
RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-96299745; PubMed-8661109;
RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
RA Brodeur G.M.;
RT "Physical mapping and genomic structure of the human TNFR2 gene."
RL Genomics 35:94-100(1996).
RN [4]
RP SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE-90349572; PubMed-2166946;
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
RA Ringold G.M.;
RT "Complementary DNA cloning of a receptor for tumor necrosis factor
and demonstration of a shed form of the receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
RN [5]
RP SEQUENCE OF 27-31.
RX MEDLINE-90110215; PubMed-2153136;
RA Engelmann H., Novick D., Wallach D.;
RT "Two tumor necrosis factor-binding proteins purified from human
urine. Evidence for immunological cross-reactivity with cell surface
tumor necrosis factor receptors."
RL J. Biol. Chem. 265:1531-1536(1990).
RN [6]
RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
RX MEDLINE-91056048; PubMed-2173696;
RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
RA Brockhaus M.;
RT "Purification and partial amino acid sequence analysis of two
distinct tumor necrosis factor receptors from HL60 cells."
RL J. Biol. Chem. 265:20131-20138(1990).
RN [7]
RP CHARACTERIZATION.
RX MEDLINE-93016040; PubMed-1328224;
RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
RA Lipari M.T., Goeddel D.V.;
RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
Characterization of ligand binding, internalization, and receptor
phosphorylation."
RL J. Biol. Chem. 267:21172-21178(1992).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.
RX MEDLINE-99221490; PubMed-10206649;
RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
RT "Structural basis for self-association and receptor recognition of
human TRAF2."
RL Nature 398:533-538(1999).
CC -|- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-ALPHA AND
APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -|- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
LEVEL ON THREONINE RESIDUES.
CC -|- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND
WYETH-AVERST). USED TO TREAT MODERATE TO SEVERE RHEUMATOID
ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING
PORTION OF TNFR2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO
TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.
CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -|- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".
CC -|- DATABASE: NAME=Enbrel; NOTE=clinical information on Enbrel;
WWW="http://www.enbrelinfo.com/".
-----

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CC CELLS.

CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

CC -1- DATABASE: NAME=PROV; NOTE=CD guide CDW137 entry;

CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw137.htm".

CC -----

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CC -----

CC EMBL; U03397; AAA53133.1; -

CC EMBL; L12964; AAA62478.2; -

CC HSSP; P19438; 1EXT.

CC MIM; 602250; -

CC InterPro; IPR001368; -

CC Pfam; PF00020; TNFR\_C6; 2.

CC PROSITE; PS00652; TNFR\_NGFR\_1; 1.

CC PROSITE; PS00050; TNFR\_NGFR\_2; 1.

CC Receptor; Glycoprotein; Repeat; Signal; Transmembrane.

CC SIGNAL 1 17 POTENTIAL.

CC CHAIN 18 255 4-1BB LIGAND RECEPTOR.

CC DOMAIN 18 186 EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 187 213 POTENTIAL.

CC DOMAIN 214 255 CYTOPLASMIC (POTENTIAL).

CC DOMAIN 47 159 3 X TNFR-CYS.

CC REPEAT 47 86 TNFR-CYS 1.

CC REPEAT 87 118 TNFR-CYS 2.

CC REPEAT 119 159 TNFR-CYS 3.

CC CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC SEQUENCE 255 AA; 27899 MW; F3A563F5E5F00460 CRC64;

Query Match 37.8%; Score 93; DB 1; Length 255;

Best Local Similarity 40.0%; Pred. No. 7e-05;

Matches 16; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 1 DCASGTFSGGHEGCKPWTCTQFGFLTVFPGNKTHNAV 40

Db 119 DCCGFTNDQKRGICRPWTNGLDGSVLVNGTKERDVVC 158

RESULT 4

OX40\_RAT

ID OX40\_RAT STANDARD; PRT; 271 AA.

AC P15725;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).

GN TNFRSF4 OR TNGPIL OR OX40.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=T-cell;

RC MEDLINE=90214614; PubMed=2157591;

RA Mallett S., Fossum S., Barclay A.N.;

RT "Characterization of the MRC OX40 antigen of activated CD4 positive T

RT lymphocytes -- a molecule related to nerve growth factor receptor.";

RL EMBO J. 9:1063-1068(1990).

CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.

CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

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CC -----

CC EMBL; X17037; CAA34897.1; -

CC PIR; S08036; S08036.

CC PIR; S12783; S12783.

CC HSSP; P25942; 1CDF.

CC InterPro; IPR001368; -

CC Pfam; PF00020; TNFR\_C6; 3.

CC PROSITE; PS00652; TNFR\_NGFR\_1; 3.

CC PROSITE; PS00050; TNFR\_NGFR\_2; 2.

CC Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;

CC SIGNAL 1 19 POTENTIAL.

CC CHAIN 20 271 OX40L RECEPTOR.

CC DOMAIN 20 210 EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 211 235 POTENTIAL.

CC DOMAIN 236 271 CYTOPLASMIC (POTENTIAL).

CC DOMAIN 25 164 4 X TNFR-CYS.

CC REPEAT 25 60 TNFR-CYS 1.

CC REPEAT 61 102 TNFR-CYS 2.

CC REPEAT 103 123 TNFR-CYS 3 (INCOMPLETE).

CC REPEAT 124 164 TNFR-CYS 4.

CC CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC SEQUENCE 271 AA; 29895 MW; C06465136B16821 CRC64;

Query Match 34.1%; Score 84; DB 1; Length 271;

Best Local Similarity 41.0%; Pred. No. 0.001;

Matches 16; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 2 CASGTFSGGHEGCKPWTCTQFGFLTVFPGNKTHNAV 40

Db 125 CPPGHFSPGSGNQACKPWTNCTLSGKQIRHPASNSLDTVC 163

RESULT 5

41BB\_MOUSE

ID 41BB\_MOUSE STANDARD; PRT; 256 AA.

AC P20334;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE 4-1BB LIGAND RECEPTOR PRECURSOR (T-CELL ANTIGEN 4-1BB).

GN TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=89184547; PubMed=2784565;

RT "cDNA sequences of two inducible T-cell genes.";

RL Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/C.

RC MEDLINE=94179805; PubMed=8133039;

RA Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;

RT "Genomic organization and chromosomal localization of the T-cell

RT antigen 4-1BB.";

RL J. Immunol. 152:2256-2262(1994).

CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.

CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

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OM protein - protein search, using sw model

Run on: September 4, 2001, 16:15:26 ; Search time 43.78 Seconds  
(without alignments)  
32.080 Million cell updates/sec.

Title: US-09-512-363-2\_COPY\_114\_154

Perfect score: 246

Sequence: 1 DCASGTFSGHGHCKPWTD.....TOGFLTFVPGNKTHNAVCV 41

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	96	39.0	277	1	OX40_HUMAN
2	95	38.6	272	1	OX40_MOUSE
3	93	37.8	255	1	41BB_HUMAN
4	84	34.1	271	1	OX40_RAT
5	70.5	28.7	256	1	41BB_MOUSE
6	63	25.6	461	1	TNR2_HUMAN
7	61	24.8	474	1	TNR2_MOUSE
8	60.5	24.6	416	1	NGFR_CHICK
9	56	22.8	880	1	ZAP1_YEAST
10	54.5	22.2	231	1	NRG1_YEAST
11	54.5	22.2	350	1	ACCO_PSEPH
12	54.5	22.2	425	1	NGFR_RAT
13	54	22.0	435	1	TNR2_HUMAN
14	53.5	21.7	152	1	IXA_TRIFL
15	53	21.5	289	1	CD40_MOUSE
16	53	21.5	1786	1	LMB1_MOUSE
17	52	21.1	415	1	TNR2_MOUSE
18	52	21.1	1786	1	LMB2_HUMAN
19	51.5	20.9	577	1	CCBS_OENBE
20	51.5	20.9	579	1	CCBS_DAUCA
21	51.5	20.9	1050	1	ITA5_XENLA
22	51	20.7	84	1	MT22_ORYSA
23	51	20.7	997	1	AT5F_HUMAN
24	50.5	20.5	327	1	GBLP_ARATH
25	50.5	20.5	327	1	GBLP_BRANA
26	50	20.3	269	1	CD40_BOVIN
27	50	20.3	269	1	CD40_HUMAN
28	50	20.3	1790	1	LMB1_DROME
29	49.5	20.1	146	1	IXB_TRIFL
30	49.5	20.1	317	1	GBLP_BAREE
31	49.5	20.1	324	1	GBLP_CAEEL
32	49.5	20.1	439	1	CK13_SCHPO
33	49.5	20.1	490	1	CPC2_RABIT

34 49.5 20.1 1168 1 LMB3\_MOUSE  
35 49 19.9 216 1 YODA\_ECOLI  
36 49 19.9 582 1 ATKA\_HALNI  
37 48.5 19.7 248 1 KLKC\_HUMAN  
38 48.5 19.7 529 1 YUOL\_CAEEL  
39 48.5 19.7 535 1 TYRL\_CHICK  
40 48.5 19.7 987 1 EPB4\_HUMAN  
41 48.5 19.7 1064 1 YY08\_METJA  
42 48 19.5 1074 1 SM5A\_HUMAN  
43 48 19.5 4655 1 LRP2\_HUMAN  
44 47.5 19.3 207 1 CYOC\_PSEPU  
45 47.5 19.3 761 1 SM3D\_CHICK

Q61087 mus musculus  
P76344 escherichia  
P57684 halobacteri  
Q9UKR0 homo sapien  
P30638 caenorhabdi  
O57A05 gallus gall  
P54760 homo sapien  
Q60307 methanococc  
Q13591 homo sapien  
P98164 homo sapien  
Q94WR3 pseudomonas  
Q90663 gallus gall

#### ALIGNMENTS

RESULT 1  
OX40\_HUMAN  
ID OX40\_HUMAN STANDARD; PRT: 277 AA.  
AC P43489; Q13663;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DE OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY  
DE ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).  
GN TNFRSF4 OR TNXP1L.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=94170844; PubMed=7510240;  
RA Latza U., Duerkop H., Schmittger S., Ringeling J., Eitelbach F.,  
Hummel M., Fonatsch C., Stein H.;  
RT "The human OX40 homolog: cDNA structure, expression and chromosomal  
assignment of the ACT35 antigen";  
RL Eur. J. Immunol. 24:677-683(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95219871; PubMed=7704935;  
RA Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A.,  
Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.;  
RT "Identification of OX40 ligand and preliminary characterization of  
its activities on OX40 receptor";  
RL Circ. Shock 44:30-34(1994).  
CC -!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD134 entry;  
WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd134.htm".  
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EMBL: X75962; CAA53576.1; -  
EMBL: S76792; AAB33944.1; ALT\_INIT.  
HSSP: P25942; ICDF.  
MIM: 600315; -  
InterPro: IPR001368; -  
Pfam: PF00020; TNFR\_C6; 3.  
PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
Signal.  
FT SIGNAL 1 28 POTENTIAL.  
FT CHAIN 29 277 OX40L RECEPTOR.

141	SEQUENCE FROM N.A.
RP	RP
RC	TISSUE=Blood;
RX	MEDLINE=95347766; PubMed=7622190;
RA	Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,
RA	Kwon B.S.;
RT	"Characterization of human homologue of 4-1BB and its ligand.";
RL	Immunol. Lett. 45:67-73(1995).
-!	FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIB
CC	ACTIVE DURING T CELL ACTIVATION.
CC	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC	-!- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T



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4. Handel, M.L. et al. Clinical and Experimental Pharmacology and Physiology (2000) 27(3): 139-144
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